

1001

```

501 GGTcaaggcc aTTGCCGaaC agcgcgcGCgt accgaTGcgcg actTTCTTcc
551 ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CAtcgTACAT
601 ACCCTcgtCT TTTTcgTTtt CAAACTACTg taa

```

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

```

g627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
201 TLVFFVFKLL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

```

m627.seq
  1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
 51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCAATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CTTTGATGAC GGGTACCCTG TTTTATTTCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

```

m627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
g627	MSGLWKPEHPGFEILGSRYALQNLVRDVILITLTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINTMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
g627	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1  ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCACATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTTT TTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCTTG TTTCAATCGC TGCTGGCGGT TTCTATGGGT
451 TCGGTATCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCTCTG CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627.pep
1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FVLVSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

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a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX
 190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq
 1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
 51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC
 101 ACACATGGAT TTTACGTTCG GTCAGGCGGC TCAATACCAA CAGGCCGCGT
 151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
 251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
 301 GATTGAATCA GGTGCGGCG CACTTTTTCG CTGCTCAATT TTGCCAGCGC
 351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep
 1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRRLLNTNRPR
 51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
 101 D*IRLRRTFS LLNFASASGT *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq
 1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT
 51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCCTTAC
 101 AAACATGGAT TTGCGTTCG GTCAAACGGC TCAATACCAA CAGGCCGCGT
 151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
 251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG
 301 GATTGGATCA GGTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAGCGC
 351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep
 1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQWILRS VKRLNTNRPR
 51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
 101 DWIRLRRTSS PLKFASASGA *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m628/g628 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQTWILRSVKRLNTNRPR	LKSSAASLIM			
g628	MCVPLKPAGCGPPNSCVSILAAFS	DGTSAPAAALHTWILRSVRRLLNTNRPR	LKSSAASLMM			
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFASASGA				
g628	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFASASGT				
	70	80	90	100	110	120
m628.pep	X					
g628	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

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a628.seq
 1 ATGTGCGTGC CACTCAAACC GGCCGGATGC GGGCCGCCGA ATTCATGTGT
 51 TTTCGATGTG GCAGCATTTC CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
 101 ACACATGGAT TTTACGCTCG GTCAAACGGC TCAATACCAG CAAACCTCGT
 151 CTGAAATCCT CGGCGGCTTC TTTGATCACA ACCACAGGGT CTGCCGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
 251 CGGCAGGGAT TTTGCTGAAC GGACGGGTAC GCAGCGCAGT CCACAAACCG
 301 GATTGGATCA GATTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAACGC
 351 TTCGGGCGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

a628.pep
 1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALHTWILRS VKRLNTSKPR
 51 LKSSAASLIT TTGSAASGLV SIALTKMANG SASTAGILLN GRVRSVAVHKP
 101 DWIRLRRRTSS PLKFANASGA *

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQ	TWILRSVKRLNTNR	PKSSAASLIM		
a628	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALHTWILRSVKRLNTSKPRLKSSAASLIT				
	10	20	30	40	50	60
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVAVHKPDWIRLRRRTSS	PLKFASASGA			
a628	TTGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVAVHKPDWIRLRRRTSS	PLKFANASGA			
	70	80	90	100	110	120

m628.pep X
 |
 a628 X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

g629.seq
 1 ATGACTGCca aacCTTTTTT CCTCAACCTG GCcaaCCTCC TGCTGCCggc
 51 ggtatTGTTT GCCGTCAGcc tGtcggTCGG cattgccgaT TTCCGCTGGT
 101 CGGATGTGTT TCGCTGTCC GACAGCCAGC AAGTGATGTT CATCAGCCGC
 151 CTGCCGCGCA CGTTTGcgaT TGTGTTGACG GGCgcgtcga tagcgGtggc
 201 gGGGAtgatt atgcagATTC TGATGCGCAA CcgtTTTGTC GAGCCTtcta
 251 tggcgGGTGC GGGCCAAAGt gcgGCTTTGG GTttgcttct gAtgtccctg
 301 ctgctgcctg CcgCgccgct gccggTcaAA ATGTCGGtag CcgccgttgC
 351 CGCGCTGATC GGGATGTTGG tctTtatgct gctaataccgC Cgcctgccac
 401 cgacggcgca gctgatgGTg ccgCTGGTGG Gg.ttATTTT CGGCGGCGTG
 451 GttgaGGCGG TGGCAGCGTT TGTCGCGTAT GAGTTTGAGA TGCTGCAAAT
 501 GTTGGGCGTG TGGCAGCAGG GCGACTTTTC AAGCGTGCTG CTGGGGCGGT
 551 ACGAGCTGCT TTGGATTACG GGCGGTTTGG CGGTGTTTGC CTACCTGATT
 601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAGACGGTGA GCGTGAATTT
 651 GGGTTTGAAC CGGACGGCGG TGTGTGGTC GGGTTTGATT ATTGTGGCAC
 701 TGATTACATC GCTGGTCATT GTAACGGTCG GCAATATTCC GTTTATCGGG
 751 CTGGTCGTGC CGAATATCGT CAGCCGCCTG ATGGGCGACA GGCTGCGCCA
 801 AAGCCTGCCT GCGGTCGCCC TCTTGGGCGC GTCTTTGGTT TTATTGTGCG
 851 ACATTATCGG ACGCATGATT GTGTTTCCGT TTGAAATTCC GGTCTCCACG
 901 GTTTTTGGTG TGTTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
 951 ACCCGCCTAT GCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

g629.pep
 1 MTAKPFSLNL ANLLPAVL AVSLSVGIAD FRWSDVFSLS DSQQVMFISR
 51 LPRTFAIVLT GASIAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLLMSL
 101 LLPAAPLPVK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGXIFGGV

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151 VEAVATFVAY EFEMLQMLGV WQQGDFSSVL LGRYELLWIT GGLAVFAYLI
201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
251 LVVPNIVSRL MGDRLRQSLP AVALLGASLV LLCDIIGRMI VFPFEIPVST
301 VFGVLGTALF LWLLLLRKPAY AV*

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2023>:

```
m629.seq
1   ATGACTGCCA AACCTTTTTT CCTCAACCTG ACCAACCTGC TGCTGCTGGC
51  GGTGTTGTTT GCCGTCAGCC TGTGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CTGATGTGTT TCTACTGTCC GACAGCCAGC AGGTCATGTT CATCAGCCGC
151 CTGCCGCGCA CTTTTCGATG TGTGCTGACG GCGCGCTCGA TGGCGGTGGC
201 CGGCATGATT ATGCAGATTT TGATGCGCAA CCGTTTTGTG GAACCGTCGA
251 TGGTGGGCGC AAGCCAAAGC GCGGCTTTAG GTTTGCTGCT GATGACCCTG
301 CTGCTGCCGG CCGCGCCGCT GCCGGCGAAA ATGTCGGTTG CCGCCGTTGC
351 CGCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC
401 CGACCGCGCA ACTGATGGTG CTTTGGTTCG GGATTATTTT CGGCGGTGTG
451 ATTGAGCGGG TAGCCACCTT TATCGCGTAT GAAAACGAAA TGCTGCAAA
501 GCTCGGCGTG TGGCAGCAGG GCGATTTTTT GAGCGTGCTG CTGGGGCGGT
551 ACGAGCTGCT TTGGATTACG GCGGTTTGG CGGTGTTTGC CTATCTGATT
601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAAACGGTAA GCGTGAATTT
651 GGGTTTGAAC CGGACGGCGG TGTTGTGGTC GGGTTTGATT ATTTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCG GTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCCCTG ATGGGCGACA GTTTGCGCCA
801 AAGCCTGCTT GCGGTGGCCT TGCTGGGCGC ATCTTTGGTG TTGCTGTGCG
851 ACATTATCGG ACGCGTGATT GTGTTTCCGT TTGAAATTC GGTCTCTACG
901 GTTTTGGTG TATTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
951 ACCCGCTAT GCGCTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

m629.pep	1	<u>MTAKPFSLNL</u>	<u>TNLLLLAVLF</u>	<u>AVSLSVGVAD</u>	<u>FRWSDVFSLS</u>	<u>DSQQVMFISR</u>
	51	<u>LPRTFAIVLT</u>	<u>GSMVAAGMI</u>	<u>GQILMRNRF</u>	<u>EPSMVGASQS</u>	<u>AALGLLLMTL</u>
	101	<u>LLPAAPLPAK</u>	<u>GASMAAVALI</u>	<u>GMVLFMLLIR</u>	<u>RLPPTAQLMW</u>	<u>PLVGIIFFGV</u>
	151	<u>IEAVATFIAIY</u>	<u>ENEMLQMLGV</u>	<u>WQQGDFSSVL</u>	<u>LGRYELLWIT</u>	<u>GLGAVFAYLI</u>
	201	<u>ADRLTILGLG</u>	<u>ETVSVNLGSL</u>	<u>RTAVLWSGLI</u>	<u>IVALITSLVI</u>	<u>VTVGNIPIFI</u>
	251	<u>LVVPNIISRL</u>	<u>MGDRLRQSLP</u>	<u>AVALLGASLV</u>	<u>LLCDIIGRVI</u>	<u>VFPFEIPVST</u>
	301	<u>VFGVLGTALF</u>	<u>WLMLLRKPAY</u>	<u>AV*</u>		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m629/g629 95.7% identity in 322 aa overlap

	10	20	30	40	50	60
m629.pep	MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
	: : : : : : : : : :					
g629	MTAKPFSLNLANLLLPVAVLFAVSLSVGIADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m629.pep	GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMTLLLPAAPLPAKMSVAAVAALI					
	: : : : : : : : : :					
g629	GASIAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLMSLLLPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIFGGVIEAVATFIAZENEMQLMGVWQQGDFSSVL					
	: : : : : : : : :					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEFEMQLMGVWQQGDFSSVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
	: : : : : : : : :					

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g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g629      VTVGNIPFIGLVVPNIVSRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```
a629.seq
  1  ATGACTGCCA AACCTTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
 51  GGTGTTGTTT GCCGTCAGCC TGTGCGGTGGG CGTTGCCGAT TTCCGCTGGT
101  CGGATGTGTT TTCGCTGTCTG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151  CTGCCGCGCA CGTTTGCGAT TGTGTTGACG GGC GCGTCGA TGGCGGTGGC
201  GGGGATGATT ATGCAGATTC TGATGCGTAA CCGTTTGTCT GAGCCTTCTA
251  TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTTGCTTCT GATGTCCTTG
301  CTGCTGCCTG CCGCGCCGCT GCCGGTCAA ATGTCGGTTG CCGCCGTTGC
351  CGCGTTAATC GGGATGTTGG TGTATTATGAT GCTTATCCGC CGCCTGCCGC
401  CGACGGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGCGTG
451  GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAA
501  GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTG CTCGGACGGT
551  ATGAACTGTT GTGGGCAACG GGGATTTTGG CTTTGTGTTG CTATTTGATT
601  GCCGACCAGC TGACGATTTT GGGTTTGGG GAAACGGTAA GCGTGAAC
651  GGGGCTGAAC CGGACGGCGA TTCTGTGGTC GGGGCTGATT ATTGTGGCTT
701  TGATTACGTC GCTGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751  CTGGTCGTGC CGAACATCAT CAGCCGCTG ATAGGCGACA GGCTGCGCCA
801  AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851  ACATTATCGG ACGAGTGATT GTGTTTCCGT TTGAAATTCC GGTATCGACC
901  GTCTTCGGCG TATTGGGTAC GCGGTTGTTT TTATGGCTTT TGTAAAGGAA
951  ACCTGCTCAT GCCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```
a629.pep
  1  MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
 51  LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLMLSL
101  LLPAAPLPVK MSVAAVAALI GMLVFMMILIR RLPPTAQLMV PLVGIIFGGV
151  VEAVATFIAY ENEMLQMLGV WQGDGDFSVL LGRYELLWAT GILALFAYLI
201  ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251  LVVPNIISRL IGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST
301  VFGVLGTALF LWLLLRKPAH AV*
```

m629/a629 95.7% identity in 322 aa overlap

```
           10      20      30      40      50      60
m629.pep  MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a629      MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           10      20      30      40      50      60

           70      80      90      100     110     120
m629.pep  GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMLTLLPAAPLPKMSVAAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a629      GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMLSLLLPAAPLPVKMSVAAVAALI
           70      80      90      100     110     120

           130     140     150     160     170     180
m629.pep  GMLVFMLLIRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMLQMLGVWQGDGDFSSVL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

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a 629      GMLVFMMLIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
              130      140      150      160      170      180

              190      200      210      220      230      240
m629.pep   LGRYELLWITGGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
              ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||
a 629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
              190      200      210      220      230      240

              250      260      270      280      290      300
m629.pep   VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a 629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
              250      260      270      280      290      300

              310      320
m629.pep   VFGVLGTALFLWLLLRKPAYAVX
              |||||:|||||
a 629      VFGVLGTALFLWLLLRKPAHAVX
              310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATTT TGGTGTGGCT ggctttgttt ccccccattgt tttacggcat
51  gtacaacgtc GGCGCACAGG CATTCGGTGC CTTAACGCCC GAtttgctgc
101 aacaaagcat cggccacgac ggcaattacg ccctcgccaa cgctttgggc
151 atcaatatgt cccccgaaGc gggcgtgtTg ggcaaatgc tgttcgGCGC
201 GATttacttc ctgccgattt acgcgaccgt aTTTATTGTG GGcggcttct
251 ggGaagtCTT GTTCGCATCc gtACGCAAAC ACGAAATCAA CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGC
451 GCCTTCCTGT TCTTCGCCTA CCCCGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG
701 CTtcttgGCG CATTATTGCC ggCGTGATGA TCGGTatGat tGcgatgTCT
751 tcgctgatta acttcatCGg ttctgacacc aaagctatgt ttgctatgca
801 cttggatcat ggcacttggT GGAaagatGa ttAtcactca ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF PPMFYGMYNV GAQAFGALTP DLLQQSIAHD GNYALANALG
51  INMSPEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLVAS VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLEFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVTGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFFVF ARIASWRIIA GVMIGMIAMS
251 SLINFIGSDT KAMFAMHLVH GTWWKDDYHS LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GTACAACGTC GGCGCGCAGG CATTCGGTGC GTTAACGCCCT GATTTGCTGC
101 AACAAAACAT CGCCAACGAC TGGCATTACG CCTTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTGC GACAAAATGC TGTTTGGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACTGT ATTTGTTGTG GGCGGTTTCT
251 GGGAAAGTTT GTTCGCCACC GTGCGCAAAC ACGAAATCAA CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCTTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCACTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCC GGCTCCATTG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG
701 CTTCTTGCGG CATTATTGCC GGCCTGATGA TCGGTATGAT TCGCATGTCT
751 TCGCTGTTCa ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC

```

1008

```

801 TTGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTGTT CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

m630.pep

```

1 MMILVWLALF PAMFYGMYNV GAQAFGALT PLDQQNIAND WHYAFANALG
51 INMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVGTQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLENFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIDYF VAQANIKRRK
351 ARSNG*

```

m630/g630 93.5% identity in 275 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALF	PAMFYGMYNV	GAQAFGALT	PLDQQNIAND	WHYAFANALG	INMSSEAGVS
g630	MMILVWLALF	PMPFYGMYNV	GAQAFGALT	PDLLQQSI	AHDGNYALAN	ALGINMSPEAGVL
	10	20	30	40	50	60
	70	80	90	100	110	120
m630.pep	DKMLFGAIYF	LPIYATVFVV	GGFWEVLFAT	VRKHEINEGF	FVTSILFALI	VPPTLPLWQA
g630	GKMLFGAIYF	LPIYATVFIV	GGFWEVLFAS	VRKHEINEGF	FVTSILFALI	VPPTLPLWQA
	70	80	90	100	110	120
	130	140	150	160	170	180
m630.pep	ALGISFGVVV	AKEVFGGTG	KNFMNPALA	GRAFLFFAY	PANLSGDAV	WTAVDGYSG
g630	ALGISFGVVV	AKEVFGGTG	KNFMNPALA	GRAFLFFAY	PANLSGDAV	WTAVDGYSG
	130	140	150	160	170	180
	190	200	210	220	230	240
m630.pep	QWAAHGADGL	KNAVGTQTIT	WMDAFIGKLP	GSIGEVSTLA	LLIGGAFIVF	ARIASWRIIA
g630	QWAAHGADGL	KNAVGTQTIT	WMDAFIGKLP	GSIGEVSTLA	LLIGGAFIVF	ARIASWRIIA
	190	200	210	220	230	240
	250	260	270	280	290	300
m630.pep	GVMIGMIAMSS	LNFFIGSDTN	AMFAMPWYW	HLVVGGFAI	GMLFMATDP	VASFTNVGK
g630	GVMIGMIAMSS	LNFFIGSDTK	AMFAM----	HLVHGTWWK	DDYHSLYIK	.
	250	260	270	280		
	310	320	330	340	350	
m630.pep	YGALIGVMCV	LIRVVNPAYP	EGMMLAILF	ANLFAPIDY	FVAQANIKR	RRKARSNGX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

a630.seq

```

1 ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51 GTACAACGTC GCGCACAGG CATTCCGGTG GTTAACGCCC GATTTGCTGC
101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GGCAAATGC TGTTCGGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GGCGGTTTCT
251 GGGAAGTTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC
301 TTTGTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAG AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAACGCCA TAACCGGTCA AACCATCACT
601 TGGATGGATG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGGCTT TATCGTGTTC GCCCGCATCG

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1009

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701 CTTCTTGGCG CATTATTGCC GGC GTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGGGTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCC GTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGCGCAT TCTGTTTGCC AACCTGTTG
1001 CCCC GATTTT C GACTATTTT GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

a 630.pep

```

1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQOSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMN PALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIAN	WHYAFANALGINMSSEAGVS				
a 630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQOSIAND	WHYALANALGINMSSEAGVL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m630.pep	DKMLFGAIYFLPIYATVFVVG	GFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA				
a 630	GKMLFGAIYFLPIYATVFIVG	GFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA				
	70	80	90	100	110	120
	130	140	150	160	170	180
m630.pep	ALGISFGVVVAKEVFGGTGKNFMN	PALAGRAFLFFAYPANLSGDAVWTA	VDGYSGATALA			
a 630	ALGISFGVVVAKEVFGGTGKNFMN	PALAGRAFLFFAYPANLSGDAVWTA	VDGYSGATALA			
	130	140	150	160	170	180
	190	200	210	220	230	240
m630.pep	QWAAHGADGLKNAVTGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
a 630	QWAAHGADGLKNAITGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
	190	200	210	220	230	240
	250	260	270	280	290	300
m630.pep	GVMIGMIAMSSLFNFIGSDTNAMFAMPWY	HLVVGGFAIGMLFMATDPVSASFTNVGKWW				
a 630	GVMIGMIAMSSLFNFIGSDTNAMFAMPWY	HLVVGGFAIGMLFMATDPVSASFTNVGKWW				
	250	260	270	280	290	300
	310	320	330	340	350	
m630.pep	YGALIGVMCVLIRVVNPAYPEGMMLAILFANL	FAPIFDYFVAQANIKRRKARSNGX				
a 630	YGALIGVMCVLIRVVNPAYPEGMMLAILFANL	FAPIFDYFVAQANIKRRKARSNGX				
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

g635.seq

```

1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTTCAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTGCGAAA GACAGGGCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTC CTTACCCAGT TTTTCCAACA CTTCTTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGGA

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1010

301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC
 351 TCTGCAATTT GATTTTCCG TAAACAACAG GATTATCGTT AAACATCGGT
 401 GCAGCATTCA AACGATAAGA CAAGGGTCTG TACCAGATTA G

This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:

g635.pep

1 MTRRRVGKQN RIAIHSAYR KMVVFVFIQI HDDGDFQLRE LFERQGIAGR
 51 LKTQIGHNAP HILKRRALHF LTQFFQHFF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IPRFPTLQF DFSVNNRIIV KHRCISQITIR QGSVPD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2035>:

m635.seq

1 ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTTCAGATA CACGATGACG
 101 GGGATTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC
 151 TTCAAACCC AAATCAGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
 201 GCATCTGCTC CTTATCCAGT TTTTAAACA CGTCTCTTC CGTCAGCTTT
 251 TGCCCGTAA AATTGTTCAA AAGCGTCAC ACCGAAGCCG CCCCAGGGA
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:

m635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFIQI HDDGDLQLCK LLERQGIAGR
 51 FKTIQIRHNP HILKRRGHLL LIQFF*HVLV RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/g635 80.0% identity in 130 aa overlap

	10	20	30	40	50	60
m635.pep	MTQRRVGKQNRIAVYTAQYREMIILAVFIQHDDGDLQLCKLLERQGIAGRFRKTQIRHNP					
	10	20	30	40	50	60
g635	MTRRRVGKQNRIAIHSAYRKMVVFVFIQHDDGDFQLRELFERQGIAGRFRKTQIGHNAP					
	70	80	90	100	110	120
m635.pep	HILKRRGHLLLIQFFXHVLFRLLPVKIVQKRRHRSRPAGKIQILLYNIEIAPFFPTLHF					
	70	80	90	100	110	120
g635	HILKRRALHFLTQFFQHFFRQLLPVKIVQKRRHRSRPAGKIQILLYNIEIPRFPTLQF					
	130					
m635.pep	DFSISNRIIVDX					
	130					
g635	DFSVNNRIIVKHRCISQITIRQGSVPDX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2037>:

a635.seq

1 ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTTCAGATA CACGATGACG
 101 GGGATTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC
 151 CTCAAACCC AAATCAGGCA TGATGCGCCG CATATCCTCA AACGACGCGC
 201 GCATCTGCTC CTTATCCAGC TTTTCAACA CGTCTCTTC CGTCAGCTTT
 251 TGCCCGTGAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGGA
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2038; ORF 635.a>:

a635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFIQI HDDGDLQLCK LLERQGIAGR
 51 LKTQIRHDAP HILKRRALHL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/a635 95.4% identity in 131 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

1011

```

m635.pep    MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHNAP
             |||||
a635        MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHDAP
             10      20      30      40      50      60

             70      80      90      100     110     120
m635.pep    HILKRRGHLLLIQFFXHVLFRLQLLPVKIVQKRHRSRPAGKI QILLYNI EIAFFPTLHF
             |||||
a635        HILKRRGHLLLIQLFQHVLFRLQLLPVKIVQKRHRSRPAGKI QILLYNI EIAFFPTLHF
             70      80      90      100     110     120

             130
m635.pep    DFSISNRIIVDX
             |||||
a635        DFSISNRIIVDX
             130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc atTGTAGGCA AAAACGCACT
51  TGCCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTTGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 AAATATTGCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCGccggg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTACAG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACC ATCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGCGCGC TGTACGGCTA TGGTACGCCC GCTCTGTGTC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GGCGCGGGCA AAAATTTCGG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 CGGCTGCCCA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCAGC
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCCGTAT GGCCGAACAA AATAAAGCAT CATTCAAATG TGCCTGTTTT
951 TATAGCGAAA CCGCTGAAA CCGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGKNALARF VDNIVVNIGI VDIVEHDA LI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAE A VVFIGVVRAG
101 IGNNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYAERI IKNIVVFNQG ARGGFFEINT GIHCWQAHTG TGNGQVAERY
201 VRRVYGYGTP ALVPFDGCGT VGRPFNRNRF VDIKFLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFI AK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCCTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTTGAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 TTTGAGCCCG TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCG
201 AAATATTGCC GCTGATTTTC CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAAT CGCTGAAGCG GTTGTTTTTC TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCGGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCGCGCACC ATCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTTCTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGCGCGC TGTACGGCTA TGGTACGCCC GCTCTGTGTC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CTTCAATCG TAATCGGTTT GTCAATGTGA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

1012

This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

m638.pep

```

1  MIGEKFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFGVVRAG
101 IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
151 RTMQIYADRI IQNIVFVNOG ARGSSFEINT GIHCGQAHTG TNGQVAERY
201 VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
251 GAGKCGIPIS IIGS*

```

m638/g638 88.2% identity in 254 aa overlap

m638.pep	10	20	30	40	50	60
	MIGEKFIVVGIIIGKYALACLVDNVVVNIGIVDIVEHNALIAAADGDIVEYFEPLGKHQHI					
g638	MIGGQFIVVGIVGKNALARFVDNVVVNIGIVDIVEHDALIAAADGDIVEHFEPFGKHQHI					
m638.pep	70	80	90	100	110	120
	AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFGVVRAGIGKNAVPPFGNVVADDLRTG					
g638	AHIVAHGNIAADFAVVGVIHVDGETQVAEAVVFIGVVRAGIGKNAVPPFGNVVADDLRTG					
m638.pep	130	140	150	160	170	180
	CVPNGNAVAAALVHAQSRVADDFILAHHRIGRTMQIYADRI IQNIVFVNOGARGSSFEINT					
g638	RVPNGNAIAALHAQGRVADDFILAHHRIGRTMKVYAEIRIKNIVFVNOGARGGFEINT					
m638.pep	190	200	210	220	230	240
	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCCTVGRPFNRNRFVNVKFGFIYA					
g638	GIHCWQAHTGTGNGQVAERYVRRVYGYGTPALVPFDGCGTVGRPFNRNRFVDIKFGLIYA					
m638.pep	250	260				
	GSQFERIARPGAGKCGIPISIIGSX					
g638	GSQFDRIARPGAGKNFGKVVLRGNVDDGCRCLKNAAGGKYQHGLQPYTERGCVHSVPLF					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

a638.seq

```

1  ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATGA TGCCTTGCTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCGG
201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
351 GCGCGCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCGCG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGTAACGC GTCAGGTTGC GGAGCGTTAC
601 GTCCGCGCGC TGTACGGCTA TGGTACGCC GCTCCTGTCT CCTTCGATGG
651 TTGCAGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATGTGA
701 AGTTTGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

a638.pep

```

1  MIGGQFIVVG IVGKNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVRAG
101 IGKNAVPPFG NIVADDLRTG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
151 RTMQIDADRI IQNIVFVNOG ARGSSFEINT GIHCGQAHTG TNGQVAERY
201 VRRVYGYGTP APVSFDGCRT VGRPFNRNRF VDVKFGFIYA GSQFERIARP

```

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251 GAGKCGIPIS IIDSW*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGKEFIVVGIIGKYALACLVDNVVNI GIVDIVEHNALIAAADGDIVEYFEPLGKHQHI					
	: : : : : : : :					
a638	MIGGQFIVVGIVGKNALARFVDNVVNI GIVDIVEHDALVAAADGDIVKHFEPLGKHQHI					
	10	20	30	40	50	60

	70	80	90	100	110	120
m638.pep	AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFVGVVRAGIGKNAVPPFGNVVADDLRTG					
	: : : : : : : :					
a638	AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFIGVVRAGIGKNAVPPFGNIVADDLRAG					
	70	80	90	100	110	120

	130	140	150	160	170	180
m638.pep	CVPNGNAVALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIIVFNQGARGSFFEINT					
	: : : : : : : :					
a638	RVPNGNAIALVHAQSRVADDFILPHHRIGRTMQIDADRIIQNIIVFNQGARGSFFEINT					
	130	140	150	160	170	180

	190	200	210	220	230	240
m638.pep	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCGTVGRPFNRNRFVNVKFGFIYA					
	: : : : : : : :					
a638	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVSFDGCRTVGRPFNRNRFVDVKFGLIYA					
	190	200	210	220	230	240

	250	260
m638.pep	GSQFERIARPGAGKCGIPISIIIGSX	
	: : : :	
a638	GSQFERIARPGAGKCGIPISIIDSWX	
	250	260

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCAAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACA CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGCGGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGGCAG GCGGGAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSVSGN ISVGNNMGYV LMFSERLKVF DNIAGVSRD*
151 GIMLNYYVNS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLHDN SFINNGSQVK YVSTRFLDWS EGGHGNYSWD NSPFDLNGDG
251 FGD SAYRPDG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEKAET RQSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1014

m639-1.seq

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTGCCTC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCGATG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGA
201 CGCACCCTGG GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACA CCTACAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCC GATATTACG ACAACATTAT
501 CAACAAGGCA GGCAAGTGGC TATTTGCCCTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAA TCCTTTATCA ACAACGAAAG
651 CCAGGTCAAA TACGTCAGCA CGCGCTTTCT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CGGCAGTCGG
1001 AATGGGGCAG GCGGGAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

m639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSSEISG ISVGNMVG YVLMFSERLKVF DNIAVGSRDQ
151 GIMLNHYVNY SDIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLDHN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNG IIDQIIWRAP VSRLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEKEVE RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
g639-1.pep	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEVSGN					
m639-1	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
g639-1.pep	ISVGNMVG YVLMFSERLKVF DNIAVGSRDQXGIMLNHYVNYSDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMVG YVLMFSERLKVF DNIAVGSRDQXGIMLNHYVNYSDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
g639-1.pep	YDKLSANHFENCQIGMHFTAIEGTSLDHNSFINNGSQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAIEGTSLDHNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
g639-1.pep	NSPFDLNGDGFSDAYRPDGIIDQIIWRAPVSRLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	NSAFDLNGDGFSDAYRPNGIIDQIIWRAPVSRLMNSPAISIVKWAQAFPAVLPGGVV					
	250	260	270	280	290	300
g639-1.pep	DSKPLMKPYAPKIQTRYQAMKDELLEKEAETRQSERGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLEKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

a639-1.seq

1015

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAC TGCCCC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTCG GTCGGCGTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA TATTTCCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAACA CCTATAAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTGTTC GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACG ACAACATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTTCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAAA TACGTCAGCA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CGGCGACGGC
751 TTCGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGACCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGC GCAGGCGCAA TTTCCCGCCG TTTTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATC AAACCCGTTA
951 TCAGGCGATG AAGGACGGGC TGCTCAAAAA AGTCGAAACG CGGCAGTTGG
1001 AATGGGGCAG GCGGAAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEISGN ISVGNNMGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLN YVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTS LHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPN IIDIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

a639-1/m639-1 98.8% identity in 344 aa overlap

a639-1.pep	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
a639-1.pep	10	20	30	40	50	60
a639-1.pep	70	80	90	100	110	120
a639-1.pep	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
m639-1	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
a639-1.pep	70	80	90	100	110	120
a639-1.pep	130	140	150	160	170	180
a639-1.pep	ISVGNNMGYVLMFSERLKVF DNIAGVSRDQ GIMLN YVNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNNMGYVLMFSERLKVF DNIAGVSRDQ GIMLN YVNYS DIHDNIINKAGKCVFAYNAN					
a639-1.pep	130	140	150	160	170	180
a639-1.pep	190	200	210	220	230	240
a639-1.pep	YDKLSANHFENCQIGIHFTA AIEGTS LHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTA AIEGTS LHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW					
a639-1.pep	190	200	210	220	230	240
a639-1.pep	250	260	270	280	290	300
a639-1.pep	NSAFDLNGDGF GDSAYRPN IIDIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV					
m639-1	NSAFDLNGDGF GDSAYRPN IIDIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV					
a639-1.pep	250	260	270	280	290	300
a639-1.pep	310	320	330	340		
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
a639-1.pep	310	320	330	340		

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1   ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCCTGT TTTTCAATCC GCGGTATGTC TCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251 GCgtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGTGCG TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCGAGCGT
501 GCGCGCCGGC GACATCATCA GcgggTGCAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601 GGTTCCGGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAAGGC CGTCGGCCAT
751 CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801 GGCCGGCGTG GCCGATCACG CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTGTGA TGTGTCCTTG GTCAGCCAGC CTTCCATCGG TAAAAGCCTG
901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACCCGGGCA
951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCCG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCGAGCTGTC
1101 TGCCGCCGAT GCGCCGCGTT TTAAAGAACT TTCTTGTTT ACCATCCCTG
1151 AAGGCGTAGC GTTTGACGGT GCGGAGCCGT GGCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1   MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIL NPPTPSVAPG DIISGATVTL MVVNDISIQR YKVIANQYRL
201 GSDKALQTA ASDVREAAAP SETRPRRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGKAGV ADHAEQGD PD DTFIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGYVVRGGI FDRIEMIQGE
351 NSFRFTDAQH ERVVELSAAD APRFKEVSWF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1   ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGGTTGCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1   MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAVFVFLTAALPAYAERLPDFLAK					
	: : : : :					
g640	MIHIISILKSIGISGIAMSCFSIRMSAFRARITAFFTAFVFLTAALPAYAERLPDFLAK					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
g640          IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAN
                70      80      90      100     110     120

                130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
                |||||||||||||||||||
g640          DGTIAGAKLVDHHEPIMLIGIPQSRVDKFIDKYIGLNFINKPPTPSVAPGDIISGATVTL
                130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGTT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKMSAFR ARITAFFAAF VFLTAALPAY
51 AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

                10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
a640          MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
                10      20      30      40      50      60

                70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
                ||||| |||||:|||||||||||||||||||||||||||||||||||:|
a640          IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAK
                70      80      90      100     110     120

                130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
                |||||||||||||||
a640          DGTIAGAKLVDHHEPIMLIGIPH
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1  ATGCGGTATC CGCCGCAATC GCGGTTTTTG CAGAATGCCG CGCGTTGCCT
51 TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTTGCCCG CTATCCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGTCTTCG TGTTCCTCCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTCG AGGGCGCAGG CGTCGGTCAG GGTGTGTTC
251 TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgtCgc gGGCAACGGC
301 GGcaaagcgG ACatcggtTT Gcacggcgtc gagCAGGGtt tggTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CCGTGGCGCG GACGAACTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATT TCGCGGCGgc gTAAGTGAT
551 TCCGTGGCGa ggTTTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCGG
651 AAACCTGATG GCGGCGTTGG ATTTGCGCGC GTTCGTAATC GACGAATCTG

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1018

```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATACGGCG
851 GTTGCAGGCA TTTCCGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTCCGAGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC Cgtttttgcg ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCCTGCCAGT ATTTTCGCGGC
1051 GttgACGTAA ATGGTTtgtt cgtcggata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAt cgCgcgcgcg gaggtTtcgg gttcggtaAc gcccaaacgg
1151 cggcttttcgc ctTTGAAAAT CATGTCCAAA CCTTGTGCGA CTTCGccttc
1201 gccgcgcgaac tCTTGACAGAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

g642.pep

```

1 MRYPPQSAVL QNAARCLLR PKSACRRICP LSAISAVQYI FADVQQEGC
51 GVVFVFLYED KKS GDDFADE DFLQAGVGQ GVFLQEAADV FKQSVVAGNG
101 GKADIGLHGV EQGLV FVQLN ACFFFGGGA DELVVNF GIK HIVRAFKNRE
151 GADIDGDIAG WVS AFKTLRA QEFLQHLRGG VSVFRGEGFD DVRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFHN
251 AVRHADQLQA AADKDV LERA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVCFGDEQQV DDFGEFAVFA LFGGNEEEVA LRIALPVFRG
351 VDVNGLFVGI FVAGLHFACN RRAGGF GFGN AQTA AF AFEN HVQTLCDLRF
401 AAELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

m642.seq (partial)

```

1 GCCTGCCGCC GTATTTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
51 CTTTGCGGAT KTCGTT CAGC AGGAAGGCTG CGGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTTG
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTT CTGCAGGAAG CTGCGGATGT
201 CTTCAGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACTTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TGCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTTCG CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGCGCG
601 GATTTGCGCG CGTTCGTAAT CGACGAATTT GATGTCGTTG CGGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTGTCAGGC ATTTTCGGAT
801 CGATGCGGTT GACGGCGTAA CCGACGGCGC GCAAGCCTTC GGTGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CACCCAAACC GCGGCCCTCG CTTTGA AAA
1101 TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATCGCCGAA CTCTGCAGT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

m642.pep (partial)

```

1 ACRRICLPEA ISAVQYIFAD VVQQEGCGVF VFLRYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADVSFQI FKDVFNHVR HADQLQAAAD KDVLERAQDTG
251 SVALGEFHG GCRHFGIDAV DGVTGDAQAF GCEGFAADV FGDQQLVDDF
301 GEFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVDIFV GLHFACNRRR
351 GGFGFNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHQR FADAGTQRNGH
401 AVMPRNP

```


1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30	
				ACRRICPLPAISAVQYIFADV	VVQEGCGVFVFR	LYED	
g642	MRYPPQSAVLQNAARCLLR	PKSACRRICPLSAISAVQYIFADV	VVQEGCGVFVFL	LYED			
	10	20	30	40	50	60	
m642.pep	40	50	60	70	80	90	
	KESGDDFADKDFLQAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV	FVQLH					
g642	KKSGDDFADEDFLQAGVGQGVFLQEAADVFGQSVVAGNGGKADIGLHGVEQGLV	FVQLN					
	70	80	90	100	110	120	
m642.pep	100	110	120	130	140	150	
	ACFFFFGGGADKL	VVNF	GIKHIVRAFKNREGADV	SDIAGGVSAFKTLRTQEF	LQHLRGG		
g642	ACFFFFGGGADEL	VVNF	GIKHIVRAFKNREGADIDGDIAGWVSAFKTLRAQEF	LQHLRGG			
	130	140	150	160	170	180	
m642.pep	160	170	180	190	200	210	
	VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVK	NLGNLMAAPDFAAFVIDE	FDDVADVS				
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVKDFGNLMAALDFAAFVIDES	DIVADIS					
	190	200	210	220	230	240	
m642.pep	220	230	240	250	260	270	
	FQIFKDVFHNAVRHADQLQAAADKDVLERAQ	TGSVALGEFHHGGCRHFGIDAVD	GVTDGA				
g642	VQVVKDVFHNAVRHADQLQAAADKDVLERAQ	TGSVAPGEFHHGGCRHFGIDAVD	GVTDGA				
	250	260	270	280	290	300	
m642.pep	280	290	300	310	320	330	
	QAFGCEGFAADV	CFGDEQQVDDFGEFAVFALFGGNEEEVALRVALPVFRGV	DVNGLSVDI				
g642	QAFGCEGFAADV	CFGDEQQVDDFGEFAVFALFGGNEEEVALRIALPVFRGV	DVNGLVFGI				
	310	320	330	340	350	360	
m642.pep	340	350	360	370	380	390	
	FVVGLHFACNRRAGGFGFGNTQTAAALAFENHLQTLRDLRFIAELLQWLQHQ	RAFDAGTQR					
g642	FVAGLHFACNRRAGGFGFGNAQTAAAFENHVQTLCDLRFIAELLQRLQHQ	RAFDAGTQR					
	370	380	390	400	410	420	
m642.pep	400						
	NGHAVMPRNP						
g642	NGHAVMPRNPX						
	430						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

1	GCCTGCCGCC	GTATTTGCC	GCTATCCGCA	ATATCGGCAG	TCCAATATGT
51	CTTTGCCGAT	GTCGTTCA	AGGAAGGCTG	CGGTGTCTTC	GTGTTCCGCC
101	TGTACGAAGA	CAAAGAGTCG	GGCGATGATT	TTGCCGATAA	AGACTTTTTG
151	CAGGGCGCAG	GCATCGGTCA	GGGTGTGTTC	CTGCAGGAAG	CTGCGGATGT
201	CTTCGGGCAA	AGTGTAGTCG	CGGGCGACGG	CGGCAAAGCG	GGCATCGGTT
251	TGCAGGCGGT	CGAGCAGGGT	TTGGTTTTTG	TCCAACCTCA	TGCCTGCTTC
301	TTTTTCTTCG	GCGGTGGCGC	GGACAACTG	GTCGTAAATT	TCGGCATAAA
351	GCAATATCGT	TTCGCGCTTCA	AAAATCGTGA	AGGGGCGGAT	GTCGATAGCG
401	ATATTGCCGG	CGGTGTGTCC	GCGTTCAAAA	CCCTTCGCGC	CCAAGAGTTT
451	TTGCAACATT	TGCGCGGCGG	CGTAAGTGTA	TTCCGTGGCG	AGGGTTTTGA
501	CGATGTTCGC	CTCCATCAGT	TGATGGGCGA	CGGGTGCAAC	GGGCGAAACG
551	GAATGGCAGA	CGTAGCGGTA	AAGAATCTCG	GAAACCTGAT	GGCGGCGCCG
601	GATTTCGCGG	CGTTCGTAAT	CGACGAATCT	GATGTCGTTG	CGGACGTATC
651	GTTCCAGGTT	TTCAAGGGTG	TATTCATAA	TGCCGTGCGT	CATGCCGATC

1020

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701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCAGGC ATTTCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GCGGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```

a642.pep Length: 407
1 ACRRICPLSA ISAVQYVFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRAQEF
151 LQHLRGGSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVFSQV FKGVFHNAVR HADQLQAAAD KDLERAQTG
251 SVALGEFHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFVV RLHFSGNRRA
351 GGFGFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

m642/a642 95.8% identity in 407 aa overlap

```

m642.pep      10      20      30      40      50      60
ACRRICPLPAISAVQYIFADV VQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
|||||:|||||
a642          10      20      30      40      50      60
ACRRICPLSAISAVQYVFADV VQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF

m642.pep      70      80      90      100     110     120
LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKL VVNFGIKHIV
|||||:|||||
a642          70      80      90      100     110     120
LQEAADVFGQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKL VVNFGIKHIV

m642.pep     130     140     150     160     170     180
RAFKNREGADVDSDIAGGVS AFKTLRTQEF LQHLRGGSVFRGEGFDDVRLHQLMGDGCN
|||||:|||||
a642         130     140     150     160     170     180
RAFKNREGADVDSDIAGGVS AFKTLRAQEF LQHLRGGSVFRGEGFDDVRLHQLMGDGCN

m642.pep     190     200     210     220     230     240
RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVFSQIFKDVFNHNAVRHADQLQAAAD
|||||:|||||
a642         190     200     210     220     230     240
GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADVFSQVFKGVFNHNAVRHADQLQAAAD

m642.pep     250     260     270     280     290     300
KDLERAQTGSVALGEFHGGCRHFGIDAVDGVT DGAQAFGCEGFAADVC FGDEQQVDDF
|||||:|||||
a642         250     260     270     280     290     300
KDLERAQTGSVALGEFHGGCRHFGIDAVDGVT DGAQAFGCEGFAADVC FGDEQQVDDF

m642.pep     310     320     330     340     350     360
GEFAVFALFGGNEEEVALRV ALPVFRGVDV NGLSVGIFVVR LHFSGNRRAGGFGFGNTQT
|||||:|||||
a642         310     320     330     340     350     360
GEFAVFALFGGNEEEVALRV ALPVFRGVDV NGLSVGIFVVR LHFSGNRRAGGFGFGNAXT

m642.pep     370     380     390     400
AALAFENHLQTLRDLRFIAE LLQWLQHORA FDAGTQRNGHAVMPRNP
|||||:|||||
a642         370     380     390     400
AALAFENHVQTLCDLRFIAE LLQWLQHORA FDAGTQRNGHAVMPRNP

```

g643.seq

1	ATGGTGTTGC	CTTTGATGTT	GTTGGCGACA	ATCAGgTcgg	CTACGCTGAc
51	gttgta ^{nc} Gt	TTGGCaATGt	tGaaCAgggt	gtcgccTTCT	ACACGCGGT
101	GGATGCTGGC	ATTGagcGGt	GAGGTTTCGG	CTTCGCGCTG	GGCAGCTTTTg
151	GCTACGCGCG	TTTCCAAACG	TGCCCGCGT	TtgcCGTCCG	CGGCAACGGT
201	ATGTTGCGGA	GATGAGGAAA	TGTTGTGTTC	GGCAACTGTG	TCAGGCGTGC
251	CGATGACGGC	GGagaTGGTT	TC ^T TCA ^G CCT	GCCGGCGCag	gTTGTTTTCGG
301	GCAACAAGCT	GCATGAGTTC	GTCTGCCGCC	TGCATGTCTG	TTGGGGGGAt
351	GACCTGCGcg	aGTGtTGGCG	TTTGGGTTTC	agacgGCATG	GCAGTCTGTT
401	TTTcggTTTG	a			

g643.pwp

1	MVLPLMLLAT	IRSATLTLXR	LAMLNRVSPS	TTRWMLAWSG	EVSASPSAAL
51	ATRVSKRARR	LPSAATVCCG	DEEMLCSATV	SGVPMTAEMV	SSACRRRLFR
101	ATSCMSSSAA	CMSFGGMTCA	SVAVVWSDGM	AVCFVS*	

m643.seq

1	ATGGTGTTGC	CTTTGATGTT	GTTGGCGACA	ATCAGGTCGG	CTACACTGAC
51	GTTGTAGCGT	TTGGCAATGT	TGAACAGGGT	GTGCGCTTCT	ACAAAGCGGT
101	GGATGCTCGC	ATGGAGCGGG	GAGATTTCGG	CTTCGCGCTG	GGCAGCTTTG
151	GCTATGCCGC	TTTCCAAACG	TACCGCGCGT	TTGCGCTCGC	CGCAGCGCGT
201	ATGTTGCGGA	GATGCGGAAA	TTTTGTGTTT	GGCAACTGTG	TGACGGCTGC
251	CGATGACGGC	GGAGATGGTT	TCTTCAGCCT	GTCGGCGCAG	GTTGTTTCGG
301	GCAACAAGCT	GCATGAGTTC	GTCTGCCGCC	TGCATGTCGT	TTTGGGGGAT
351	GATCTGCCGC	AGTGTGCGG	TTTGGGTTTC	AGACGGCATG	GCGGTCTGTT
401	TTTCGGTTTG	A			

m643 . pep

```

1  MVLPLMLLAT  IRSATLTL*R  LAMLNRVSPS  TTRWMLAWSG  EISASPSAAL
51  ATRVSKRTRR  LPSAAAVCCG  DAEILCSATV  SGVPMTAEMV  SSACRRRLFR
101 ATSCMSSSAA  CMSFWGMICA  SVAVVWSDGM  AVCFSV*

```

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

m643/g643

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2067>:

1022

```

a643.seq
1   ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTTTCG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
351 GATCTGCGCG AGTGTTCGCG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTTCGGTTT A

```

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

```

a643.pep
1   MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGTICA SVAVWVSDGM AVCFSV*

```

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
a643	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGMICA					
a643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGTICA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMAVCFSVX					
a643	SVAVWVSDGMAVCFSVX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

```

g644.seq
1   ATGCCGCTCG AAAGGccgGC GGATTGTTCG CCGGTGCACT TTGTGGTAAA
51  GTTTAGAAAA TTAACCTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CCATGGACAC GGCTGCTTTT TTAAagcaca tcgaatCCGC
201 ATTCcccccG ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCCCTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC
301 GACAAAAAAC ACGGCGGGCG CAAGGGCAGT CAGTTTGAAA TCCAAGAAGT
351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
401 TCGAAGGCGC GCTGGTGTTC CAGCCTCTGC AAGagttcgg cggcgaagcG
451 CAAGTCGCAC AAGGTTTGA CATGATTTTC AAaggcgaaa gccgcggttt
501 gggcgTtacc gaaccgaAa cctccggcgc gGcgaTTGCA CGCGAAAtgc
551 agtcctgcta cgaatatacc gacgaacaAA CCATTTACGT caaCGCCGCG
601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCCTcctcg ttgccgcaaa
651 agagcgcaaa aacGGcaaac tcgcaaaagt CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCCTG CATCCGAAGG CCTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAAACTC TCCCGGGGCG ACGCTGCCGG TTGCGCGCGG TTCCAAAACA
851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACATCC TTGACAACCT GAACCGATAT GTCCGCAACG ATATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCAACG CCGCCATCAG GTTTCGAAAA
1001 TCCTTTACCG CTACGTCTGC CATTCCGTTT CGcccgtcgC GCcgcTCGCC
1051 CATCAATTGA TGGAGGCGAA catcgTCAAA ACcctCGCCA CGGAATACAC
1101 TTAcgcCGCC GCGCAAATGT TGCAAAACT CTGGGGCGCG AAGGGTTTTG
1151 AACGCGGACA CCCAGCCGGC AATATCGCCA TCGATATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1251 CCTCCGCGCC ACCGCCGAAG AAAAAAGAGC AGGCATTAAG TTGGACAAAA
1301 accaaaCCCT Gctcgacgcc gtgCAAcacc atGTCcgctt tgCCGCCGTT
1351 GCCcgcGacT ACGCTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GACGCCTGCG CCTGCAAAA AGTCTTCATC GGCAAAATCA

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1023

1451 TCGCCCCGACT TTTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pep

1 MPSEPADCC PVHFVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KOAGLLLPFL
 101 DKKHGGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGGGA
 151 QVAQGLDMIF KGESRRRLGVT EPETSGAAIA REMQSCYEYT DEQTIYVNAA
 201 KYWQGNQSOSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNIIFIRSRL QLIGMTHGIM
 301 EYILDNLNRY VRNDIRFVDY ERREIQRRHQ VSEILYRYVC HSVSPVAPVA
 351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHPAG NIAIDIRPFT
 401 IFEGPNDMLY AEIYDQFVRA TAEKEAGIK LDKNQTL LDA VQTDVRFVAV
 451 ARDYALPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQEEHEDTTA
 501 FLLNDIRKDI LDCRYCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq

1 ATGCCGCTCG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAG CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
 201 ATTCCGCCGC ATTTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
 301 GACAAAAAAT ACGGCGGGCG CAAGGCGAGC CAGTTTGAAA TCCAAGAAGT
 351 CcTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
 451 CAAGTCGCGC AAGGTTTGGA GATGATTTTC AAAGCGGAGG GCGGCGGTTT
 501 GGGTGTTACC GAACCCGAAA CCTCCGCGCG GCGATTGCA CGCGAAATGC
 551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCGCG
 601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
 651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
 701 CCAAAACATA CATCCGCTGC GAAACCCCTG CATCCGAAGG CTTGCGCGCC
 751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACGCCCGT
 801 GATGAAACTC TCCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
 851 TCTTTATCCG CAGCCGCTTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT
 951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CCGCCATCAG GTTTCCGAGA
 1001 TTCTTTACCG CTACGCTGTC CATTCGTTT CGCCTGTTGC CCCCCTCGCC
 1051 CATCAGCTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
 1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGTGCG AAGGTTTTTG
 1151 AACGCCGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
 1201 ATTTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATT ACACCAGTT
 1251 TGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
 1301 ACCAAACCTT GCTCGACCGC CTGCAAAACG ATGCCCGCTT TGCCGCCGTC
 1351 GCCCCGACT ACACCTTGCC TGAAGACAT CGCAGCTTCC TGCAGGAACA
 1401 CACCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
 1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGA AACACGAAGA CACCGCAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 GTAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pep

1 MPSEPADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KOAGLLLPFL
 101 DKKYGGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGDEA
 151 QVAQGLEMIF KEGGGGLGVT EPETSGAAIA REMQSYEYI DGQTIYVNAA
 201 KYWQGNQSOSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSRL QLIGMTHGIM
 301 EYILENLERY VRNDIKFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
 351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
 401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTL LDR LQTDARFVAV
 451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQAKHEDTAA
 501 FLLNDIRKDI LDCRYCG*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSEPADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
g644	MPSEPADCCPVHFVVKFRKLTNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					

1024

	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
g644	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
g644	AGHYGVPVTLRTGIEGALVLPQLEFGDEAQAQGLEMIFKGEGLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
g644	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
g644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
g644	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLM EANIVK					
	310	320	330	340	350	360
m644.pep	370	380	390	400	410	420
g644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
m644.pep	430	440	450	460	470	480
g644	TAEKEAGMKLDKNQTL DRLQTDARFAAVARDYTL PEDIRSFLOEHTLTDACALQKVFI					
	430	440	450	460	470	480
m644.pep	490	500	510			
g644	GKIIARLFVQAKHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

```

a644.seq
1  ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGCGAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCAG ACGGTATCGA CCTGATGCCA TACCTGCCCC
251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGCGGGGCG CAAGGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGGTTTGA CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
501 AGGCGTTACC GAACCCGAAA CCTCCGGCGC GGCGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTTACGT CAACGCCGCG
601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACGCCCGT
801 GATGAAACTC TCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA

```

1025

```

851 TCTTTATCCG CAGCCGCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CCGCCATCAG GTTTCCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTTG
1151 AACGCGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTTGAAG GCCCGAACGA TATGCTTAT GCCGAAATTT ACGACCAGTT
1251 TGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCTT GCTCGACCGC CTGCAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACCTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGCGCG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644.pep
1  MPSERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGRRKS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYET DGQTIYVNAA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI FRSRL QLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEEAGMK LDKNQTLDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

```

m644/a644 97.3% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
a644	MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
	10	20	30	40	50	60
m644.pep	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRRKGSQFEIQEVLRI					
a644	LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQVAQGLEMIFKGGGGGLGVTEPETSGAAIA					
a644	AGHYGVPVXXXXXXEGALVLQPLQEFGDEAQIAQGLDMVFKGGGGGLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644.pep	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLLVPKTYIRC					
a644	REMQSYEYTDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FRSRLQLIGMTHGIM					
a644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FRSRLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	EYILENLERIVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					
a644	EYTLLENLERYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					

1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a644						
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEEAGMKLDKNQTLRLQTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
a644						
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVVFVQAKHEDTAAFLNDIRKDILDCRYCGX					
a644						
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645 . seq

```

1  ATGATGATGG  TGTGGCGTT  GGGGATGTCG  ATGCCGGTTT  CGATGATGGT
51  GGAACAGAGC  AACACATTGA  ATCTTTGCTG  CAAAAAGTCG  CGCATGACTT
101 GTTCCAGCTC  GCGCTCACGC  AGTTGTCCGT  GCGCCACGCC  GATACGGGCT
151 TCGGGCAGCA  GGGTTTCCAG  CCGCTCGCGC  ATATTCTCAA  TCGTATCTAC
201 TTCATTGTGC  AGGAAAAata  cTGTCTCTCC  GCGTTTGAGT  TCGCGCAACA
251 CGGCTTCGCG  CACGCTGCCT  TCGCTGAACG  GTTTGACAAA  GGTTTTACAG
301 GCGAGGCGGC  GGCTCGGTGC  AGTGGAATC  AGCGAGAAGT  CGCGCAGACC
351 TTCGAGCGCC  ATGCTGAGGG  TCGCGGAAT  CGGCGTGGCG  GTCATGGTTA
401 GGATGTCGAC  ATTGGCGCGC  AGGCGTTTGA  GCTGCTCTTT  CTGTGCGACG
451 CCGAAGCGGT  GTTCTTCATC  GATAATCAAT  AAACCTAAGT  TTTGAATTT
501 TATGTCGTCC  TGCACCAATT  TGTGCGTACC  GATAACGATA  TCGACAGTAC
551 CGTCCGCCAT  GCCTTCGAGC  GTGGCTTTGG  TGGCTTTGCT  GTTGTGAAA
601 CGCGAAAGGC  TGGCGACTTT  CACGGGGAAA  TCGGCGAAAC  GGTGCGCGAA
651 GTTTTGC GCG  TGCTGCTCGA  CCAGAAGCGT  GGTGCGGGCG  AGTACGGCGA
701 CCTGTTTGCC  GCCCATCACC  GCCACAAACG  CGGCGCGAAG  GGCAGCTTCG
751 GTTTTGCCGA  AACCGACATC  GCCGCACACA  AGTCGGTCCA  TCGGCTTCGC
801 CTGCGTCAAA  TCTTTAATCA  CGGcggcgat  ggcggcggcC  TGGTCTTCGG
851 TTTCCTCGTA  G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

g645 . pep

```

1  MMVLALGMS MPVSMMEQ NTLNLCCKKS RMTCS SSRSR SCPCATPIRA
51  SGRVSSRSR  IFSIVSTSLC  RKNTCPPLRS  SRNTASRTLP  SLNGLTKVFT
101 ARRLGAVVI  SEKSRRPSSA  MLRVRGIGVA  VMVRMSTLAR  RRLSCSFRT
151 PKRCSSSIIN  KPKFLNFMSS  CTNLCVPITI  STVPSAMPSS  VALVALLLLK
201 RERLATFTGK  SAKRSAKFCA  CCSTRSVVGA  STATCLPPIT  ATNAARRATS
251 VLPKPTSPT  SRSIGFACVK  SLITAAMAAA  WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645 . seq

```

1  ATGATGATGG  TGTGGCGTT  GGGGATATCG  ATACCGGTTT  CGATGATGGT
51  GGAACAGAGC  AACACGTAA  ATCGTTGCTG  CAAAAAGTCG  CGCATGACTT
101 GTTCCAGCTC  GCGCTCGCGC  AGTTGTCCGT  GCGCCACGCC  GATGCGGGCT
151 TCGGGCAGCA  GGGTTTCCAG  CCGCTCGCGC  ATATTTTCAA  TCGTATCTAC
201 TTCATTGTGC  AGGAAAAATA  CCTGTCTCTC  GCGTTTGAGT  TCGCGCAACA
251 CGGCTTCGCG  CACGCTGCCT  TCGCTAAAGG  GTTTGACAAA  GGTTTTGACG
301 GCGAGGCGGC  GGCTGGGCGC  GGTGGAATC  AGCGAGAAGT  CGCGCAGTCC
351 TTCCAACGCC  ATACTTAAAG  TACGCGGAAT  CGGCGTGGCG  GTCATGGTAA
401 GGATATCAAC  ATTGGCGCGC  AGGCGTTTGA  GCTGCTCTTT  CTGACGCACG
451 CCGAAGCGGT  GTTCTTCGTC  GATAATCACT  AAACCTAAGT  TTTGAATTT
501 GATGTCGTCC  TGCACCAATT  TGTGCGTACC  GATAACAATA  TCGACCGTGC
551 CGTCTGCCAT  GCCTTCCAGC  GCGGCTTTGG  TGGCTTTGCT  GTTGTGAAA
601 CGCGAAAGGC  TGGCGACTTT  CACGGGGAAA  TCGGCGAAAC  GGTGCGCGAA
651 GTTTTGC GCG  TGCTGCTCGA  CCAAAAGCGT  GGTGCGAGCA  AGTACGGCGA
701 CCTGTTTGCC  GCCCATCACC  GCCACAAACG  CGGCGCGCAG  GGCAGCTTCG
751 GTTTTGCCGA  AGCCGACATC  GCCGCACACA  AGGCGATCCA  TCGGCTTCGC
801 TTGCGTCAAA  TCTTTAATCA  CGGCGGCGAT  GCGGCGGGCC  TGGTCTTCGG

```


851 TTTCTTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

m645.pep

```

1   MMMVLALGIS IPVSMMEQSN TLNRCCKKS RMTCSSSRSR SCPCATPMRA
51  SGRVSSRSR IFSIVSTSLC RKNTCPPRLS SRNTASRTL PSLKGLTKVLT
101 ARRRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRLTLAR RRLSCSF*RT
151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSKFCFCA CCSTKSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMMVLALGISIPVSMMEQSN	TLNRCCKKS	RMTCSSSRSR	SCPCATPMRA	SGRSRVSSRSR	
g645	MMMVLALGMSMPVSMMEQSN	TLNRCCKKS	RMTCSSSRSR	SCPCATPIRA	SGRSRVSSRSR	
	10	20	30	40	50	60
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPPRLSS	RNTASRTLPSL	KGLTKVLTARRRL	GAVVISEKSR	SPSNA	
g645	IFSIVSTSLCRKNTCPPRLSS	RNTASRTLPSL	NGLTKVFTARRRL	GAVVISEKSR	SPSSA	
	70	80	90	100	110	120
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRISTLAR	RRRLSCSFXRTP	KRCSSSIITKPK	FLNLMSSCTSL	CVPITI	
g645	MLRVRGIGVAVMVRISTLAR	RRRLSCSFCRTP	KRCSSSIINKPK	FLNFMSSCTNL	CVPITI	
	130	140	150	160	170	180
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALLLLK	RERLATFTGKS	AKRSKFCACCS	TKSVMVGAST	ATCLPPIT	
g645	STVPSAMPSSVALVALLLLK	RERLATFTGKS	AKRSKFCACCS	TRSVVGAST	ATCLPPIT	
	190	200	210	220	230	240
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPTSPHT	RRSIGFACVKSL	ITAAMAAWSSV	SSSX		
g645	ATNAARRATSVLPKPTSPHT	RSIGFACVKSL	ITAAMAAWSSV	SSSX		
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq

```

1   ATGATGATGG TGTGGCGTT GGGAAATGTCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
201 TTCATTGTGC AGGAAAAATA CTTGCCCGCC GCGTTTGAGT TCGCGCAATA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
501 TATGTCGTCC TGCACCAGTT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCCGCCAT GCCTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAGC GGTGCGCAAA
651 ATTTTGC GCG TGCTGCTCGA CCAGAAGCGT GGTGCGTGCG AGTACGGCAA
701 CTTGTTTGCC ACCCATTACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGCGGCGAT GCGGCTGCC TGGTCTTCGC
851 TTTCTTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep

```

1   MMMVLALGMS IPVSMMEQSN TLNRCCKKS RMTCSSSRSR SCPCATPMRA

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1028

```

51  SGSRVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTL P SLNGLTKVLT
101 ARRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSAKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKTPSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/a645 96.9% identity in 286 aa overlap

```

              10      20      30      40      50      60
m645.pep     MMMVLALGISIPVSMMEQSNLTNRCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645         MMMVLALGMSIPVSMMEQSNLTNRCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
              10      20      30      40      50      60

              70      80      90     100     110     120
m645.pep     IFSIVSTSLCRKNTCPPLRSSRNTASRTLPSLKGLTKVLTARRRLGAVVISEKSRSPSNA
              :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645         MFSMVSTSLCRKNTCPPLRSSRNTASRTLPSLNGLTKVLTARRRLGAVVISEKSRSPSSA
              70      80      90     100     110     120

              130     140     150     160     170     180
m645.pep     ILKVRGIGVAVMVRISTLARRRLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645         ILKVRGIGVAVMVRMSTLARRRLSCSFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI
              130     140     150     160     170     180

              190     200     210     220     230     240
m645.pep     STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645         STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT
              190     200     210     220     230     240

              250     260     270     280
m645.pep     ATNAARRATSVLPKTPSPHTRRSIGFACVKSLITAAMAAWSSVSSX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645         ATNAARRATSVLPKTPSPHTRRSIGFACVKSLITAAMAAWSSVSSX
              250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

g647.seq

```

1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTGCGA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

g647.pep

```

1  MQRLAADGIQ IFFVGVGQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51  GFKGTVGQTE RGTVAADTV FRQIVGVDD TDAERTAVHS RGTRGFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

m647.seq

```

1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCGA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

m647.pep

```

1  MQRLAADGIQ IFFVSDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSVDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGOTE					
	: : : : : : : : : : : : : : : :					
g647	MQRLAADGIQIFFVGVDGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFKGTVGOTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTVAVADTVFRQIISIVNHADAERTAHSRGTRGFYRISLIIX					
	: : : : : : : : : : : : :					
g647	RGTVAVADTVFRQIVGVDDTDAERTAVHSRGTRGFYRISLIIX					
	70	80	90	100		

```
a647.seq
1  GTGCAAAGGC  TCGTTACACA  CAGCGTCCAA  GTCTTTTTTG  TAGGTGTCTGA
51  TGGGTCAGTTT  GCCTTGCCAA  TAAACGGTTT  GGTAAAGAG  CAGTGCACGCA
101 CCGTATTCTT  TGGCAAGGTT  TCCCGATGCT  TTGAGCAGGT  AATACTGTAT
151 GGCTTCAAAG  GTACGGTGGG  TCAGACCGAG  CGCGGAGCCG  TCGCTGTAGC
201 GGACACCGTT  TTTTCGCCAA  TAATACGCAT  AGTTGATCAC  GCCGATACCG
251 AGCGAACGGC  GGCCCATAGT  GGAGGTACGC  GCGGCTTCTA  CCGGATATCC
301 CTGATAATCT  AA
```

```
a647.pep
  1  VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
 51  GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAHS GGTRGFYRIS
101  LII*
```

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSV	DGQFALRINGLVKERARTVF	FGKVCRCFEQVILYGF	KGTVGQTE		
a647	VQRLVTHSVQVFFVGV	DGQFALRINGLVKERARTVF	FGKVCRCFEQVILYGF	KGTVGQTE		
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTVA	ADTVFRQII	SIVNHADAERTAAHSR	GTRGFYRISLIIX		
a647	RGAVA	ADTVFRQIIR	IVDHADTERTAASGG	TGRGFYRISLIIX		
	70	80	90	100		

g648.seq

```
1 ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGTAT
51 CGACGTTTTG AATGTAGATG GCCCGGTGCC CGGCACGCTC TCGCATCAGC
101 TTGGAAAAACA GGTTCGCAGC CGGAATGATA CGTGTGCGTA TGTTCGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAA TTCTGCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAACCCCGAA ACCTCGTTGG GCGAAACAG CGTAATGTTG
251 CGCCCTTAA TCAAGCGGGT GTACAGCAGC CGGTTGATT GACAGGCATA
301 ATCAAGCTGG CGGATACGGT TGTCTTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCA ATATGCCACA AGGGGTAGAA CAAAGTTGCC
401 GCGCCGCGCG GCACGCCACC TTGCGAATAA GATTTGACC CCGCTTAA
451 CATCTTAAAG AAGGGATATG AGCCGGTATC CCGGGCTTCA CGCCCGGGA
501 TTTCGCTGTC CAGCCCGCGG ATACGTCGCG CATTGATGCC GATGCCCGCG
551 CGTTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGATTTCAA TCAGCACACA GCTTGA
```

g648 . pep

```

1  MNRNRNARIER  AVRIAVIDVL  NVDAPGPGTL  LHQRGKQVGS  RNDTLAYVRV
51  LLVFRIEPLK  FVLVGKKRFV  QPRNLVGRKQ  RNVAALNQAG  VQQAVDLHAI
101 IKLADTVVFH  APVVFQHQQA  FGFNMPQGVF  QGCRAAAHAT  LRTFRDRLK
151 HLKEGNAAGM  PGFTAPDFAV  QPADTSGIDA  DARALGNVHF  NRAGSGIDGI
201 QTIVAFNQHT  A*

```

m648.seq

m648 . pep

	10	20	30	40	50	60
m648 .pep	MNRRDARIERAVRIA	IDVNLVDAPGSGTLL	HQRGKQVGS	RNDALADIRVLL	VFRIEPLK	
g648	:					
	MNRRNARIERAVRIA	IDVNLVDAPGPTLL	HQRGKQVGS	RNDTLAYVRVLL	VFRIEPLK	
	10	20	30	40	50	60
m648 .pep	70	80	90	100	110	120
	FVLVGKKRFVQSRNLV	GRKQRNVAALNQAGV	QQAVDLHAVIKLTD	TVVVFHTAVVFQHQQA		
g648						
	FVLVGKKRFVQPRNLV	GRKQRNVAALNQAGV	QQAVDLHAIK	LADTVVFHAPVVFQHQQA		
	70	80	90	100	110	120
m648 .pep	130	140	150	160	170	180
	FGFDMPPQGVQGCRAAA	HAALRTGFDRLKH	FKEGNAAGMPRFAAP	PDFAVQQTADTSGIDA		
g648	:					
	FGFNMPQGVQGCRAAA	HATLRTFRDRLKHL	KEGNAAGMPGTAPD	FAVQPADTSGIDA		
	130	140	150	160	170	180
m648 .pep	190	200	210			
	DARTLGNVFHN	RAGSGIDGIQTIVAF	NQHTAX			
g648	:					
	DARALGNVFHN	RAGSGIDGIQTIVAF	NQHTAX			
	190	200	210			

a648.seq

1	ATGAACAGGC	GCAACGCGCG	GATCGAACGG	GCTGTGCGTA	TTGCAGTGTAT
51	CGACGTTTTG	AATGTAGATG	CGCCGGGTTT	CGGCACGCTC	CTGCATCAGC
101	TGTGAAAAAC	GGTCGGCAGC	CGGAATGATG	CGCTTGCCTG	TATCAGGGTTA
151	TTGCTCGTAT	TTCTGTATAG	ACCGCTCAAA	TTCTGTTTGG	TCGGGAAAAA
201	ACGCTTCGTA	CAATCCCGGA	GCTTCGTTGG	GCAGAAAACAG	CGTAATGTGTG
251	CCGCCCTTAA	TCAGGCGGGT	GTACAGCAGG	CGGTTGATTT	GCACGCCGTA
301	ATCAAGCTCA	CGGATACGGT	TGPTTCCAC	GCCCCGGTTG	TTTTTCAACA
351	CCAGCAGGCT	TTCCGGCTTC	ATATGCCACA	AGGGGTAGAA	CAAGGTTGCC
401	GCGCCGCCCG	GACGCCACC	TTTCGGAACAG	GATTTGACTG	CCGCCTGAAA
451	CATTTTAAAG	AAGGGAATGC	AGCCGGTATG	CGGTGCTTCG	CCGCCCCGGA

1031

501 TTTGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA
 551 CGCTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
 601 CAGGCTGTCTG TCGCATTCGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648.pep
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVDLHAV
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGFDCRLK
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
 201 QAVVAFDQYA A*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
a648	MNRRNARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVDLHAVIKLTDTVVFHTAVVFQHQQA					
a648	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVDLHAVIKLTDTVVFHAPVVFQHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPQGV E QGCRAAAHAALRTGFDRRLKHFEKNAAGMPRFAAPDFAVQTADTSGIDA					
a648	FGFDMPQGV E QGCRAAAHATLRTGFDCRLKHFEKNAAGMPCFAAPDFAVQSADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRAAGSGIDGIQTIVAFNQHTAX					
a648	DARTLGNVFHNRAAGSGVDGIQAVVAFDQYAA					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGA CTGGTAT CAACA ACTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAAA CATATCAGCA
 101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649.pep
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECKRYLER
 51 RAAWYRSQGN VQELRENKKA RKAFTLPYA EQKIQCRAAY EAFDDFDGGR
 101 FRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGA CTGGTAT CGACA ACTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
 101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGT
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

```

1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCRAAY EAFDDFDGGS
101 FRR*

```

m649/g649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
g649           MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
g649           VQELRENKKARKAFRTLPYAEQKIQCRAAYEAFDDFDGGRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

```

a649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
51  CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTGGAACGC
151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
251 CCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCAGCAGG
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

```

a649.pep
1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKTQCRAAY EAFDDFDGSR
101 FRR*

```

m649/a649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
a649           MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
a649           VQELRENKKARKAFRSLPYKEQKTQCRAAYEAFDDFDGSRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

```

g650.seq
1  ATGTCCAAC TCAAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCGCAG CTATTTGAC AGGGTCGTCA ACCGAGCCG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGAAAA AAACaccgGT TTACGacggc aggcacGacg TTtacgcaGc
501 taccgatgcc gcacTCAACT AtctGcAATA TCTCTatggA CTGTTCCGGC
551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCGTC ACCGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCAACGAAA CGCGCAACTA TGCCCCAAG CTGCTCGCCG
701 TGCGCAACAT TATTGCCACC CCCCATCTT TCGGCATGAA TATCAGCGAC

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1033

```

751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTGAATCC TGCATTC AAC GTCCCGCGt tcatCCCCAA AAaCaacgc
901 aaacTGCTGC TTCCTGTGCG GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCTTTTC CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCCggcag gcaCGGTGAA CGTCAGCATt gccCgaatcc aacCCgccc
1251 cgcaCAGACA gcgacatta ccgtcgcacc tttgccgcaa gaaaccgtcc
1301 gtacgggaac ccgatcccct tgtccgcaTt accgaaccgc ccctTGCAGC
1351 AGCCGCAGCG CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

g650 . pep

```

1 MSKLKTIALT ASGLSVCPGF LYAQTSSHQ VGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWDE LRQGRMGEV NPFLVRRHES KFIASRSYFD RVVNRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPDYRSN
401 MPAGTVNVSI ARIQFAAAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

m650 . seq

```

1 ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATACGCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCGAAT CCGGCAGCCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGAAA AAACACCGGT TTACGACGGC AGGCACGACG TTTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCGGCG
551 ACTGGCCGCT TGCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
701 TGCCCAACAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGCA
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCTTAAACCC CGCATTC AAC GTCCCGCGT TTATCCCCAA AAGCAAACGC
901 AAATGCTGC TTCCTGTGCG GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG . AAC CCGATCCCC TGTCCGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

m650 . pep

```

1 MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWGE LRQGRMGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLOLYG LFGDWPLAFA AYNWEGENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPDYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1034

m650.pep	10	20	30	40	50	60
	MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPTKQYFQSGSLWGE					
g650	MSKLKTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPTKQYFQSGSLWDE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGFMRGEVNPVLVRRHESKFIASHSYFNRVINRSRPYMYHIANEVKKRNMPAEAAALLP					
g650	LRQGFMRGEVNPVLVRRHESKFIASRSYFDRVVNRSRPYMYHIANEVKKRNMPAEAAALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNWGEVNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
g650	LFGDWPLAFAAYNWGEVNVGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSFGMNIISDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR					
g650	PQSFGMNIISDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPFIPKNKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDTPYRSNMPAGTVNVGIARIRPAAAQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSIDIDNTPDTPYRSNMPAGTVNVSIARIQAAAQT					
	370	380	390	400	410	420
m650.pep	430	440	450	460		
	ADITVAPLPQKTVRXTXTRSPCPYCRTCPCDSRSATSNRKTDHRAVX					
g650	ADITVAPLPQETVRTGTRSPCPHYRTRPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

```

a650.seq
1  ATGTCCAAAC  TCAAAACCAT  CGCCCTGACC  GCGTCAGGTC  TGTCCGTTTG
51  TCCGGGTTTC  CTATACGCCC  AAAACACCTC  ATCACACCAA  ATCGGTTTGG
101 CGATTATGCG  CTTAAACTCT  TCAATACTCG  ACCTGCCACC  GACAAAACAA
151 TATTTCCAAT  CCGGCAGCCT  GTGGAGCGAG  CTGCGCCAAG  GCTTCCGGAT
201 GGGCGAAGTC  AATCCCGAAC  TGGTACGCCG  CCACGAAAGC  AAATTCATCG
251 CAAGCCACAG  CTATTTCAAC  AGGGTCATCA  ACCGGAGTAG  ACCCTATATG
301 TACCATATCG  CCAACGAAGT  CAAAAACGC  AATATGCCCG  CCGAAGCCGC
351 CCTGCTTCCC  TTCATCGAAA  GCGCGTTCGT  CACCAAAGCC  AAATCACACG
401 TCGGCGCATC  GGGCCTGTGG  CAGTTCATGC  CCGCTACCGG  CAGGCATTAC
451 GGCCCTGGAAA  AAACACCGGT  TTACGACGGC  AGGCACGACA  TTTACGCCGC
501 CACCGATGCC  GCACTCAACT  ATCTGCAATA  CCTCTATGGA  CTGTTCCGGC
551 ACTGGCCGCT  CGCCTTTGCC  GCCTACAAC  T  GGGGTGAAGG  CAACGTCGGA
601 CGCGCCATCA  ACCGCGCCCG  CGCCCAAGGG  CTCGAACCGA  CCTACGAAAA
651 CCTGCGTATG  CCCAACGAAA  CGCGCAACTA  TGTTCCCAAG  CTGCTCGCCG
701 TGCGCAACAT  CATTGCCGCC  CCCCAATCTT  TCGGCATGAA  TATCAGCGAC
751 ATAGACAACA  AACCGTATTT  TCAGGCAGTC  GAACCGGACC  GTCCGCTCGA
801 CAACGAAGCC  ATCGCCCGGC  TTGCCGGCAT  CACGCAAAGC  GAGCTGCTCG
851 CCCTAAACCC  CGCATTCAAC  GTCCCGCGT  TCATCCCCAA  AAGCAAACGC

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1035

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901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAACCAG CTGTGTCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCCT TGTCGGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

a650.pep

```

1  MSKLKTIALT ASGLSVCPGF LYAQNTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWSE LRQGFMRGEV NPELVRRHES KFIASHSYFN RVINRSRPFY
101 YHIANEVKKR NMPAEAAALL FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDIIYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

```

m650/a650 99.1% identity in 465 aa overlap

	10	20	30	40	50	60
m650.pep	MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
a650	MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
	10	20	30	40	50	60
m650.pep	LRQGFMRGEVNPELVRRHESKFIASHSYFN RVINRSRPFYHIANEVKKRNMPAEAAALLP					
a650	LRQGFMRGEVNPELVRRHESKFIASHSYFN RVINRSRPFYHIANEVKKRNMPAEAAALLP					
	70	80	90	100	110	120
m650.pep	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
a650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	LFGDWPLAFAAYNWEGENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
a650	LFGDWPLAFAAYNWEGENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAA					
	190	200	210	220	230	240
m650.pep	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR					
a650	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR					
	250	260	270	280	290	300
m650.pep	KLLLPVASVQTFQSNYLNAAPDSLFSWEVYTTPAAKTSLSDISTATGMSIADIKRLNNLNG					
a650	KLLLPVASVQTFQSNYLNAAPDSLFSWEVYTTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTYRSNMPAGTVNVGIARIRPAAQT					
a650	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTYRSNMPAGTVNVGIARIRPAAQT					

1036

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRXTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
a650	ADITVAPLPQKTVRXTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652.seq

```

1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCGGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCCGG CTACAAGGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATACTTGGA GGCTTGGTGA
551 ACGAATTCCC GATTATTTC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATTG GGCAAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTCTGTA CCAATCCGAA AATTCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCCTGAAAGc cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCAccgct ccggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTAaaaccgG TCCTTTGAGc
901 cgTTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCcgctACT ACCCCGGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652.pep

```

1  MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW
201 EGWKLLEFKL GKKVQLVGDD LFTVNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAKYNQ LLRIEELAE AAYYPGKAFF YQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652.seq

```

1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAGGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATATCTGGA GGCTTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GGCGGTAGAG TTCAATTGGT
651 TGCGCAGCAC TTGTTCTGTA CCAATCCAAA AATCTTGGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCCTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAa CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652.pep

```

1  MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC

```

1037

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
 151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW
 201 EGWKLLETKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAKYNQ LLRIEEELAE AADYPSKAAF YQLGK*

m652/g652 98.2% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
g652	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN					
g652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
g652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFPPIISIEDGMDENDWEGWKLLETKLGGVQLVGDDLFVTNPKILAEGIEKGVANA					
g652	GLVNEFPPIISIEDGMDENDWEGWKLLETKLGGVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
g652	LLVKVNQIGTLSETLKAVDLAKCNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAKYNQLLRIEEELAEAADYPSKAAFYQLGKX					
g652	RSDRMAKYNQLLRIEEELAEAAAYPGKAAFYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

a652.seq

1	ATGATCGAAT	TGGACGGTAC	TGAAAACAAA	GGCAATTTGG	GTGCGAATGC
51	GACTTTTGCG	GTTTCTATGG	CGGTTGCACG	CGCCGCTGCC	GAAGACTCAG
101	GCCTGCCGCT	TTACCGCTAC	TTGGGCGGCG	CAGGCCCGAT	GTCCCTGCCC
151	GTACCGATGA	TGAACGTCAT	CAACGGCGGC	GAACACGCCA	ACAACAGCCT
201	GAACATCCAA	GAGTTTATGA	TTATGCCCGT	CGGCGCAAAA	TCTTTCCGCG
251	AAGCGTTGCG	CTGCGGTGCG	GAAATTTTCC	ACGCCTTGAA	AAACTGTGTC
301	GACAGCAAAG	GCTTCCCGAC	CACAGTCGGC	GACGAAGGCG	GTTTCGCCCC
351	CAACCTGAAC	AGCCACAAAG	AAGCCCTGCA	ACTGATGGTC	GAGGCGACCG
401	AAGCCGCCGG	CTACAAAGCG	GGCGAAGACG	TATTATTCGC	ATTGGACTGC
451	GCGTCCAGCG	AGTTCTACAA	AGACGGCAAA	TACCACTTGG	AAGCCGAAGG
501	CCGCTCCTAC	ACCAACGCGG	AATTTGCCGA	ATATCTGGAA	GGCCTGGTCA
551	ACGAGTTCCC	CATCATCTCC	ATCGAAGACG	GGATGGATGA	AAACGACTGG
601	GAAGGCTGGA	AACTGCTGAC	CGAAAACTG	GGCGGCAAG	TCCAACCTCGT
651	TGGCGACGAC	CTCTTCGTTA	CCAACCCGAA	AATCCTTGCC	GAAGGCATTG
701	AAAAAGGCGT	GGCAAACGCA	CTATTGGTCA	AAGTCAACCA	AATCGGTACT
751	TTGAGTGAAA	CCCTGAAAGC	CGTCGACTTA	GCCAAACGCA	ACCGCTACGC
801	CAGCGTAATG	AGCCACCGCT	CCGGCGAAAC	CGAAGACAGC	ACCATGCGCG
851	ACTTGGCAGT	CGCCACCAAC	TGTATGCAGA	TCAAAACCGG	TTCTTTGAGC
901	CGTTCCGACC	GCATGGCGAA	ATACAACCAA	CTGCTGCGTA	TCGAGGAAGA
951	ATTGGCGGAA	GCCGCCGACT	ACCCAGCAA	AGCCGCATTG	TACCAACTGG
1001	GCAAATAA				

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

a652.pep

1	MIELDGTENK	GNLGNATLA	VSMVARAAA	EDSGLPLYRY	LGGAGPMSLP
51	VPMNVINGG	EHANNSLNIQ	EFMIMPVGAK	SFREALRCGA	EIFHALKKLC
101	DSKGFPTTVG	DEGGFAPNLN	SHKEALQLMV	EATEAAGYKA	GEDVLFALDC

1038

151 ASSEFYKDGG YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW
 201 EGWKLLETKL GGKVLVGGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAKYNQ LLRIEEELAE AADYPSKAAF YQLGK*

m652/a652 99.7% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
a652	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNLSNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
a652	EHANNLSNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGGKYHLEAEGRSYTNAEFAEYLE					
a652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
a652	GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGTLSETLKAVDLAKRNRYASVMHRSGETEDSTIADLAVATNCMQIKTGSLS					
a652	LLVKVNQIGTLSETLKAVDLAKRNRYASVMHRSGETEDSTIADLAVATNCMQIKTGSLS*					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAKYNQLLRIEEELAEAADYPSKAAFYQLGKX					
a652	RSDRMAKYNQLLRIEEELAEAADYPSKAAFYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA  TCGTTGATAT  TTTCCGCCGC  GAAATTTTGG  ACTCACGCGG
51  CAACCCACAC  GTCGAGTGTG  ATGTATTGCT  CGAATCCGGC  GTAATGGGAC
101 GTGCGCCCGT  ACCGAGCGGC  GCATCCACCG  GTCAGAAAGA  AGCTTTGGAA
151 CTTCCGCACG  GCGACAAATC  CCGCTATTCC  GGCAAAGGCG  TATTGAAGGC
201 CGTCGAACAC  GTCAACAACC  AAATCGCCCA  AGCCCTCATC  GGTATCGATG
251 CCAACGAGCA  ATCTTATATC  GACCAAAATCA  TGATCGAATT  GGACGGTACT
301 GAAAACAAAG  GCAATTGGGG  TGCGAATGCG  ACTTTGGCGG  TCTCTATGGC
351 GGTTCACGCG  GCCGCTGCCG  AAGACTCAGG  CCTGCCGCTT  TACCGCTACT
401 TGGGGGGCGC  AGGTCCGATG  TCCCTGCCCG  TACCGATGAT  GAACGTCATC
451 AACGGCGGCG  AACACGCCAA  CAACAGCCTG  AACATCCAAG  AGTTTATGAT
501 TATGCCCGTC  GGCGCAAAAT  CTTTCCGCGA  AGCGTTGCGC  TGCGGTGCGG
551 AAATTTTCCA  CGCCTTGAAA  AAACGTGTGC  ACAGTAAAGG  CTTCCCGACC
601 ACAGTCGGCG  ACGAAGGCGG  TTTCCGCCCC  AACCTGAACA  GCCACAAAGA
651 AGCCCTGCAA  CTGATGGTGC  AAGCGGCCGA  AGCCGCCGGC  TACAAGGCGG
701 GCGAAGACGT  ATTATTCGCA  TTGGACTGCG  CGTCCAGCGA  GTTCTACAAA
751 GACGGCAAA  ACCACTTGG  AGCCGAAGGC  CGCTCCTACA  CCAACGCGGA
801 ATTTGCCGAA  TACTTGGAAG  GCTTGGTTAA  CGAATTCCTG  ATTATTTCCA
851 TTGAAGACGG  GATGGACGAA  AACGACTGGG  AAGGCTGGAA  ACTGCTGACC
901 GAAAAATTGG  GCAAAAAAGT  TCAATTGGTC  GGCGACGACT  TGTTCGTAAC
951 CAATCCGAAA  ATTCTTGCCG  AAGGCATCGA  AAAAGGCGTA  GCAAACGCAT
1001 TGCTGGTCAA  AGTCAACCAA  ATCGGTACTT  TAAGCGAAAC  CCTGAAAGCC
1051 GTCGATCTGG  CAAAATGCAA  CCGCTACGCC  AGCGTGATGA  GCCACGCTC
1101 CGGCGAAACC  GAAGACAGTA  CCATTGCCGA  CTTGGCAGTC  GCCACCAACT
1151 GTATGCAGAT  TAAACCGGT  TCTTTGAGCC  GTTCCGACCG  CATGGCGAAA
1201 TACAACCAAC  TGCTGCGTAT  CGAGGAAGAA  TTGGCGGAAG  CCGCCTACTA
1251 CCCCAGCAAA  GCCGCATTCT  ACCAACTGGG  CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

1039

g652-1.pap

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAEAAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEF AE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKQVLV GDDLFTNPK ILAEGIEKGV ANALLVKVNO IGTLSLTLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAYYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCCG GAAATTTTGG ACTCACGCGG
51  CAACCCCACA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTTATTCG GGCAAGGGCG TATTGAAGGC
201 GGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGTGACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGGCG AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGGC AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCGAAAT CTTTCCGCGA AGCGTTGCGC TGCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCGCGACC
601 ACAGTCGCGC ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCCGGC TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGG AAGCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGTAGAGT TCAATTGGTT GCGGACGACT TGTTCGTAAC
951 CAATCCAAAA ATCTTGGCGG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CCGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCAGCAAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pap

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEF AE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKQVLV GDDLFTNPK ILAEGIEKGV ANALLVKVNO IGTLSLTLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLLES GVMGRAAVPSGASTGQKEALELRDGDKSRY S					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLLES GVMGRAAVPSGASTGQKEALELRDGDKSRY S					
	10	20	30	40	50	60
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVI NGGEHANNSLNIQEFMIMPV GAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVI NGGEHANNSLNIQEFMIMPV GAKSFREALR					
	130	140	150	160	170	180

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA					
g652-1	CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEAAEAAGYKAGEDVLFA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFP IISIEDGMDENDWEGWKLLT					
g652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFP IISIEDGMDENDWEGWKLLT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA					
g652-1	EKLGGKVLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKCNRYA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEAAADYPSK					
g652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEAAAYPGK					
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCCG GAAATTTTGG ACTCACGCGG
51  CAACCCACCA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTTATTCG GGCAGGGCGG TATTGAAGGC
201 GGTGCAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGACACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGGCG AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGCGGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GGCACAAAT CTTTCGCGCA AGCGTTGCGC TGCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCGC ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGGCG TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCGCAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGCAAGT CCAACTCGTT GCGGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGAGPM SLPVPMNVI
151 NGGEHANNSL NIOEFMIMPV GAKSFREALR CGAEIFHALK KLDCSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMD E NDWEGWKLLT
301 EKLGGKVLV GDDLFVTNPK ILAEGIEKGV ANALLVKVNQ IGTLSLTKA
351 VDLAKRNRYA SVMSHRSGE EDSTIADLAV ATNCMQIKTG SLSRSDRMAK
401 YNQLLRIEE LAEAADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLLESQVMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLLESQVMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

m652-1      70      80      90      100     110     120
            GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

m652-1      130     140     150     160     170     180
            AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
              130     140     150     160     170     180

m652-1      190     200     210     220     230     240
            CGAEIFHALKKLCDKSGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      CGAEIFHALKKLCDKSGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

m652-1      250     260     270     280     290     300
            LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPFIISIEDGMDENDWEGWKLLT
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPFIISIEDGMDENDWEGWKLLT
              250     260     270     280     290     300

m652-1      310     320     330     340     350     360
            EKLGGRVQLVGDDLFTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1      EKLGGRVQLVGDDLFTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

m652-1      370     380     390     400     410     420
            SVMSHRSGETEDSTIADLAVATNCMIKTGSLRSRDRMAKYNQLLRIEEELAEAAADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMIKTGSLRSRDRMAKYNQLLRIEEELAEAAADYPSK
              370     380     390     400     410     420

m652-1      429
            AAFYQLGKX
a652-1      AAFYQLGKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

g653.seq

```

1   ATGCGCGGcgg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGTtgacggT GATGTGCGCt ttgccccAAG
101 CGGCTtcggc ggctttgcCg gtgaTTTCA TCGGTTGCAG GtcgacgaGG
151 AAaacgTGGC TTTCGGTGCG GCCGGAaacg atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTTCACTTGT TTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgGCGGCG
301 ATAACGTgca tcaACGGAcc gCCTTGcAGG CTTGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTTGTGG GTGGTAGTgG ttACgaaGTc GCAGAatggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

g653.pep

```

1   MAAEPMRME VTYGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMTAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRLVW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

m653.seq

```

1   ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTtgacggT GATGTGCGCt TTGCCCCAAG
101 CGGCTTCGGC GGCTTTCGG GTAATTTTCA TCGGTTGCAG GTCAACGAGG

```

1042

```

151 AAAACGTGGC TTTCGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCACCTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAAG CTTGGGAAGA TGGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTGGG GATATTCGCC GCCGGAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

```

              10      20      30      40      50      60
m653.pep      MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              |||||
g653           MAAEPMRMPEVTYGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              10      20      30      40      50      60

              70      80      90      100     110     120
m653.pep      MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              |||||
g653           MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF
              70      80      90      100     110     120

              130     140     150     160
m653.pep      SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX
              |||||
g653           SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATSPAX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
1  ATGGCGGCGG AACCGATGCG GATGCCGAG GTAACGAAGG GTTTTCCGG
51  ATCATTCTGG ATGGCGTTT TGTTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG
151 AAAACGTGGC TTTCGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCACCTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAAG CTTGGGAAGA TGGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGGATTGG GATATTCGCC GCCGGAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

```

              10      20      30      40      50      60
m653.pep      MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              |||||
a653           MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              10      20      30      40      50      60

              70      80      90      100     110     120
m653.pep      MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              |||||
a653           MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              70      80      90      100     110     120

              130     140     150     160
m653.pep      SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX
              |||||
a653           SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX

```


1043

130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2123>:

```
g656.seq
1  ATGCCGCGTT TCTCCGGTTC GATTCTTCG ATGATTCCA TCGCGCGGAC
51  TTTtggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGc ctTCGACGTT GGAAACGATG
151 TGCATCACAT GGGAGTATTT TTCAATCACC ATTTTGTCCG TGACTTTGAC
201 TTCGCCTGTT TTGCTGATGC GTCCGACATC GTTGCGCCCC AAATCGATAA
251 GCATAACGTG TTCGGCgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACGTcat CGCGTTCGCG GCGGACGAGG ATTTCGGGCG
401 AGGAACCGAC GATGTGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2124; ORF 656.ng>:

```
g656.pep
1  MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIITCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRTS ISGEEPTMWK SPKS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2125>:

```
m656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTCCA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTCGACGTT GGAAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCCG TAACTTTGAC
201 TTCGCCGGTT TTA CTGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATAACGTCTG TGCGTTCGCG TCGGACGAGG ATTTCGGGCG
401 AGGAGCCGAC GATGTGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2126; ORF 656>:

```
m656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPS FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT ITSLRSRRTS ISGEEPTMWK SPKS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m656/g656 91.0% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGA	PESVPAGKVAARMSMLVMPS	FRRPSTLETMCITWEYFSIT			
g656	MPRFSGSISSMISIARTFGA	PESVPAGKVAARMSILVTPS	FKQPSTLETMCITWEYFSIT			
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRP	KSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
g656	ILSVTLTSPVLLMRPTSLRP	KSITCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
	70	80	90	100	110	120
m656.pep	ITSLRSRRTSISGEEPTMWK	SPKSX				
g656	MTSSRSRRTSISGEEPTMWK	SPKSX				
	130	140				

1044

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTGACGTT GGAAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTGTGTCG TAACTTTGAC
201 TTCGCCGTT TTTACTGATG GCGCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTGCGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTTGCGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPS FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP K SINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRTR ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGA	PESVPAGKVAARMSMLVMPS	FRRPSTLETMCITWEYFSIT			
a656.	MPRLLGSTSSMISMARTLGA	PESVPAGKVAARMSMLVMPS	FRRPSTLETMCITWEYFSIT			
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRP	KSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
a656	ILSVTLTSPVLLMRPTSLRP	KSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRP	KSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
a656	ILSVTLTSPVLLMRPTSLRP	KSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
	70	80	90	100	110	120
m656.pep	ITSLRSRRTRISGEEPTMWK	SPKSX				
a656	MTSSRSRRTRISGEEPTMWK	SPKSX				
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
201 GGCAAAATGC GCGGCGGTta cgACCGAATT TGAAAacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTACAGGAA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGT GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattcC ATCGTCcccg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GGCGCAACgc tTGGCGGACG AATTGGATTA TGTCGGCgta
751 TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACACATGAAT TGCTCGTCAA
801 TGAAACCGCC CCGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCGAGA CAGTTCCAA CAGCAGGTAC GCATTATGTG CAACctGCCG
901 cccGccgACA CCAAATTATT aTCCCcttgC TGTATGGCGA ATATTTTGGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGCGCGAA TGCACACCTG CACCTATACG GAAAAAAAAC CGCAGAGAAA
1051 GGTCGGAAAA TGGGACACTT TaccgTTTTG ACCACCGATT CGGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657.ppep

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GVDGKGQIRV	KTLDLKAFF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQARQTAQR	LADELGYVGV

1046

251 LAVEMFVVG D THELVNETA PRTHNSGHHT IDACAADQFQ QQVRIMCNLP
 301 PADTKLLSP C MANILGDVW QEDGGE PDWL PLQSRPNAHL HLYGKKTAQK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2131>:

m657.seq
 1 ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGGCA TCCTCGGCGG
 51 CGGACAATTA GGCAGAATGT TTACCGTTGC CGCCAAAACC ATGGGCTACA
 101 AAGTAACCGT TCTCGACCCC GATCCGGACG CGCCGGCAGC AGAATTTGCC
 151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT
 201 GGCAAAATGC GCGGCGGTGA CCACTGAATT TGAAAACGTC AATGCGGATG
 251 CGATGCGCTT TTTGGCAAAA CATACCAATG TTTCCCTAG CGGCGATTGT
 301 GTGGCGATTG CACAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAAGC
 351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA
 401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
 451 GGCTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAACTCAA
 501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
 551 TGGATTGCG CAGTGAAATT TCCGTAATCG TATGCCGTTT GAACAATGAC
 601 AACGTGCAAA CTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT
 651 GGCTTATTCC ATCGTCCCCG CGCGACTGAG TGCCGACGTG CAGCAACAGG
 701 CGCGGCAGAT GCGCAACGC TTGGCGGACG AATTGGATTA TGTGCGCGTA
 751 TTGGCGGTAG AAATGTTTGT TGTGCGTGAC ACGCATGAAT TGGTCGTCAA
 801 CGAAATCGCC CCGCGCCCGC ACAATTCGG ACACCATACG ATAGATGCCT
 851 GCGCAGCAGA CCAGTTCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG
 901 CCTGCCGATA CCAAATTACT GAGTTCTTGC TGTATGGCAA ATATTTTGGG
 951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGCTG CCCTTGCAAA
 1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
 1051 GGGCGGAAAA TGGGACACTT TACCGTTTTA ACCACCGATT CGGACACCGC
 1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657.pep
 1 MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDAPAAEFA
 51 DRHLCAPFND QAALDELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
 101 VAIAQNRIQE KAWIRKAGLQ TAPYQVCKA EDITEASAQF LPGILKTATL
 151 GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRSEI SVIVCRLNND
 201 NVQTFDPAEN IHENGILAYS IVPARLSADV QQARQMAQR LADEL DYGV
 251 LAVEMFVVG D THELVNEIA PRPHNSGHHT IDACAADQFQ QQVRIMCNLP
 301 PADTKLLSS C MANILGDVW QEDGGE PDWL PLQSHNAHL HLYGKKTAHK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m657/g657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	DPDAPAAEFA	DRHLCAPFND
g657	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA	DRHLCAPFDD
	70	80	90	100	110	120
m657.pep	QAALDELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC	VAIAQNRIQE	KAWIRKAGLQ
g657	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC	VSIAQNRIQE	KAWIRKAGLQ
	130	140	150	160	170	180
m657.pep	TAPYQVCKA	EDITEASAQF	LPGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL
g657	TAPYQAVCKA	EDITEASAQF	LPGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR					
	: : : : : :					
g657	EKMVDLRGEISVIVCRLNNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGLAVEMFVVGDTHEL VVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
	: : : : : :					
g657	LADEL DYVGLAVEMFVVGDTHELLVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAHKGRKMGHFTVL					
	: : : : : :					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAQKGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSLX					
	: : : : :					
g657	TTDSDTAFQEAKKLHQSLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGCGCG
51  CGGACAATTA GGCAGAATGT TTACTGTTGC TGCCAAAACC ATGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATTACAGGA AAGGCATGGA TACGCAAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCAGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAACTCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTGG GAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGTCT GAACAATGAC
601 AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATTCACGAAA ACGGTATCCT
651 CGCCTACTCC ATCGTCCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GGCGCAGCGT TTGGCCGATG AATTGAACTA CGTCGGCGTA
751 TTGGCGGTAG AAATGTTTGT TGTGCGCGAC ACGCATGAAT TGGTCGTCAA
801 CGAAATCGCG CCGCGTCCGC ACAATTCCGG CCACCATACC GTCGACGCT
851 GCGCGGCAGA CCAATTCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGCTGACA CCAAATGCT GAGTTCTTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCCGCGCGGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTAL EELAK AAVTTEFENV NADAMRFLAK HTNVSPSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESI QF LPGILKTATL
151 GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQQARQMAQR LADELNYVGV
251 LAVEMFVVGDT HELVVNEIA PRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGEPDWF PLQSRPDAHL HLYGKKTAHK
351 GRKMGHFTIL STDSDTAFQE AKKLHQSL*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPAPAAEFADRHLCA PFND					

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```

|||||
a657      MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCAFPDN
           10      20      30      40      50      60

           70      80      90      100     110     120
m657.pep  QAALDELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
           |||||
a657      QTALEELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
           70      80      90      100     110     120

           130     140     150     160     170     180
m657.pep  TAPYQVVCKAEDITEASAQFLPGILKTATLGVDGKGQIRVKTLDLKAFAEHGGVDCVL
           |||||
a657      TAPYQAICKAEDITEESIQLFLPGILKTATLGVDGKGQIRVKTVDLKAFAEHRGVDCVL
           130     140     150     160     170     180

           190     200     210     220     230     240
m657.pep  EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR
           |||||
a657      EKMVDLRGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQQARQMAQR
           190     200     210     220     230     240

           250     260     270     280     290     300
m657.pep  LADEL DYVGLAVEMFVVGDTHEL VVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP
           |||||
a657      LADEL NYVGLAVEMFVVGDTHEL VVNEIAPRPHNSGHHTVDACAADQFQQQVRLMCNLP
           250     260     270     280     290     300

           310     320     330     340     350     360
m657.pep  PADTKLLSSCCMANILGDVWQEDGGE PDWLP LQSHPN AHLHL YGKKT AHKGR KMGHFTVL
           |||||
a657      PADTKLLSSCCMANILGDVWQEDGGE PDWFP LQSRPD AHLHL YGKKT AHKGR KMGHFTIL
           310     320     330     340     350     360

           370     379
m657.pep  TTDSDTAFQEAKKLHQSLX
           :|||||
a657      STDSDTAFQEAKKLHQSLX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2135>:

```

g658.seq
1  ATGGTGGCCG GAATTGTGCG TGC GCGGGGCG GGTTCATTG ACGAGCAATT
51  CATGTGTGTC GCCGACAACA AACATTCTA CCGCCAAtac GCCGACATAA
101 TCCAATTTCGT CCGCCAagcG TTGCGCCGTC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGCCGCGcgg gGACGATGga atAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCGGGG TCGAAGGTTT GCACGTTTTC ATCGTTCAGA
251 CGGCATACGA TCACGGAAAT CTCGCCGCGC AAGTCCACCA TTTTTTCCAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTTG AGTTTCGTCCA
351 ACGTTTTGAC GCGGATTTGA CCTTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGCACAAAA TTGCGCGCTT GCTTCAGTAA TGTCTTCGGC
451 CTTGCAAAACC GCCTGATACG GCGCGGTTT CAAGCCTGCT TTGCGTATCC
501 ACGCTTTTTT CTGAATGCGG TTTTGTGCAA TGGACACGCA GTCGCGCTG
551 GGGGAAACGT TGGTATGCTT TGCCAGAGAG CGCATCGCGT CGGCAttgac
601 gtTTTCAAAT TCGGTcgtaA CCGCCGCGCA TTTTGCCAAT TCGTCCAACG
651 CGGCCCGGTC GTCAAACGGC GCGCACAAAT GCGGTCGGC AAATTCGGCC
701 GCCGGCGCAT TCGGGTCGGG ATCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTAGCGGCA ACGGCAACA TTctgcctAA

```

This corresponds to the amino acid sequence <SEQ ID 2136; ORF 658.ng>:

```

g658.pep
1  MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRRLPRLLLL
51  VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAQVHHFFQ

```

1049

```

101 NAIHAAVFGK RGFEFVQRF ADLTFVVAQ RSRFQDAGQK LRACFSNVFG
151 LANRLIRRL QACFAYPRFF LNAVLCNGHA VAAGGNVGM L CQRAHRVGID
201 VFKFGRNRR FCQFVQRPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG
251 FSGNGKHS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```

m658.seq
  1 ATGGTGTCCG GAATTGTGCG GGCGCGGGGC GATTCGTTG ACACCAATT
 51 CATGCGTGTC ACCGACAACA AACATTCTA CCGCAATAC GCCGACATAA
101 TCCAATTCGT CCGCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTTGTC ATTGTTCAAA
251 CGGCATACGA TTACGGAAAT TTTACTGCGC AAATCCACCA TTTTTCCTAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAA CGCGGCTTTG AGTTCATCCA
351 ATGTTTTTAC GCGGATTGTA CCTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGGCAAAA TTGCGCGCTT GCTTCAGTGA TGTCTCAGC
451 CTTACAAACC ACTTGATACG GCGCGGTTTG CAATCCCGCT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTTGTGCAA TCGCCACACA ATCGCCGCTA
551 GGGGAAACAT TGGTATGTTT TGCCAAAAG CGCATCGCAT CGGCATTGAC
601 GTTTTTCAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCCAAAG
651 CAGCTTGGTC GTTAAACGGC GCGCACAAAT GGCGGTCGGC AAATCTGCT
701 GCCGGCGCGT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTTGGCGGCA ACGGTAAACA TTCTGCCTAA
```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```

m658.pep
  1 MVSGIVRARG DFVDDQFMRV TDNKHFYRQY ADIIQFVRQA LRHLPRLLLH
 51 VGTQSRGDDG ISQDAVFVDV FGRVESLHV IVQTAYDYG N FTAQIHFFQ
101 NAIHAAVFGK RGFEFIQCFY ADLTFVVAQ RSRFQDAGQK LRACFSNVFG
151 LTNHLIRRL QSRFAYPCF LNAVLCNRHT IAARGNIGMF CQKAHRIGID
201 VFKFSGHRR FCQFVQSSLV VKRRAQMAVG KFCCRRVRIG VENG YFVAHG
251 FGGNGKHS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

```

m658.pep      10      20      30      40      50      60
MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLHVGTQSRGDDG
||:||||| |:|:| |:|||||||||||||||||:||||| ||||
g658          10      20      30      40      50      60
MVAGIVRARGGFIDEQFMCVADNKHFYRQYADIIQFVRQALRRLPRLLLHVGTQPRGDDG

m658.pep      70      80      90      100     110     120
ISQDAVFVDVDFGRVESLHVIVQTAYDYG NFTAQIHFFQNAIHAAVFGKRGFEFIQCFY
||||| |:|:| |:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|
g658          70      80      90      100     110     120
ISQDAVFVDVDFGGVEGLHVFIQTAYDHGNLAAQVHHFFQNAIHAAVFGKRGFEFVQRF

m658.pep     130     140     150     160     170     180
ADLTFVVAQRSRFQDAGQKLRACFSDFSLTNHLIRRLQSRFAYPCFLNAVLCNRHT
||||| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
g658         130     140     150     160     170     180
ADLTFVVAQRSRFQDAGQKLRACFSNVFGLANRLIRRLQACFAYPRFFLNAVLCNGHA

m658.pep     190     200     210     220     230     240
IAARGNIGMFCQKAHRIGIDVFKFSGHRR AFCQFVQSSLVVKRRAQMAVGKFCCRRVRIG
:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
g658         190     200     210     220     230     240
VAAGGNVGM LQRAHRVGIDVFKFGRNRR AFCQFVQRPVVKRRAQMAVGKFRRRRIRVG

m658.pep     250     260
VENGYFVAHGFGGNGKHSAX
```

1050

```

          :|||||:|||||
g658      IENGYFVAHGFSNGKHSAX
          250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

```

a658.seq
1  ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTTCGTTG ACGACCAATT
51  CATGCGTGTC GCCGACAACA AACATTCTA CCGCCAATAC GCCGACGTAG
101 TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT
151 GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT
201 CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTTGTC ATTGTTTCTG
251 CGGCATACGA TAACGGAAAT TTCGCGGCGC AAGTCCACCA TTTTTCCTCA
301 AACGCAATCC ACGCCGCGGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 CCGTTTTGAC GCGGATTTGG CCTTTGCCGT CATAGCCCAA TGTCGCGGTT
401 TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC
451 TTTGCAAATT GCTTGATACG GCGCGGTTTG CAGGCCTGCT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTTGCGCGA TGGCAACGCA GTCGCGCGTG
551 GGGGAAACAT TGGTATGTTT GGCGAGAAAA CGCATCGCAT CGGCATTGAC
601 GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAAT TCTTCCAAAG
651 CGGTTTGGTT GTCAAACGGC GCACACAAAT GGCGGTCGGC AAATTCGCGT
701 GCCGGCGCAT TCGGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT
751 TTTGGCAGCA ACAGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

```

a658.pep
1  MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGQT LRHLSRLLLN
51  VGTQSGWDDG VGEDTVFVNV FGRIESLHV IVQTAYDNGN FAAQVHFFQ
101 NAIHAAVFGK RGFEFIHRFD ADLAFVIAQ CSGFDAGQK LYAFFSDVFG
151 FANCLIRRLG QACFAYPCLF LNAVLRDNGA VAAGGNIGMF GEKTHRIGID
201 VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFCRRIRVG IEYGYFVAHG
251 FGSNSKHSAX*

```

m658/a658 75.3% identity in 259 aa overlap

```

          10      20      30      40      50      60
m658.pep  MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLVGTQSRGDDG
          ||:||||:| |||||:|||||:|||||:|||||:|||||:|||||:|||||
a658      MVAGIVRTRRDFVDDQFMRVADNKHFYRQYADVQFIGQTLRHLRLLLVGTQSGWDDG
          10      20      30      40      50      60

          70      80      90      100     110     120
m658.pep  ISQDAVFVDVFGRVESLHVIVQTAYDYGNFQAIIHFFQNAIHAAVFGKRGFEFIQCFY
          ::||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a658      VGEDTVFVNVFGRIESLHVIVQTAYDNGNFAAQVHFFQNAIHAAVFGKRGFEFIHRFD
          70      80      90      100     110     120

          130     140     150     160     170     180
m658.pep  ADLTFVAVQSRFQDAGQKLRACFSDVFSLTNHLIRRLGLQSRFAYPCLFLNAVLCNRHT
          |||:||||:| | ||||| | |||||:| | |||||: |||||: ||||| : ::
a658      ADLAFVIAQCSGFQDAGQKLYAFFSDVFGFANCLIRRLGLQACFAYPCLFLNAVLRDNGA
          130     140     150     160     170     180

          190     200     210     220     230     240
m658.pep  IAARGNIGMFCQKAHRIGIDVFKFSGHRRAFQCFVQSSLVVKRRRAQMAVGKFCRRVRIG
          :|| ||||| :||:|||||:|:| : |:||| ||:|||||:||||| |||:|:|
a658      VAAGGNIGMFEKTHRIGIDVFELGRNSRTFCQFFQSGLVVKRRTQMAVGKFCRRIRVG
          190     200     210     220     230     240

          250     260
m658.pep  VENGYFVAHGFGNGKHSAX
          :| |||||:|:|
a658      IEYGYFVAHGFGSNSKHSAX
          250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

g661.seq
 1 ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51 GGCGGGCATT GCCGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
 151 ACCGGAAAAA CCTtgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
 201 TGCCGTGCAG ATTGCCGGCA GCGACCCga acaGATGGCG Gatgcggcgc
 251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
 301 cccgccaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
 351 CGAGccgctg gttgcCgcca tTTtggaggc ggtggtcAAG GCGGCGGcg
 401 TACCCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
 451 ctgcCcgccg tcgccaaaat cgccgaagat tgcggcattg ccgccCttgc
 501 cgttccacgg gcgCGCgcgc ACGCAAATGT ACAAAGGCGA GGCgcGTTAC
 551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
 601 CGGCGACATC actTCgccc AAAAAAGCCGC GccgTCCTC AAACAAACCG
 651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
 701 TTCCGCGATT TGAAGCATTA TGCCGAACAC GGCGTTTAC CGCCTGCCTT
 751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACACATC CGCGCCATGC
 801 ACGCGTTTTA TGGTGAAGACC GTCGGTGTGC GCATCGCAGC CAAACACATA
 851 GGCTGGTACA TCGGCGAAAT GCCCGACGGC GAACAGGCGC GCGGTGA

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

g661.pep
 1 MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
 51 TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
 101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDHQQN
 151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
 201 RRHFFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPREFAL CRTRRFACL
 251 EFGRMQSRHF EPHPRHARVL WXDRCARHT QTHRLVHRRN ARRRTGAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

m661.seq
 1 ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51 GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
 151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
 201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
 251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
 301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
 351 CGAGCCGCTG GTTGCCGCCA TTTTGGGAAG CGTCGTCCGT GCGGCAGGCG
 401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
 451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC
 501 CGTCC.ACGG ACGCACGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
 551 GAACATCATC CGGAAACCAA ATGCCGCTG AACATCCCGG TCTGGGTCAA
 601 CGGCGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG
 651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
 701 TTCCGCGATT TGAAACATTA TGCCGAACAC GGTGTTTTC GCCTGCCTT
 751 GAGTTTGGCA GAATGCGCCG CCGCTATTTT GAACACATC CGCGCCATAC
 801 ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCAGC CAAACACATA
 851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

m661.pep
 1 MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
 51 TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
 101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDHQQN
 151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
 201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPREFETL CRTRCFACL
 251 EFGRMRRRYF EPHPRHTRVL RRHRCARHT QTHRLVHRRN ARRRDTS*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
g661	MHIGGYFIDNPIALAPMAGIADKPFRRLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
g661	ADEGGIVAVQIAGSDPEQMADAARYNVGLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
g661	VAAILEAVVKAAGVPVTLKTRLGWHDDQNLPVAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHDRARRARQAVVLPFRFETL					
g661	GALRTHRRDQKPSEHPGLGQRRHHFAAKSRRRPQTNRRRRHDRARRARQAVVFPRFEAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
g661	CRTRRFTACLEFGRMQSRHFEPHPRHARVLWXDRRCARHTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGCGGCATT ACCGACAAAC CGTTCGCCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGGAGGC GGTGGTCAAA GCGGCGGGCG
401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCACGCGC ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CCGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAAACATTA CGCCGAACAC GGTGTTTAC CGCCTGCCTT
751 GAGTTTGGCA GAATGTACCG CCACTATTTT GAACCACATC CGAGCCATGC
801 ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQQMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRHYLAAKSP SRPQTNRRRR HYDRARRARQ TVVLPFRFETL RRTRCFTACL
251 EFGRMYRHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					

1053

```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10          20          30          40          50          60

           70          80          90          100         110         120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70          80          90          100         110         120

           130         140         150         160         170         180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||||:|||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130         140         150         160         170         180

           190         200         210         220         230         240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPFRFETL
           |:|:|
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPFRFETL
           190         200         210         220         230         240

           250         260         270         280         290         299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           |||||:||||| |:||||| |:|||||
a661      RRTRCFTACLEFGRMYRHYFEPHPSHARVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           250         260         270         280         290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGtctGC CAAATGCCTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAA gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggctg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTTCGGAC GCAACAATTC GGTTTTTGTG
601 GATTTTTTCG GCATtcagac GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAG TGATACCCGC CATTCCCGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTTGGAAATC CTTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTTA TCGAAGAACG
801 CGTGCGCGAA CACCCGGAAC AATATTTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLQFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVIIILPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNNNSVFN
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPIV READNTVTLO FYPAWSFSPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK REKTRPEGSP DFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTTGAAACA

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1054

```

201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TGCCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTG GGTTTTTGTG
601 GATTTTTTTCG GTATTCAGAC GGCAACGATT ACCGATTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGAAATC CTTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCGTTTTA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTTG GCTGCACAAG CGTTTTAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
  1 MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
 51 KCFSEWSEEK RKTVLKQHFK HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIIILYPHFT AFEMAVYALN QDIPLISMSY HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFF
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PVREADNTVTLH FYPAWSFPG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

	10	20	30	40	50	60
m663.pep	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKP RRRIGEINLAKCFSEWSEEK					
g663	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKP RRRIGEINLAKCFPEWDEEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m663.pep	RKTVLKQHFKHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH YLDDALAAGEKVIIILYPHFT					
g663	RKTVLKQHFKHMAKLMLEYGLYWYASAKCLKSLVRYRNKH YLDDALAAGEKVIIILYPHFT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m663.pep	AFEMAVYALNQDIPLISMSYHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS					
g663	AFEMAVYALNQDVPLISMSYHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m663.pep	SAPFLYLPDQDFGRNDSVFFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVTLH					
g663	SAPFLYLPDQDFGRNNSVFFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVTLQ					
	190	200	210	220	230	240
	250	260	270	280	290	
m663.pep	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
g663	FYPAWSFPSDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
  1 ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAATT
 51 TCTGCCGTTT GCGCTGCTGC ACAAACTTGC TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCGCCGTA TCGGCGAAAT CAATTTGGCA

```

1055

```

151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAACCG TGTTGAAACA
201 GCATTTCAAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATGGT
251 ACGCGCCCGC CGGGCGTTTG AAATCACTGG TCGCTACCG CAACAAACAT
301 TATTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACITCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCGATCAG GATTTCGGAC GCAACGATTG GGTTTTGTG
601 GATTTCCTCG GTATTTCGGAC GGCAACGATT ACCGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCGT CTTGGGAATC CTTTCCGAGT
751 GAAGATGCGC AGGCCGACGC GCAGCGCATG AACCGTTTGA TCGAGGAACG
801 CGTGCGCGAA CATCCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

a663.pep

```

1 MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51 KCFPEWDGKK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNRDSVFV
201 DFFGIRTATI TGLSRIAALA NAKVIPAI PV READNTVTLH FYPAWESFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

m663/a663 96.2% identity in 293 aa overlap

	10	20	30	40	50	60
m663.pep	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP	RRRIGEINLAKCFSEWSEEK				
a663	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP	RRRIGEINLAKCFPEWDGKK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m663.pep	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
a663	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
	70	80	90	100	110	120
	130	140	150	160	170	180
m663.pep	AFEMAVYALNQDIPISMYSHQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
a663	AFEMAVYALNQDVPLISMYSHQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
	130	140	150	160	170	180
	190	200	210	220	230	240
m663.pep	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAAL	ANAKVIPAI PV READNTVTLH				
a663	SAPFLYLPDQDFGRNDSVFVDFFGIRTATITGLSRIAAL	ANAKVIPAI PV READNTVTLH				
	190	200	210	220	230	240
	250	260	270	280	290	
m663.pep	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHK	RFKTRPEGSPDFYX				
a663	FYPAWESFSEDAQADAQRMNRFIEERVREHPEQYFWLHK	RFKTRPEGSPDFYX				
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

g664.seq

```

1 ATGATACATC CGCACCACTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51 AGAAATTGTT CATCTCCTCA TAGCTGAagg gGCGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTTCCGGGAA CTGGTCTTGG CGCAGCAGGC GGATGTCTTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGGAAAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGAAA TATTCTGTGC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT TGTTTCCAT CGCGCCATA
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCcaa
451 cCgaagcgc gtttcgtcCc acttcategC gtTTTTTCAA cgaTTCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT

```

551 GA

This corresponds to the amino acid sequence <SEQ ID 2154; ORF 664.ng>:

g664.pep

```

1  MIHPHHFRAF FINGHGVEIV HLLIADGAHR MGGRACVFGE LVLAQQADVL
51  DAAHGAAGAV AGKLLVAEHG QPFLQRKLEP VAAGYAVARP VVEIFVSDHG
101 FNAFEIGIGG GAAVGEDELG VKNVQTLVFH RAHIEIAYGD DHENIQVIFQ
151 PEARFVPLHR VFSTIPRQSR PWVCPLRWCK TRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

m664.seq

```

1  GTGATACATC CGCACTACTT CCGCGCCTTT TTCATAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TAGCTGGCGG GCGCACCCG ATGGGCGGTC
101 GGGCCTGCGT CTTCGGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTT
151 GATGCGGCGC ACGGCGCGGC TGGCGCGGTC GCCGAAAAT TCTTGCTCGC
201 GGAAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGAAA TACTCGTGTG CGACCACGGA
301 TTCGATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCCAT CGCGCCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ATTTTCATCGC GTTTTT.CAA CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGAAA ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:

m664.pep

```

1  VIHPHYFRAF FINGHGVEIV HLLIAGGAHR MGGRACVFGE LVLAQQADVF
51  DAAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGYAVARP VVEILVSDHG
101 FDAFEIGIGG GAAVGKDELG VKDVQTLVFH RAHIEIAHGD DHENIQVVFQ
151 TEARFVPFHR VFXTIPRQSR PWACPLRWCK TRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFF	FINGHGVEIV	HLLIAGGAHR	MGGRACVFGE	LVLAQQADVF	DAAHGAAGAV
	:	:	:	:	:	:
g664	MIHPHHFRAFF	FINGHGVEIV	HLLIADGAHR	MGGRACVFGE	LVLAQQADVL	DAAHGAAGAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m664.pep	AGKFLVAEHG	QPFLQRKLEP	VAAGYAVARP	VVEILVSDHG	FDAFEIGIGG	GAAVGKDELG
	:	:	:	:	:	:
g664	AGKLLVAEHG	QPFLQRKLEP	VAAGYAVARP	VVEIFVSDHG	FNAFEIGIGG	GAAVGEDELG
	70	80	90	100	110	120
	130	140	150	160	170	180
m664.pep	VKDVQTLVFH	RAHIEIAHGD	DHENIQVVFQ	TEARFVPFHR	VFXTIPRQSR	PWACPLRWCK
	:	:	:	:	:	:
g664	VKNVQTLVFH	RAHIEIAYGD	DHENIQVIFQ	PEARFVPLHR	VFSTIPRQSR	PWVCPLRWCK
	130	140	150	160	170	180
m664.pep	TRFX					
g664	TRFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

a664.seq

```

1  GTGATACATC CGCACCCTT CCGCGCCTTT TTCATAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TATCGGGCGG GCGCACCCG ATGTGCGGTC
101 GGACCTGCGT CTTCGGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTT
151 GATACGGCGC ACGGCGCGGC TGGCGCGGTC GCCGAAAAT TCTTGCTCGC

```

1057

```

201 GGAACACGGT CAACCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCCAT CGACCCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CTTGGGGCTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
1  VIHPHHFRAF  FINGHGVEIV  HLLISGGAHR  MCGRTCVFGE  LVLAQQADV
51  DTAHGAAGAV  AGKFLVAEHG  QPFLQRKLEP  VAAGHAVARP  VVEIFVSDHG
101 FDAFKIGIGG  GTAVGKDELG  VKDVQTLVFH  RTHIEIAHGD  DHENIQVVFQ
151 TEARFVPLHC  VFXAIPRQSR  PWACPLRWCK  TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

          10      20      30      40      50      60
m664.pep  VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGGRCVFGELVLAQQADVDAHGAAGAV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664       VIHPHHFRAFFINGHGVEIVHLLISGGAHRMCGRTCVFGEVLAQQADVDTAHGAAGAV
          10      20      30      40      50      60

          70      80      90     100     110     120
m664.pep  AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVGKDELG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664       AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
          70      80      90     100     110     120

          130     140     150     160     170     180
m664.pep  VKDVQTLVFHRAHIEIAHGDHENIQVVFQTEARFVPFHRVFXTPRQSRPWACPLRWCK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664       VKDVQTLVFHRTHIEIAHGDHENIQVVFQTEARFVPLHCVFXAIPRQSRPWACPLRWCK
          130     140     150     160     170     180

m664.pep  TRFX
          ||||
a664      TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
1  atgaagtGg  acgaaacgcg  cttcgGggtg  GAAtatgact  tggatatTTT
51  CATGGTCGTC  GCCGTAGGCG  ATTTCAATAT  GGGCGCGATG  GAAAACAAGG
101 GTTTGAACAT  TTTTAACACC  AAGTTCGTCC  TCGCCGACAG  CCGCACCGCC
151 ACCGATACCG  ATTTCAAGG  CATTGAATCC  GTGGTCGGAC  ACGAATATTT
201 CCACAACCTGG  ACGGGCAACC  GCGTAACCTG  CCGCGACTGG  TTCCAGCTTT
251 CGCTGAAGGA  AGGGCTGACC  GTGTTCCGCG  ACCAAGAGTT  TTCCGGCGAC
301 CGCGCCGGCC  GCGCCGTGCG  CCGCATCGAG  AACATCCGCC  TGCTGCGCCA
351 GAACCAAGTTC  CCCGAAGACG  CAGGCCCGAC  CGCCCATCCG  GTGCGCcccg
401 TCAGCTATGA  GGAGATGAAC  AATTTCTACA  CCATGACCGT  TTATGAAAAA
451 GCGCGCGAAG  TGGTGCGGAT  GTATCATACC  CTGCTCGGCG  AAGAGGGCTT
501 CCAAAAAGGC  ATGAAGCTAT  ATTTcCaacg  CCACGACGGA  CAGGCAGTGA
551 CCTGCGACGA  TTTCCGCGCG  GCGatggcgg  ATGCGAACGG  CATCAATCTC
601 GACCAGTTCG  CCTTGTGGTA  CAGCCAGGCG  GGCACGCCCG  TTTTGGGAAGC
651 CGAAGGCCGT  CTGAAAAACA  ATGTTTTCGA  GTTAACCATT  AAACAAACCG
701 TGCCGCCCAC  GCCGATATG  GCGGACAAAC  AGCCGATGAT  GATTCCCGTC
751 AAAGTCGGGC  TTCTGAACCG  CAACGGCGAA  GCGGTGGCAT  TCGATTATCA
801 GGGCAAACGC  GCAACCGAAG  CCGTGTGCT  GATGACCGAA  GCCGAACagg
851 CCTTCCCGCT  CGAAGGTGTA  ACCGAAGCCG  TCGTTCCTC  GCTGCTGCGC
901 GGGTTACGCG  CGCCAGTGTA  TCTGAACTAT  CCGTACAGCG  ACGACGACCT
951 GCTGCTCCTG  CTCGCCACG  .ACAGCGACGC  TTTCACGTGC  TGGGAAGCCG

```

```

1001 CCCC AACGCT CTACCGTCGC GCCGTGCGCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTGCGCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAa ctGTGGGACG GCACGGAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctgcCG AAATGGCAGC AATTGGaccg tcaggcgggcg aagCAGgaaa
1301 accaaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGTCTGCC GCGCCTTcgt cctGCGCGCC GACCCCGCGC acatcgAAAC
1401 TGTTGCGGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTC AAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGAaa gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCC CTTATCGGCT CAAGccgccc cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCACACAA
1651 GCGCGTTTCG TCATCGGCAG CTTAGCCGCG AACGTCCGCG ATTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cCCGCAggtc gccGCCGCG TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGCATTTCG GCGCAGGAAG GATTGTCGAA AGacGTGGGC GAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

```

g665.pep
  1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VRPVSYEEMN NFYTMVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNVFELTI KQTVPPPTDM ADKQPMMPV
251 KVGLLLNRNGE AVAFDYQGR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYLYN PYSDDDLLLL LAHDSDAFTC WEAQAOTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDLLDNFKA LLLGVPSAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDROQA KQENQSYEYS PETADWRTL
451 NVCRAFVLRA DPAHIETVAE KYGEMAQNMT HEWGILSAVN GNESDTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLNPNK
551 ARSLIGSFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

```

m665.seq
  1 ATGAAATGGG ACGAAACGCG CTTGCGTTTG GAATACGACT TGGATATTTT
 51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCTGAAG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACCTG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCAAGTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCCCCG
401 CCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GCGCGGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCCGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCAAGTTC CCTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCAC GCGCGATATG ACGGATAAAC AGCCGATGAT GATTTCCGTC
751 AAGTTCGGG TGCTGAACCG CAACGCGGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTTCCT GCTGACCGAA GCCGAACAGA
851 CCTTCCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCAACAGCT CTACCGCCG GCCGTCGCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCGG AAATGGCAGC AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CACGCTGCGC

```


1059

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1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTCGGCT CAAGCCGCGC CAGCGACACC CTGCAACAGG
1601 TTGGAACCGC CTGTCAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
1651 GCCCGTTTCG TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGCAGGTC GCCGCCCGCT TAGTGCAAGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTGCGA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNIFELTV KQTVPPPTDM TDKQPMMPV
251 KVGLLNRNGE AVAFDYQGKR ATEAVLLLTE AEQTFLLLEGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLNDNAFKA LLLGVPEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQAAA KQENQSYEYS PEAAGWRTL
451 NVCRAFLRA DPAHIETVAE KYGEMAQNM T HEWGILSAVN GNESDTRNRL
501 LAQFADKFS DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSR NVPFHAEDEG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQRIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

	10	20	30	40	50	60
m665.pep	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRTATDTDFEGIES					
g665	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRTATDTDFEGIES					
	10	20	30	40	50	60
m665.pep	VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIE NIRLLRQHOF					
g665	VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIE NIRLLRQHF					
	70	80	90	100	110	120
m665.pep	VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIE NIRLLRQHOF					
g665	VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIE NIRLLRQHF					
	70	80	90	100	110	120
m665.pep	PEDAGPTAHPVRPASYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG					
g665	PEDAGPTAHPVRPVSYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG					
	130	140	150	160	170	180
m665.pep	PEDAGPTAHPVRPASYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG					
g665	PEDAGPTAHPVRPVSYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG					
	130	140	150	160	170	180
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPPTDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPPPTDM					
	190	200	210	220	230	240
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPPTDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPPPTDM					
	190	200	210	220	230	240
m665.pep	TDKQPMMPV KVGLLNRNGE AVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLR					
g665	ADKQPMMPV KVGLLNRNGE AVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300
m665.pep	TDKQPMMPV KVGLLNRNGE AVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLR					
g665	ADKQPMMPV KVGLLNRNGE AVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

1060

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLHSDAFTRWEEAQTLYRRVAANLATLSDGVLPKHEK					
	: : : : : :					
g665	GFSAPVYLNYPYSDDDLLLHSDAFTCWEEAQTLYRRVAANLAALSDGIGLPKHEK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
	: : : : : :					
g665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNQAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
	: : : : : :					
g665	KWHELDQAAKQENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQH					
	: : : : : :					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFNRNVPFHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	: : : : : :					
g665	PKFSLENPNKARSLIGSFNRNVPFHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILDX					
	: : : : :					
g665	CNKLEPHRKNLVKQELQCIHQEGLSKDVGEIVGKILGX					
	610	620	630			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

```

a665.seq
1  ATGAAGTGGG  ACGAAACGCG  CTCGGTGTG  GAATACGACT  TGGATATTTT
51  CATGGTCGTC  GCCGTGGGCG  ATTTCAATAT  GGGTGCGATG  GAAAACAAGG
101  GTTTGAACAT  CTTTAACACC  AAGTTCGTCC  TTGCCGACAG  CCGTACCGCC
151  ACCGATACCG  ATTTGAAGG  CATCGAATCC  GTGGTCGGAC  ACGAATATTT
201  CCACAACCTG  ACGGGCAACC  GCGTGACCTG  CCGCGACTGG  TTCCAGCTTT
251  CGCTGAAGGA  AGGGTTGACC  GTGTTCCGCG  ACCAAGAATT  TTCCGGCGAC
301  CGCGCCAGCC  GCGCCGTGCG  CCGTATCGAA  AACATCCGCC  TGCTGCGCCA
351  GCACCACTTC  CCCGAAGACG  CAGGTCCGAC  CGCACATCCG  GTGCGCCCCG
401  CCCGATATGA  GGAGATGAAC  AATTTCTACA  CCATGACCGT  TTATGAAAAA
451  GGCGCGGAAG  TGGTGCGGAT  GTATCACACC  TTGCTCGGCG  AAGAGGGCTT
501  CCAAAAAGGT  ATGAAGCTCT  ATTTCCAACG  CCACGACGGA  CAGGCTGTTA
551  CCTGCGACGA  TTTCCGCGCG  GCGATGGTGG  ACGCGAACGG  CATCAACCTC
601  GACCAATTCT  CCTGTGGTGA  CAGCCAAGCA  GGTACGCCGG  TTTTAGATGC
651  TCAAGGGCGT  CTGAAAAACA  ATGTGTTTGA  GTTAACCATC  AAACAAACCG
701  TGCCGCCAC  GCCGATATG  GCGGACAAAC  AGCCGATGAT  GATTCCTGTC
751  AAAATCGGGC  TGCTGAACCT  CAACGCGGAA  GCGGTGGCAT  TTGATTATCA
801  GGGCAAACGC  GCGACCGAAG  CCGTGTGCT  GCTGACCGAA  GCCGAACAGA
851  CCTTCCAGTT  CGAAAGCGTA  ACCGAAGCCG  TCGTTCCCTC  GCTGCTGCGC
901  GGGTTCAGCG  CGCGGTGCA  TCTGAACAT  CCGTACAGCG  ACGACGACCT
951  GCTGCTTCTG  CTCGCCCATG  ACAGCGACGC  CTTACAGCGC  TGGGAAGCCG
1001  CACAAACGCT  CTACCGCCGT  GCCGTGCGCG  CCAACCTTGC  CGCGCTTTCA
1051  GACGGCGTCG  AGTTGCCGAA  ACACGAAAAA  CTGCTTGCCG  CCGTCGAAAA
1101  AGTCATTTCA  GACGACCTCT  TAGACAACGC  TTTCAAAGCC  CTGCTTTTGG
1151  GTGTGCCGTC  TGAAGCCGAG  CTGTGGGACG  GCGCGGAAAA  CATCGACCCG
1201  CTGCGCTACC  ATCAGGCGCG  CGAAGCCTTG  TTGGATATAC  TTGCCGTCCG
1251  CTTTCTGCGC  AAATGGCACG  AATTGAACCG  TCAGGCGGCG  AAGCAGGAAA
1301  ACCAAAGCTA  CGAGTACAGC  CCCGAAGCCG  CCGGTTGGCG  CACGCTGCGC
1351  AATGTCTGCC  GCGCCTTCGT  CCTGCGCGCC  GATCCCGCGC  ACATCGAAAC

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTCCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCGCTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCCGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

```

a665.pep
  1 MKWDETRFGL EYDLDFIMVV AVGDFNMGAM ENKGLNIFNT KFLVADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAENVVMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPTPDM ADKQPMIPIV
251 KIGLLNCNGE AVAFDYQGKR ATEAVLLLTE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDL LLAHSDAFTR WEAAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNQRAA KQENQSYEYS PEAAGWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYAEMAQNMW HEWGILSAVN GNESDTRNRL
501 LAQFADKFSO DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFHAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIRI AQEGLSKDVG EIVGKILD*

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m665/a665 97.3% identity in 638 aa overlap

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              10      20      30      40      50      60
m665.pep      MKWDETRFGL EYDLDFIMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES
a665           MKWDETRFGL EYDLDFIMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES
              10      20      30      40      50      60

              70      80      90     100     110     120
m665.pep      VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
a665           VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
              70      80      90     100     110     120

              130     140     150     160     170     180
m665.pep      PEDAGPTAHPVRPASYEEMN NFYTMTVYEKGAENVVMYHTLLGEEGFQKGMKLYFQRHDG
a665           PEDAGPTAHPVRPARYEEMN NFYTMTVYEKGAENVVMYHTLLGEEGFQKGMKLYFQRHDG
              130     140     150     160     170     180

              190     200     210     220     230     240
m665.pep      QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM
a665           QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTVPTPDM
              190     200     210     220     230     240

              250     260     270     280     290     300
m665.pep      TDKQPMIPIVKVGLLN RGEAVAFDYQGKRATEAVLLLTEAEQTFLLGCVTEAVVPSLLR
a665           ADKQPMIPIVKIGLLNCNGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVPSLLR
              250     260     270     280     290     300

              310     320     330     340     350     360
m665.pep      GFSAPVHLNYPYSDDDL LLAHSDAFTRWEAAQTLYRRAVAANLATLS DGVELPKHEK
a665           GFSAPVHLNYPYSDDDL LLAHSDAFTRWEAAQTLYRRAVAANLAALSDGVELPKHEK
              310     320     330     340     350     360

```

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNRQAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKGEMAQNMT					
a665	KWHELNRQAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVVRTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQRIQAQEGLSKDVGEIVGKILDX					
a665	CNKLEPHRKNLVKQALQRIQAQEGLSKDVGEIVGKILDX					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATTCCTTGAA ACCGAACCTGC ATTCGACAT  TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTC GAGCCGCAGA GGGCGGGCGA GCGCTGGTG
151 TTGGACGGTT CGGCAAAACT CTGTCCGTC AAAATCAACG GCGCGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAAACAAA
301 TCCTGTATGG GGCTGTATGC TTCCGGCGGC AATCTGTGTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTT CAGACGCCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTCGC GGGCGATTG GCGGTAACGG AAGACCGTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAACC
651 CAAGGTCCGC TTGCGCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGTTGGAA TATGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTAGGCGATT TCAATATGGG CCGGATGGAA AACAAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCTCG CCGACAGCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTGCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCGGCGCGC
1001 CCGTGCGCGC CATCGAGAAC ATCCGCCTGC TCGCCAGAA CCAGTTCCCC
1051 GAAGACGCGA GCCCGACCGC CCATCCGTTG CGCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCATACCTG CTCGGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTTCGCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTT TGGAAGCCGA AGCCCGTCTG
1351 AAAAACAATG TTTTCGAGTT AACCATTAAA CAAACCGTGC CGCCACGCCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA GTCGGGCTTC
1451 TGAACCGCAA CGCGAAGCG GTGGCATTCT ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCCG TGTGCTGAT GACCGAAGCC GAACAGGCTT TCCCGCTCGA
1551 AGGTGTAACC GAAGCCGTGC TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGATCTT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCACGACA GCGACGCTT CACGTGCTGG GAAGCCGCC AAACGCTCTA
1701 CCGTCGCGCC GTCGCGCCA ACCTTGCCGC GCTTTCAGAC GGCATCGGGT

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCCT CAAAGCCCTG CTTTGGGGCG TGCCGTCCGA
1851 AGCCGAACATG TGGGACGGCA CGGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTTG CCGTCCGCTT CCTGCCGAAA
1951 TGGCACGAAT TGGACCGTCA GCGCGCGAAG CAGGAAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCCGCGCACA TCGAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTT
2251 ATCGGCTCAA GCCGCCGCGA CGACACCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCT GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG AATTGCAGTG CATTGCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pep

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YLDLIFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTDPEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRVRRRIEN IRLLRQNFPP
351 EDAGPTAHPV RPVSYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDOG AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPTPDMA DKQPMMPVK VGLLRNNGEA VAFDYQGKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNYP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNAFKAL LLGVPSEAEI WDGTEINIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTRLN VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSSRRSDTL QQVQTALQHP KFSLENPNKA RSLIGSFERN VPHFHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVG E IVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTAC ATTTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCGCG TTGACGGTT GAGCCGCAGA GGGTAGGGGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTGTATG TTGGAAGGAG AGACGCTGAC GATTGCGGGC TGCCGTCCG
251 AACGCTTAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAACAAA
301 TCCTGTATGG GGCTGTATGC TTCCGGCGGC AATTTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCTG CCGGATGTGA
401 TGTCCAAGTT CACCACCACC ATCGTCGCGG ACAAACACCG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTTG
551 CTTTGGTTCG GGGCGATTTC GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTGCGCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGGCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTTC CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG CATCGAAAAA ATCCGCTTGC TCGCCAGCA CCAGTTCCCC
1051 GAAGACGCGA GCCCGACCGC CCATCCGGTG CGCCCCGCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAGGC GCGGAAGTAG
1151 TCGGGATGTA TCACACCCTG CTCGGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTTACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCTT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGGAAGCGGA AGGTCGTCTG
1351 AAAACAATA TTTTCGAGTT GACCGTCAAA CAAACCGTGC CGCCCACGCC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCGCTCAAG GTCCGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTCG ACTATCAGGG CAAACGCGCG

```

```

1501 ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGCCGCGCC GTCGCCGCCA ACCTTGCCAC GCTTTGAGAC GCGTTGAGC
1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTGAGAC
1801 GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
1851 AGCCGAGCTG TGGGACGGCG CAGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTTG GATACGCTTG CCGTCCACTT CCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA
2001 ATACAGCCCC GAAGCCGCCG GCTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTTGCTCT GCGCGCCGAC CCCGCGCACA TCGAAACCGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCCTGCTG GCGCAGTTT
2201 CCGACAAAGT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCTC
2251 GTCGGCTCAA GCGCGCCGAG CGACACCCTG CAACAGGTTT GAACCGCCTT
2301 GCAGCATCCG AAATTCAGCC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCGCCGATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTGCGC GCGCGCTTAG TGCAGCGGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCACCG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AAATTTTGGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YLDLIFMVVA
251 VGFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDFW QLSLKEGLTV FRDQFSGDR ASRAVRRIEN IRLLRQHQP
351 EDAGPTAHPV RPASYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPTPDMT DKQPMIPVK VGLLNRNGEA VAFDYQKRA
501 TEAVLLLTEA EQTFLLLEGVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVLEPKHEKL LAAEKVISD
601 DLLDNFAKAL LLGVPSAEAL WDGAENIDPL RYHQAREALL DTLAVHFLPK
651 WHELNROAAK QENQSYEYSP EAAGWRTLNR VCRAFLVRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNRL AQAADKFSDD ALVMDKYFAL
751 VGSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIRA
851 QEGLSKDVGE IVGKILD*

```

m665-1/g665-1 96.1% identity in 866 aa overlap

```

          10      20      30      40      50      60
m665-1.pep MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV LDGSAKLLSV
g665-1      MSKTVRYLKDY QTPAYRILE TELHFDIAEP QTVVKSRLTV EPQVRAGEPLV LDGSAKLLSV
          10      20      30      40      50      60

          70      80      90      100     110     120
m665-1.pep KINGAAADYV LEGETLTIAG VPSERFTVEV ETEILPAENK SLMGLYASGG NLFTQCEPEG
g665-1      KINGAAADYV LEGETLTIADVP SERFTVEV ETEILPAENK SLMGLYASGG NLFTQCEPEG
          70      80      90      100     110     120

          130     140     150     160     170     180
m665-1.pep FRKITFYIDR PDVMSKFTTT IVADKKRYPV LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS
g665-1      FRKITFYIDR PDVMSKFTTT IVADKKRYPV LLSNGNKIDG GEFSDGRHWV KWEDPFAKPS
          130     140     150     160     170     180

          190     200     210     220     230     240
m665-1.pep YLFALVAGDL AVTEDYFTTMSGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE
g665-1      YLFALVAGDL AVTEDRFTTMSGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE
          190     200     210     220     230     240

          250     260     270     280     290     300
m665-1.pep YLDLIFMVVA VGDFNMGAMENK GLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
g665-1      YLDLIFMVVA VGDFNMGAMENK GLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT

```

1065

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV					
	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
g665-1	RPASYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDMTDKQPMIIPVK					
	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
g665-1	VGLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLEGVTEAVVPSLLRGFSAPVHLNYP					
	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
g665-1	YSDDDLLLLLAHDSDAFTWEAAQTLYRRVAANLATLSDGVELPKHEKLLAAVEKVISD					
	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
g665-1	DLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNROAAK					
	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
g665-1	QENQSYEYSPEAAGWRTLNRNVCRAFVLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
g665-1	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQOVRTALQHPKFSLENPNKA					
	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
g665-1	RSLIGSF SRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
m665-1.pep	850	860				
g665-1	VKQALQIRAQEGLSKDVGEIVGKILDX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTAC  ATTTTGATAT TAACGAACCG CAAACCATTG
101 TGAAGTCGCG TTTGACGGTC  GAGCCGAAGA GGGTGGGAGA GCCGTGGTG
151 TTGGACGGTT CGGCGAAACT  CTTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGCG  AGACGCTGAC GATTGCGGAC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG  GAAACCGAAA TCCTGCCGGC GAAAAACAAA
301 TCGCTGATGC GGCTGTATGC  GTCCGCCGGT AACCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA  TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC  ATCGTCGCGG ACAAAAAACG CTATCCCGTT
451 TTGCTCTCCA ACGCAACAA  AATCGACGGC GGCGAGTATT CAGACGGCCG

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501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTTCG GGGCGATTTG GCGGTCACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTGCGCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTGGGCGATT TCAATATGGG TCGATGGAA AACAAGGGT TGAACATCTT
801 TAACACCAAG TTCGTCTTGG CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTTCG TGAAGGAAGG
951 GTTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG TATCGAAAAC ATCCGCCTGC TCGCCACGCA CCAGTTCCCC
1051 GAAGACGCAG GTCCGACCGC ACATCCGGTG CGCCCCGCCG GATATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTTACCT GCGACGATT
1251 CCGCGCGGCG ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTGCGCT
1301 TGTGGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
1351 AAAACAATG TGTTCGAGT AACCATCAA CAAACCGTGC CGCCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA ATCGGGCTGC
1451 TGAAGTGAAG CGGCGAAGCG GTGGCATTTG ATTATCAGGG CAAACGCGCG
1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCGA
1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CCGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
1701 CGCCCGTGCC GTCCCGGCCA ACCTTGCCGC GCTTTCAGAC GCGCTCGAGT
1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTTCAGAC
1801 GACCTCTTAG ACAACGCTT CAAAGCCCTG CTTTGGGTG TGCCGTCTGA
1851 AGCCGAGCTG TGGGACGGCG CGGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGCGCGCGCA AGCCTTGTG GATATACTTG CCGTCCGCTT TCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGGCGGAAG CAGGAAAACC AAAGCTACGA
2001 GTACAGCCCC GAAGCCGCCG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CCTTCGTCTT CCGCGCCGAT CCGCGCACCA TCGAAAACCG TGCCGAGAAA
2101 TACGCCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCCTGCTG GCGCAGTTTG
2201 CCGACAAGT TACAGACGAC GCGCTGGTGA TGGACAAATA TTTCCGCCCTC
2251 GTCGGCTCAA GCGCGCCGAG CGACACCTGA CAACAGTTTC AAACCGCCTT
2301 GCAGCATCCG AAGTTCAGCC TCGAAAATCC CAACAAGGCC CGCTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACCC
2451 GCAGGTCGCC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG CATTCAGCGC CATTCGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV
51 LDGSAKLLSV KINGVAADYV LEGETLTIAD VPSEFRTVEV ETEILPAENK
101 SLMGLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYSDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDFW QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRHQHFP
351 EDAGPTAHPV RPARYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
451 KNNVFELTIK QTVPPTPDMA DKQPMMPVK IGLLNCNGEA VAFDYQGKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLAALSD GVELPKHEKL LAAVEKVISD
601 DLLDNAFAKAL LLGVPSEAEL WDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNROAKA QENQSYEYSP EAAGWRTLNR VCRAFVLRAD PAHIETVAEK
701 YAEMAQNMTN EWGILSAVNG NESDTRNRL L AQFADKFSD ALVMDKYFAL
751 VGSRRSDTL QOVQTAHQH KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVG EIVGKILD*

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a665-1/m665-1 97.2% identity in 867 aa overlap

	10	20	30	40	50	60
a665-1.pep	MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV LDGSAKLLSV					
	: : : : :					
m665-1	MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV LDGSAKLLSV					
	10	20	30	40	50	60
	70	80	90	100	110	120

a665-1.pep	KINGVAADYVLEGETLTIADVPSERFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
m665-1	KINGAAADYVLEGETLTIAGVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
	70 80 90 100 110 120
a665-1.pep	130 140 150 160 170 180
	FRKITFYIDRPDVMKSKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
m665-1	FRKITFYIDRPDVMKSKFTTTIVADKKRYPVLLSNGNKIDGGEFS DGRHWVKWEDPFSKPS
	130 140 150 160 170 180
a665-1.pep	190 200 210 220 230 240
	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTTEADKPKVGF AVESLKNAMKWDETRFGLE
m665-1	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTTEADKPKVGF AVESLKNAMKWDETRFGLE
	190 200 210 220 230 240
a665-1.pep	250 260 270 280 290 300
	YDLDFIMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIESVVGHEYFHNWT
m665-1	YDLDFIMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIESVVGHEYFHNWT
	250 260 270 280 290 300
a665-1.pep	310 320 330 340 350 360
	GNRVTCRWFQLSLKEGLTVFRDQEFSGDRASRAVRRRIENIRLLRQHQPEDAGPTAHPV
m665-1	GNRVTCRWFQLSLKEGLTVFRDQEFSGDRASRAVRRRIENIRLLRQHQPEDAGPTAHPV
	310 320 330 340 350 360
a665-1.pep	370 380 390 400 410 420
	RPARYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFORH DQAVTCDDFRAA
m665-1	RPASYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFORH DQAVTCDDFRAA
	370 380 390 400 410 420
a665-1.pep	430 440 450 460 470 480
	MVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTVPTPDMADKQPMMPVK
m665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDMTDKQPMMPVK
	430 440 450 460 470 480
a665-1.pep	490 500 510 520 530 540
	IGLLNCNGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVPSLLRGFSAPVHLNYP
m665-1	VGLNLRNGEAVAFDYQGKRATEAVLLLTEAEQTFLEGVTEAVVPSLLRGFSAPVHLNYP
	490 500 510 520 530 540
a665-1.pep	550 560 570 580 590 600
	YSDDDLLLLLAHSDAFTRWEEAAQTL YRRAVAANLAALSDGVLPKHEKLLAAVEKVISD
m665-1	YSDDDLLLLLAHSDAFTRWEEAAQTL YRRAVAANLATLS DGVLPKHEKLLAAVEKVISD
	550 560 570 580 590 600
a665-1.pep	610 620 630 640 650 660
	DLLDNAFKALLGVPSEAE LWDGAENIDPLRYHQAREALLDILAVRFLPKWHELN RQA AK
m665-1	DLLDNAFKALLGVPSEAE LWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELN RQA AK
	610 620 630 640 650 660
a665-1.pep	670 680 690 700 710 720
	QENQSYEYSPEAAGWRTL RNVCRAFVLRADPAHIETVAEKYAEMAQNMTHEWGILSAVNG
m665-1	QENQSYEYSPEAAGWRTL RNVCRAFVLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG
	670 680 690 700 710 720
a665-1.pep	730 740 750 760 770 780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQHPKFSLENPNKA
m665-1	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQHPKFSLENPNKA
	730 740 750 760 770 780
a665-1.pep	790 800 810 820 830 840
	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL
m665-1	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL

1068

	790	800	810	820	830	840
	850	860				
a665-1.pep	VKQALQRI	RAQEGLSKDVGEIVGKILDX				
m665-1	VKQALQRI	RAQEGLSKDVGEIVGKILDX				
	850	860				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2171>:

```
g666.seq
1   ATGCTTTGTA TGAATTATCA ATCAAACCTCA GCGAAGGAG TGCTTGTAGC
51  TAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
151 ATCGCAGGTG CAGACGCTCA CACGCCTGAA CATGTAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGGTGGTG CATTGTGTGT GTATTGGGAC AATACCGCCA
401 AACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCAGAATTAT TTTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGCT CGGTAGGTAC GCCTGCTATC CCTAAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:

```
g666.pep
1   MLCMNYQSNS GEGVLVAKTY LLTALIMSMV ISGCQVIHAN QGKVNTNSAV
51  IAGADAHTPE HVTGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GREAPMRAT
151 PELFLDKDGX PLKFMEAVVA RXVRLSLN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2173>:

```
m666.seq
1   ATGCCTTGTA TGAATCATCA ATCAAACCTCA GCGAAGGAG TGCTTGTGGC
51  TAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGGTGGTG CATTGTGTGT GTATTGGGAT AATACCGCCA
401 AACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA
```

This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:

```
m666.pep
1   MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTNSAV
51  ITGADAHTPE HATGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GREAPMRAT
151 PELFLDKDGQ PLKFMEAVVV VARWVRLSL N*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m666/g666 93.9% identity in 181 aa overlap

	10	20	30	40	50	60
m666.pep	MPCMNHQSNS	GEGVLVAKTY	LLTALIMSMT	ISGCQVIHAN	QGKVNTNSAV	ITGADAHTPE
g666	MLCMNYQSNS	GEGVLVAKTY	LLTALIMSMV	ISGCQVIHAN	QGKVNTNSAV	IAGADAHTPE
	10	20	30	40	50	60
	70	80	90	100	110	120
m666.pep	HATGLTEQKQ	VIASDFIVAS	ANPLATQAGY	DILKQGGSAA	DAMVAVQTTL	SLVEPQSSGL

```

g666      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
HVTGLTEQKQVIASDFIVASANPLATQAGYDILKQGGSAADAMVAVQTTLSSLVEPQSSGL
          70          80          90          100          110          120

          130          140          150          160          170          180
m666.pep  GGGAFVLYWDNTAKTLTTFDGRETAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g666      GGGAFVLYWDNTAKTLTTFDGRETAPMRATPELFLDKDGXPLKFMEAVV--ARXVRLLSL
          130          140          150          160          170

m666.pep  NX
          ||
g666      NX
          180

```

```
a666.seq
1  ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTTGGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCGTGAA CATGCAACGG GACTGACCGA
201 ACAAAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GGCGGTGGTG CATTTGTGTT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGGAACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CATTGGAAT TTATGGAAGC
501 GGTGGTCTGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA
```

a666.pep

1	MPCMNHQSNS	GEGVLVAKTY	<u>LLTALIMSMT</u>	<u>ISGQCVIHAN</u>	QGKVNTHSAV
51	ITGADAHTPE	HATGLTEQKQ	VIASDFMVAS	ANPLATQAGY	DILKQGGSA
101	DAMVAVQTTL	SLVPEQSSGL	GGGAFVLYWD	NTAKLTTFD	GRETAPMRAT
151	PELFLDKDGQ	PLKFMEAVVU	VARWVRLLSL	N*	

		10	20	30	40	50	60
m666.pep		MPCMNHQNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
a666		MPCMNHQNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
a666		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWDNTAKTLTTFDGRETAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL					
a666		GGGAFVLYWDNTAKTLTTFDGRETAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL					
		130	140	150	160	170	180
m666.pep		NX					
a666		NX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1   atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  tttccAtttg gtattcgtcc gcgtcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAAttgcg
151 GAtttccttc agcgtgcccg cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTcgCcat atcgtccagC
251 GGCACATTcg ccctcggtcG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GGC GTTATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCCGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCGCGAA CAGCACCAC TCGTCATCCG GCAGGGAAGA CGGCAAGTCA
701 TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCAg tACCTTGCAT tcaAAAACAG ACtTGCGCCT
801 ATTgTgtcaT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1   MRFVFLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQRRARVER FPFHAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAAVAE IAVARIPIAR GVDVYQGAV MQYGVVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMNVLVLP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHFVIRQGR RQVIQRTDTL HIGYGFNIES
251 QNRIHGSTLH SKTDLRLLCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1   ATGCGGCTTT TCCCCGCTT GTGCGGACAG GTAATCCGC ATCCGTTTGA
51  TTTCCATTTC GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCTTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCAGC CTGCGCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GGC GTTATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCCGCC
451 GTTCCAACTG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCAC TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1   MRLFPGLCGQ VIPHPDFHF VVRIQPAAD QTETQVHQIS VCRVGFALIA
51  DFLQPARMEC LPNLAHVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101 VALVITADV VPLEIAAAVAE IAVAHIPIAR GVDVYQGAV MQYQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHLN
201 MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

              10      20      30      40      50      60
m667.pep    MRLFPGLCGQVIPHPDFHFVVRIQPAADQTETQVHQISVCRVGFALIA DFLQPARMEC
              ||:  | |: :  | ||: |||: : ||| |||: ||| :  : ||| ||| ||| ||: |
```

[illegible]

```
a667.seq
1  ATGCGGTTTG TCTTCTGT TT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51  TTTCCATTTC GTATTCTGCT GCGTCGAATC TGCCGCTGAC CAGACAGAAA
101 CGCAGATACA TCAGATAGGT ATTTACCGCA TCGGTTTTCG AATAATTGCG
151 GATTTCTCTC AGCCTGCCCG CGTGGAACGC CTCCCACACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAAC
251 GGCACATTGG CCCTCGGCTG GTAAAGCGCG AGCAAAATCCA TCAAATCGCA
301 ATGACGTTGG TGGTAGCGGC TGATGTAGTT GTTCCACTTG AAATCGCGCG
351 TGTCGCCGAA ATAGCCGCTCG CCGATATCCC AATAGCGCGC GGGCTTGATG
401 CCGTGTAGCA GCGAACGGTA ATGCAGAACC GGCAGGTCGA AACCGCCGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CACTTCTCTG CCGTCATCCA TCTCGCCGAT TGTACCGACA
551 TGGACTTTAT CTTGCCCCCA ACGCATGCGC CACGAAATCG CCACAACTCG
601 ATGAAGATGA TGCTGCATAA AATCCCCACC CGTCTGAGCA CGGCGTTTTT
651 GCTGGGCAA CAGCACC ACT TCATCGTCGG GCAGCGAGGA CGGCAAGTCA
701 TACAGCGTAT GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCTGT GTCATGACAG CACCTTGTTT TTA AAA. CAG ACTTGCGCCT
801 ATATGTGTCAT TAA
```

a667.pep

1	MRFVFC LGGE	IVSDPLDFHF	VFVCVESAAD	QTETQIHQIG	IYRIGFAIIA
51	DFLQPARVER	LPHLAAVHTQ	LARKTAQFRH	IVQRHIRPRL	VKREQIHQIA
101	MTLVVAADV	VPLEIAAAVE	IATAHIPIAR	GVDAV*QRTV	MQNRQVETAA
151	VPTDQLRRMF	FNQLEKFGDN	HFLAVIHLAD	CTDMDFILPP	THAARNRHNH
201	MKMMHLKIPT	RLSTAFLLGK	QHHFIVGQRG	RQVIQRDTL	HIGYGFNISS
251	ONRGHSDSTLY	LKXDLRLLLCH	*		

[illegible]

1072

	70	80	90	100	110	120
	130	140	150	160	170	180
m667.pep	IAVAHIPIARGVDAVYQGAVMQYGGIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD					
	: : : : :					
a667	IAVAHIPIARGVDAVXQRTVMQNRQVETAAVPTDQLRRMFFNQLEKFGDNHFLAVIHLAD					
	130	140	150	160	170	180
	190	200	210	220		
m667.pep	GADMYFILPPTHAAARNRHNLMKMMLHKIAARLSTAFVLGNQHHL					
	: : : : : :					
a667	CTDMDFILPPTHAAARNRHNLMKMMLHKIPTRLSTAFLLGKQHHFIVGQRGRQVIQRTDTL					
	190	200	210	220	230	240
a667	HIGYGFNIESQNRGHDSTLYLKXDLRLCHX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2183>:

```

g669.seq
1   ATGCGCCGCA TCGTTAAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAATTT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2184; ORF 669.ng>:

```

g669.pep
1   MRRIVKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2185>:

```

m669.seq
1   ATGCGCCGCA TCATTAAAAA ACACCAGCCC ATAAACGCGC CACATATCGT
51  TTTGGAATTT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACAGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2186; ORF 669>:

```

m669.pep
1   MRRIIKKHQP INAPHIVLEI RIMKLHRAFV FLGRKRPHHH DSSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m669/g669 96.2% identity in 106 aa overlap

	10	20	30	40	50	60
m669.pep	MRRIIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHH DSSLRRQHGI EGMGFDFKQI					
	: : : : :					
g669	MRRIVKKHQPVNAPHIVLEIRIMKLHRAFVFLGRKRPHHH DRSLRRQHGI EGMGFDFKQI					
	10	20	30	40	50	60
	70	80	90	100		

1073

```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1  ATGCGCCGCA TCATTAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51 TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATT TCAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1  MRRIIKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
51 EGMGDFDKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

m669.pep    10      20      30      40      50      60
             MRRIIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHHDSLRRQHGI EGMGDFDKQI
             |||||:|||||
a669        MRRIIKKHQPVNAPHIVLEIRIMKLHRAFVFLGRKRPHHHDRSLRRQHGI EGMGDFDKQI
             10      20      30      40      50      60

m669.pep    70      80      90      100
             FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
a669        FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1  ATGACTTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTCG GGTGGTGAA
51 AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGAAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAAGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNTVRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1  ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTCG GGTGGTGAA
51 AAACGCTTCG GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTTCGTCA AACAACTTA

```

1074

```

251  CGCGCGGTTT CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301  CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351  GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401  CCTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTCAGGTGC
451  GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51  IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCRW
101  PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151  G*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              |||||||
g670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep      FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK
              |||||||:|||||:|||||
g670           FITFNTSPTISGSSAEVGSSNSITRGSIASPRAIATRCWPPEWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep      SSIAFFSACS AFCPLTFIGARVMFSNTVRCGX
              |||||||:|||||
g670           SSIAFFSACS AFCPLTFIGARVMSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1  ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTTCG GGTGTTGTA
 51  AAACGCTTCC GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAA
101  TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151  ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201  GCCGACCATT TCGGGTTCGA GTGCGGAGGT CGGTTCGTCA AACACATTA
251  CGCGCGGTTT CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301  CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351  GCGTTCCAAA AGTTCCATCG CTTTTTCTC TGCTGTTC GCATTTGAC
401  CTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTCAGGTGC
451  GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51  IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCRW
101  PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151  G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              |||||||:|||||:|||||
a670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```


1075

	70	80	90	100	110	120
m670.pep	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK					
a670	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK					
	70	80	90	100	110	120
	130	140	150			
m670.pep	SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX					
a670	SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

```

g671.seq
1  ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51  GCCCAAAATG CGGTTGGCAA AGCCCAGACC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAATG ACAGagccaa TGCAAAcAgg cggggTTGGA ACGagGCAAA
201 GGCGAGGTcg gcgaaggGTG CGGCaaAGAG TTTggcaaAA AAGAaggAAA
251 ccaccCATGC cACCATCgaa cctGCTTCGG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCGGC GATGACGGcg gAGGCGAGGA GGTGCGCAAT
351 GGGGAGGCTA TTCATTCGTT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

```

g671.pep
1  MISRVTIKTP FNAPNTPPKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKGAAKSLAK KKETTHATIE PASAITPRIV
101 EMTMQAAMTA EARRSAMGRL FIRYLAGDAV HAQFVQIAFG IPCVFIVA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

```

m671.seq
1  ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAAcAGG CGGGGTTGGA ACGAGGCAAA
201 GGCGAGGTcG GCGAAGGAGG CGGCaaAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCCATGC CGCCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTGCGCAAT
351 GGGGAGGCTA TTCATTCGTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

```

m671.pep
1  MTSRVTIKTP FNAPNTPPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETTHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*
  
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

	10	20	30	40	50	60
m671.pep	MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDANANR					
g671	MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.pep	RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRSMGRL					

```
a671.seq
1  ATGACCAGCA GGGTAATAAT CAAATGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTTGGCAA AGCCCAAACC GACCGCGGAA ACTGCCCCGG
101 TCAGCAGCGA CGCGAGTATT TTCTGGATCA GACAGGCAAT GACGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTCGA ACGATGCAAA
201 GGCGATGTCG GCGAAGGGTG CGGCAAAGAG TTTGGCGAAA AAAAAGGCAA
251 CCACCCATGC CGCCATTGAG CCAGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCAGCA TGCAGGCCGT GTGATGCGCG GAGACGAGGA GGTTCGGCAAC
351 GGGGAGGTTA TTCATTTCGT ACTGACCCGC CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTTCGC ATCCCTTCGG TTTTATAGT TGCTTGA
```

```
a671.pep
1  MTSRVIIKMP FNAPNTPPKM RLAKPKPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNDAKAMS AKGAAAKSLAK KKATTHAAIE PASAITPRIA
101 DSTMOAAMMA ETRRSATGRL FIRYLTGDTV YAOFVOIAFG IPCVFIVA*
```

	10	20	30	40	50	60
m671.pep	MTSRVTIKTFFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
a671	MTSRVVIKMPFNAPNTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.pep	RGWNEAKARSAKEAAKSLAKKKETHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL					
	::					
a671	RGWNDAKAMSAKGAASKLAKKKATTHAAIEPASAITPRIADSTMQAAMMAETRRSATGRL					
	70	80	90	100	110	120
	130	140	149			
m671.pep	FIRYLTGDTVYAQFVQIAFGIPC VFIVAX					
a671	FIRYLTGDTVYAQFVQIAFGIPC VFIVAX					
	130	140				

g672.seq

1	ATGAGGAAAA	TCCGCACCAA	AATCTGCGGC	ATCACCACAC	CGGAAGACGC
51	ACTGTATGCC	GCCCACGCCG	GCGCAGACGC	ATTGGGACCT	GT'TTTT'TACC
101	CCCAAAGCCC	CCGCGCTATC	GACATCATT	AAGCAAAAT	AATCGCCGCC
151	GCACTGCGCG	CGTTTGTCTAG	CGTTGTCGCC	CTTTTCTGTA	ACGAAAGCGC
201	GCAAAACATC	CGCCGCATCC	TTGCCGAAGT	GCCGATACAC	ATCATCCAAT
251	TCCACGGCGA	CGAAGACGAT	GCATTCTGCC	GGCAGTTCGA	CCGCCCTTAT
301	ATTAAAGCCA	TTCGTGTTCA	GACGGCATCA	GACATCCGAA	ACGCCGCCAC
351	GCGCTTCCCC	AACGCTCAGG	CGTCTGCTTT	CGATGCCCTAT	CACCTTTCGG
401	AATACGGCGG	CACCGGACAC	CGCTTCGact	GGacgctggt	ggcggAATAT
451	TCGGGCAAGC	CGTGGGTGCT	TGCCGGCGGG	CTGACCCCTG	AAAACGTCTG
501	CGAAGCCGTC	CGCATCACCG	GAGCGGAAGC	GGTCGACGTA	TCCGCGGGCG
551	TGGAAGCGTC	TAAAGGCAAA	AAAGACCCCG	CCAAAGTCGC	CGCCTTTATC
601	GCAACCGCCA	ACCGCTATC	CCGTTAA		

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```
g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LEVNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATRFN NAQALLFDAY HPSEYGGTGH RFDWTLAEY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDPKVAFAFI
201 ATANRLSR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```
m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTGAG CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGCGCA CGAAGACGAC GCATTCTGCC GCCAGTCCA CCGCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GGCGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAATC GGTGATGTA TCCGGCGGTG
551 TGGAAGCGTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```
m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQSSRAV DIARAKKITA
 51 ALPPFVSVVA LEVNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATRFN DAQALLFDAY HPSEYGGTGN RFDWTLAEY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDAKVAFAFI
201 ATANRLSR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

m672.pep	10	20	30	40	50	60
	MRKIRTKICG	ITTPEDAAAA	AAGADAVGL	VFFQSSRAV	DIARAKKITA	ALPPFVSVVA
g672	10	20	30	40	50	60
	MRKIRTKICG	ITTPEDALYA	AHAGADALGL	VFYQSPRAI	DIIKAQKIAA	ALPPFVSVVA
m672.pep	70	80	90	100	110	120
	LFVNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFHRPY	IKAIRVQTAS	DIRNAATRFN
g672	70	80	90	100	110	120
	LFVNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFDRPY	IKAIRVQTAS	DIRNAATRFN
m672.pep	130	140	150	160	170	180
	DAQALLFDAY	HPSEYGGTGN	RFDWTLAEY	SGKPWVLAGG	LTPENVGEAV	RITGAESVDV
g672	130	140	150	160	170	180
	NAQALLFDAY	HPSEYGGTGH	RFDWTLAEY	SGKPWVLAGG	LTPENVGEAV	RITGAESVDV
m672.pep	190	200	209			
	SGGVEASKGK	KDAKVAFAFI	ATANRLSRX			
g672	190	200				
	SGGVEASKGK	KDPKVAFAFI	ATANRLSRX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

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```

1   ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCGCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAGCCC  CCGCGCTGTC GACATCATT AAGCACAAAA AATCACCGCC
151 GCACTGCCGC  CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC  CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
251 TCCACGGCGA  CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCTAT
301 ATCAAGGCCA  TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
351 CCGCTTCCCC  GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG  CACCGGACAC CGCTTCGACT GGACGCTGTT GGCGGAATAT
451 TCGGGCAAAC  CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGA
501 CGAAGCCATC  CGCATCACCG GAGCGGAAGC GGTCTGATGTA TCCGGCGGCG
551 TGAAGCGTC   TAAAGCAAA  AAAGACCCAG CCAAAGTTGC  CGCCTTTATC
601 GCAACGCCA   ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

```

a672.pep
1   MRKIRTKICG ITTPEDALYA AHAGADALGL VFYPQSPRAV DIKAQKITA
51  ALPPFVSVVA LFNESAQNI RRILAEPVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAADRFP DAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAEFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICGITTTPEDAAAAAGADAVGLVFFQGSRAVDIARAKKITAALPPFVSVVA					
a672	MRKIRTKICGITTTPEDALYAAHAGADALGLVFYPQSPRAVDIKAQKITAALPPFVSVVA					
	10	20	30	40	50	60
m672.pep	LFVNESAQNIRRILAEPVPIHIIQFHGDEDDAFRCRQFHRPYIKAIRVQTASDIRNAATRF					
a672	LFVNESAQNIRRILAEPVPIHIIQFHGDEDDAFRCRQFHRPYIKAIRVQTASDIRNAADRFP					
	70	80	90	100	110	120
m672.pep	LFVNESAQNIRRILAEPVPIHIIQFHGDEDDAFRCRQFHRPYIKAIRVQTASDIRNAATRF					
a672	LFVNESAQNIRRILAEPVPIHIIQFHGDEDDAFRCRQFHRPYIKAIRVQTASDIRNAADRFP					
	70	80	90	100	110	120
m672.pep	DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVGEAVRITGAESVDV					
a672	DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVDEAIRITGAEAVDV					
	130	140	150	160	170	180
m672.pep	DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVGEAVRITGAESVDV					
a672	DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVDEAIRITGAEAVDV					
	130	140	150	160	170	180
m672.pep	SGGVEASKGKKDAAKVAEFIATANRLSRX					
a672	SGGVEASKGKKDPKVAEFIATANRLSRX					
	190	200	209			
m672.pep	SGGVEASKGKKDAAKVAEFIATANRLSRX					
a672	SGGVEASKGKKDPKVAEFIATANRLSRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

```

g673.seq
1   ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51  TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC  GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT  GTCGATACGC CGGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG  GCTGAATCAA AATGTTACCG AGGCGCTCGG CCGTGTGGAT
301 GTGGTGGTTT  TCGTCGTGGA GCGATGCGC CTTACCGATG CCGACCGCGT
351 CGTGTGTAAG  CAACTGCCCA AGCACACGCC GGTCAATTTA GTGATCAACA
401 AAATCGACAA  GGACAAGGCG AAAGACCGTT ACGCGCTGGA GGCGTTTGT
451 GCGCAAGTGC  GCGCCGAATT TGAATTTCG GCGCGGAGG CGGTCAAGTC
501 GAAACACGGT  TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCGAAAG  CGTACCGATG TATCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT  TGGCGATGGA AATCGTGCCT GAAAACTCT TCCGCTATTT

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651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAAAAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
  1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
 51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEDGGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
  1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
 51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGCATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GGCCTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
  1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
 51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEDGGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

          10      20      30      40      50      60
m673.pep MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
          |||
g673      MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
          10      20      30      40      50      60

          70      80      90     100     110     120
m673.pep YTDDTAQFVFVDTPGFQTDH RNALNDRLNQ NVTEALGGVDVVVFVVEAMRFTDADRVVLK
          |||

```

1080

```

g673      YDDTAQFVFVDTPGFQTDHRNALNDRNLQNVTALGGVDVVVFVVEAMRLTDADRVVLK
           70          80          90          100          110          120

           130          140          150          160          170          180
m673.pep  QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELL
           130          140          150          160          170          180

           190          200          210          220          230          240
m673.pep  KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           190          200          210          220          230          240

           250          260          270          280          290          300
m673.pep  IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDNKVFLKVWVKVSGWADDIR
           250          260          270          280          290          300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51  TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTTGTGTTT GTCGATACGC CCGGTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTGTG
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CCGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAATA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAA GTCAAATCCG GTTGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51  OTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRNLQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPLESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFDTKVFLKVWVKVSGWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10          20          30          40          50          60
m673.pep  MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a673      MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           10          20          30          40          50          60

```

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	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVEAMRFTDADRVVLK					
a673	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVEAMRFTDADRVVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
a673	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGGGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR					
a673	IYIAVLVDKESQKAILIGKGGGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAAACAG CCGCGCGCCG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCGCGGCC CGAAATGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETYPY
101 VIINEAIEVT KTFGGTDGKH FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAAACAG CCGCGCGCCG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCGCGGCC CGAAATGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGGCAGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCGGCAGAG TATATCCGAC AAATCCGCCC
201 GTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCCGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```

1082

51 FFGTQTNAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
g674	YIQKIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq
 1 ATGAAAACAG CCCGCCGCCG TTCCCGCGAG CTGCGGTAC AAGCCGTTTA
 51 CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAGATTGCT AAAAACATCC
 101 GCGAAATGCC CGACTTTGCC AAGGCAGACG AAGAATTGTT CAACAAACTT
 151 TTCTTCGGCA CGCAAACCAA TCGGCAGAG TACATCCGAC AAATCCGCC
 201 CCTGCTCGAC CGCGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTCC
 251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
 301 GTCATCATCA ACGAAGCCAT CGAAGTAACC AAAACCTTCG GCGGCACGGA
 351 CGGGCACAAA TCGTCAACG GCATCCTCGA CAACTCGCC GCCCAAATCC
 401 GTCCCGACGA GCCCAAACGC CGTTGA

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep
 1 MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMPDFA KADEELFNKL
 51 FFGTQTNAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

g675.seq

```
1  ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcacgctc
151 gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAAC TTGC
201 CTCTTCCGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301 GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351 CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

1084

g675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCRTLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
 101 GRVALDYNIP IANAVLT TEN DAQAIERIGE KASDAKVAV ECANLVNLLL
 151 EEQFEDEE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq
 1 ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
 151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
 201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
 251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
 301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
 351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
 401 ATGCCGCCAA AGTCGCGCTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC
 451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV
 101 SRVALDYNIP IANAVLT TEN DAQAIERIEE KASDAKVAV ECANLVNLLL
 151 EEQFEDEE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFE LVSNEGAGVSRVALDYNIPIANAVLT TEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFE LVANESGAGIGRVALDYNIPIANAVLT TEN					
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFE LVSNEGAGVSRVALDYNIPIANAVLT TEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFE LVANESGAGIGRVALDYNIPIANAVLT TEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGEKASDAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq
 1 ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
 151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
 201 CTCTTCTGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
 251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
 301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
 351 CACGGAAAAC GACGCACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
 401 ATGCCGCCAA AGTCGCGCTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
 451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV

1085

101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAKVAV ECANLVNLLL
151 EEQFEDEE*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX					
a675	DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq
1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg
51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCATT TCCTCACGGC CTTCCGGCGT
151 GTTCAAAACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGG CAACGCGCCA
201 ACGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGACG
251 CCGACGATT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
301 GGTGCGCGCG AAAAATACTT GGTGCGTCGC TTCGCGCAAT TCGGGATCGA
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG
401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG
451 GTCGCGGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep
1 MPQILVRIFL IRYSEFIWETV RLCRFRRHSR SVDFDVFDK DFNFLTAFRR
51 VQNHFAFAR FNQATRRRN PRNFVLRIG FIDADDFDGL LAPVAAQQT
101 GRAEKYLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
151 VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq
1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTG
51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCATT TCCTCACGCC CTTCCGGCGT
151 GTTCAAAACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGA CAACGAGCCA
201 GCGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGATG
251 CCGACGATT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCCGAC
301 CGTCGCGCG AAAAATACTT GGTGCGTCGC TTCGCGCAAT TCGGGATCGA
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG
401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG
451 GTCGCGGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTGTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep
1 MPQILVRIFL IRYSEFIWETA RLCRFRRHSR SVDFDVFDK DFNFLTFFRR

```

51  VQNHFAFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD
101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
151 VAVACRPVDD LDDEGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

```

              10      20      30      40      50      60
m677.pep      MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLTFFRRVQNHFAFAR
              |||||
g677           MPQILVRIFLIRYSFIWETVRLCRFRHRSVDFDVFDRKDFNFLTAFRRVQNHFAFAR
              10      20      30      40      50      60

              70      80      90      100     110     120
m677.pep      FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
              |||:|
g677           FNQATRQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGGRAEKYLVRFAQFGIDDDG
              70      80      90      100     110     120

              130     140     150     160     170     180
m677.pep      SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
              |||||
g677           SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFIDQLIKLVFQCL
              130     140     150     160     170     180

              190     199
m677.pep      PSGGRNVVFGFGTHIVCGX
              |||||
g677           PSGGRNVVFGFGTHIVCGX
              190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

```

a677.seq
1  ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTTG
51  GGAAACGCGC CGTTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCGGGCGT
151 GTTTAAACCC ACTTCGTCGC CTTACGCGC TTTAATCAGA CAACGAGCCA
201 GCGGCGAAAT CCAAGAAATT TTGTTTGGCG CGGTATCGAT TTCATCGATG
251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
301 GGTGCGCGCG AAAAACACTT GGTGCGTCGC TTCGCGCAAT TCGGGATCAA
351 CGACGACGGC GGCTTCCAAA CGCTTGGTCA GGAAACGGAT GCGGCGGTGCG
401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGG TAGTCGCCGT TTTGCGTGGC
451 GTCGCGGTTG CCTGCCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTATTAAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

```

a677.pep
1  MPQILVRIFL IRYSEFIWETA RLCRFRHRSR SVDFDVFDRK DFNFLTFFRR
51  V*NHFVAFTR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT
101 GRAEKHLVGR FAQFGINDDG GFQTLGQETD AAVDFAHTAF AVKVVAVFAA
151 VAVACRPVDD LDDFGAFFIN QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

```

m677/a677 93.4% identity in 198 aa overlap

```

              10      20      30      40      50      60
m677.pep      MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLTFFRRVQNHFAFAR
              |||||
a677           MPQILVRIFLIRYSFIWETARLCRFRHRSVDFDVFDRKDFNFLTFFRRVXNHFAFTR
              10      20      30      40      50      60

              70      80      90      100     110     120

```

1087

```

m677.pep      FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a677          FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQTDGRAEKHLVGRFAQFGINDDG
                70      80      90      100     110     120

                130     140     150     160     170     180
m677.pep      SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDFFGAFFVDQLIKLVFQCL
                ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a677          GFQTLGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDFFGAFFINQLIKLVFQCL
                130     140     150     160     170     180

                190     199
m677.pep      PSGGRNVVFGFGTHIVCGX
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a677          PSGGRNVVFGFGTHIVCGX
                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1   ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTcgcCGG TCATCGCCCGC
51  CTGCATCGTC ATTTCCACGA TCGCGGCGGT GATTGCGGAA GCAGgttcGA
101 TGGTgGCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
151 ttcgcgcACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTCATTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCGGC GCAGTTTCGG CGGTCGGTCT GGGCTTTGCC
301 AACCGCATT TGGGCGGTGT ATTCGGTGCA TTGAAAGCG TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC atacggaCAA CGCaccgaa tCCctcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1   MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51  FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGV LIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1   ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCCGC
51  CTGCATCGTG CTATCCGCGA TCGCGGCGGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTCT TGCCGCCTCC
151 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCgcCTGT TTGCATTGGC
201 TCTGTCTGTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCAGC GCAGTTTCGG CGGTCGGTTC GGGCTTTGCC
301 AACCGCATT TGGGCGGCGT ATTCGGTGCA TTGAAAGCG TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1   MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51  FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLTTS AVSAVGLGFA
101 NRILGGVFGA LKGV LIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1088

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFALFAASFADLAFASFQ					
	: : : : :					
g678	MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFALFAAPFADLAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	: : : : :					
g678	PRLFALALSFISLFVIACLIQKMLRSLTGAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	: : : : : :					
g678	IMLASKTDLPDTEEWQSYTVFFVSLSEAVLNHTDNAPESLDDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```

a678.seq
1  ATGAATAACC TCCCCGTTGC CGACCTCCTC GTCTCCGCCA TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGC GCGGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTT TTTTCG CCAA ACTCTT TGCCGCACCC
151 TTCGCCGACA TCGCCTTTGC ATCGTTCCAA CCCC GCCTGT TTGCATTGGC
201 TCTGTCTGTC ATTTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTTGATTAT
351 TACCCTGCTG GTCATGCTCG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```

a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLEAAP
51 FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGILIIITLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

m678/a678 93.9% identity in 165 aa overlap

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFALFAASFADLAFASFQ					
	: : : : :					
a678	MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLEAAPFADIAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	: : : : :					
a678	PRLFALALSFISLFVIACLIQKILRSLTGAVSAVGLGFANRILGGVFGALKGILIIITLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	: : : : :					
a678	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```

g680.seq
1  ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51 GGCGACGAGG ACGCGCAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCTGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG

```

1089

```

151  CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201  AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251  GGTTCGCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301  GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351  GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401  GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451  TCGATAAACC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501  TTCGGCTTTG TTTAAACTGA TGTTTTTCTG TTTCACATGG TCGAGCAGCC
551  GTCCGACGGT GGCACGACT ATTTGCGAGC CGGCACGCAG GTCGGCGGTT
601  TGTTTGTTCCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651  GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
  1  MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
 51  RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101  ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151  SINPISNMRS ASSRTTISAL FKLMMFCFTW SSSRPTVATT ISQPARRSAV
201  CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
  1  ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
 51  GGCGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101  GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151  CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTGCA
201  GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251  GGTTCGCGCTT CTGAATGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301  GCGTTGGTGG TGTTTTGGCG GCGCACTTCG ACGGTTTCGG GCGCGTTCAT
351  GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401  GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451  TCGATAAAAC CCATATCCAG CATAAGGTCG GCTTCGTCCA AAACGACGAT
501  TTCGACTTTG TTCAAATGGA TGTTTTTCTG TTTCACGTGG TCGAGCAGCC
551  GTCCGACGGT GGCACGACG ATTTGCGAGC CGGCACGCAG GTCGGCGGTC
601  TGTTTGTTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651  GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
  1  MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
 51  RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101  ALVFCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151  SIKPISSIRS ASSKTTISTL FKWMFCFTW SSSRPTVATT ISQPARRSAV
201  CLSIFIPPNK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||||
g680      MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90     100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRFKXVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||||:|||||:|||||
g680      TLCLVLQKTTWFIKSTISRSSRLRFWKVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          70      80      90     100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFCFTW

```

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```

|||||
g680      ASLRIGAEKVAEKSRVWRWRGSICMILRMSSINPISNMRSASSRTTISALFKLMFFCFTW
              130      140      150      160      170      180

              190      200      210      220
m680.pep   SSSRPTVATTISQPARRSAVCLSIFIPPNTVWRSGRFLMX
              |||||
g680      SSSRPTVATTISQPARRSAVCLSM LTPPKRTVCRSGRFLMX
              190      200      210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2241>:

```

a680.seq
1   ATGACGAAGG GCAGTTCGGC AATATCCAGC CCCCGCGCGG CGATATCGGT
51  GGCGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTCGA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTCTTGCGC GGCGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CATACGGTCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GGCGACGACG ATTTTCGCAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>:

```

a680.pep
1   MTKGSSAISS PRAAISVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51  RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVSCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPNK TVWRSGRFLM *

```

m680/a680 98.6% identity in 220 aa overlap

```

              10      20      30      40      50      60
m680.pep     MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
              |||||:|||||:|||||
a680          MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
              10      20      30      40      50      60

              70      80      90      100     110     120
m680.pep     TLCLVLQNTMTWFICKSTISRSSRLRFXMVSTAMMCCSTLALVVCAATSTVSGAFMKSC
              |||||
a680          TLCLVLQNTMTWFICKSTISRSSRLRFXMVSTAMMCCSTLALVVCAATSTVSGAFMKSC
              70      80      90      100     110     120

              130     140     150     160     170     180
m680.pep     ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW
              |||||
a680          ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW
              130     140     150     160     170     180

              190     200     210     220
m680.pep     SSSRPTVATTISQPARRSAVCLSIFIPPNTVWRSGRFLMX
              |||||
a680          SSSRPTVATTISQPARRSAVCLSIFIPPNTVWRSGRFLMX
              190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2243>:

```

g681.seq
1   ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTCAAGCGC GCCGGGTACG GTGGcgacgg

```



```

101  tgatgtTTTC  GTCTGCTACG  CCCAATTCTT  GGAGGGTGCG  GCAGCAGACT
151  TTGAGCATT  GGCTGCCGAT  TTCGTTGGTG  AAGCGTGCCT  GTACGATGCC
201  GATGCGGAGG  TGTTTGcgt  cgaggttgGG  GGCGATGGTG  TTCATTGGGT
251  GTCCTTTGGT  ATTCGGGGTT  TCGGAATGCC  GTCTGAAGGT  TTCAGTCTTG
301  CGGCTGCCAG  TCGGCAACGG  TTTGGAATGT  GCCGTCTTCG  GCAAGCTCCC
351  ACGCGTGCC  TTCGGGTTGG  GAAAGCAGTG  CGGCGGTTTC  AGGGTTGGTT
401  TTGGTGATGT  CGGCGAGGCT  GACGATGCTG  AAGTTGTCCG  GGTCGTCGGT
451  GTATTCGTCG  GTTTCGTCGC  CGCTGAAGAA  ACGCCAGCCG  CTGTCGTTTT
501  CAAAAACGGG  GGCTTCGCGG  TAAAGGAAGC  CGACGGGCCG  GTTTTGTTTG
551  GCGACGGTGT  TGGTGGCGAT  GCAGCGGTCG  AGTGCCGAGG  AAAGTGCTTG
601  TGCAAATGCG  TTCATTGCGG  GAATACGTTG  GGGGGGGGGA  AACTTGCGGA
651  TTTTACCACG  ATTCCGCGT  TGTCGGCAGA  CGGCGGCGGT  TTGGTGGTAC
701  AATGTGCGCC  GTTTGCAGCC  TTAAGGTGTT  TCTGTATTTT  TGGAGTATGG
751  AAACGCATTC  GGGCTGTTTT  TTGCGGAAGA  CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

```

g681.pep
1  MTTTPMAISAS  NFSEEAKFIS  AMGISSAPGT  VATVMFSSAT  PNSWRVRQQT
51  LSIWLPISLV  KRACTMPMRR  CLPSRLGAMV  FIGCPLVFGV  SECRLKVSVL
101 RLPVGNGLC  AVFGKLPRAA  FGLGKQCGGF  RVGFGDVGEA  DDAEVVGVVG
151 VFVGFVAEE  TPAAVVFKN  GFAVKEADGP  VLFGDVGVD  AAVECRGKCL
201 CKCVHCGNTL  GGGKLADFTT  IPALSADGGG  LVVQCAPFAA  LRCFCIFGVW
251 KRIRAVFCGR  R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

```

m681.seq
1  ATGACGACGC  CGATGGCAAT  CAGTGCCTCA  AACTTTTCGG  AAGAGGCAAA
51  GTTCATCAGC  GCGATGGGGA  TTTCAAGCGC  GCCGGGTACG  GTGGCGACGG
101 TAATGTTTTT  GTCTGCCACG  CCCAATTCTT  GGAGGGTGCG  GCAGCAGACT
151 TTGAGCATT  CGCTGCCGAT  TTCGTTGGTG  AAGCGTGCCT  GTACGATGCC
201 GATGCGGAGG  TGTTTGCCGT  CGAGGTTGGG  GGCGATGGTG  TTCATTGGGT
251 GTCCTTTGGT  ATTCGGAGTT  TCGGAATGCC  GTCTGAAGGT  TTCAGTCTTG
301 CGGCTGCCAG  TCGGCGACGG  TTTGGAATGT  GCCGTCTTCG  GCAAGCTCCC
351 ATGCGCTGCC  TTCGGGTTGG  GAGAGCAGTG  CGGCGGTTTC  AGGGTTGGTT
401 TTGGCGATGT  CGGCGAGGCT  GACGATGCTG  AAGTTGTCCG  GATCGTCGGT
451 GTATTCGTCG  GTCTCGTCGC  CGCTGAAGAA  ACGCCAGCCG  CTGTCGTTTT
501 CAAAAACGGG  GGCTTCGCGG  TAGAGGAAGC  CGACGGGCCG  GTTTTGTTTG
551 GCGACGGTGT  TGGTGGCGAT  ACAGCGGTCG  AGTGCCGAGG  AAAGTGCTTG
601 TGCAAATGCG  TTCATTACGG  GAATACGTTG  GGGG.AAAAC  TTACGATT
651 TACCACGATT  CGTGCGTTGT  CGGCAGACGG  CGGCGGTTTG  GTGGTACAA
701 GTGCGCCGTT  TGCAGCCTTA  AGGTGTTTCT  GTATTTTGG  AGTATGGAAA
751 CGCATTCGGG  CTGTTTTTTG  CGGAAGACGG  TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

```

m681.pep
1  MTTTPMAISAS  NFSEEAKFIS  AMGISSAPGT  VATVMFSSAT  PNSWRVRQQT
51  LSIWLPISLV  KRACTMPMRR  CLPSRLGAMV  FIGCPLVFGV  SECRLKVSVL
101 RLPVGDGLEC  AVFGKLPCAA  FGLGEQCGGF  RVGFGDVGEA  DDAEVVRIVG
151 VFVGLVAEE  TPAAVVFKN  GFAVEEADGP  VLFGDVGVD  TAVECRGKCL
201 CKCVHYGNTL  GXKLDTFTI  RALSADGGGL  VVQCAPFAAL  RCFCIFGVWK
251 RIRAVFCGR  *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

          10      20      30      40      50      60
m681.pep  MTTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPLISLV
          |||||
g681      MTTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPLISLV
          10      20      30      40      50      60

```

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	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGDGLECAVFGKLPCAA					
g681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGNGLCAVFGKLPRAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVFGDVGGEADDAEVVRIVGVFVGLVAAEETPAAVVFNKGGFAVEEADGP					
g681	FGLGKQCGGFRVFGDVGGEADDAEVVGVGVFVGFVAAEETPAAVVFNKGGFAVKEADGP					
	130	140	150	160	170	180
	190	200	210	220	230	239
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVQCAPFAA					
g681	VLFGDGVGGDAAVECRGKCLCKVHCGNTLGGGKLADFTTIPALSADGGGLVVQCAPFAA					
	190	200	210	220	230	240
	240	250	260			
m681.pep	LRCFCIFGVWKRIRAVFCGRRX					
g681	LRCFCIFGVWKRIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1  ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTG CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GGCATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCGTCGGT
451 GTATTTCGTC GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAACGGG GGCCTTCGCG TAGAGGAAGC CGACGGGCTG GTTTTGTGTT
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGGTTG
601 TGCAATGCG TTCATTGCGG GAATACGTT. GGGGGAAC TTGCGGATTT
651 TACCACGATT CTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCGGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTGCGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1  ITPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFESSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVGFGDIGEA DDAEVVRVVG
151 VFVGLVAAEE TPAAVVFKN GFAVEEADGL VLFGDVGVDG AAVECRGKCL
201 CKCVHCGNTX GGKLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

	10	20	30	40	50	60
m681.pep	MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFESSATPNSWRVRQQTLSISLPISLV					
a681	ITTPMAISASNFSEEAKFISAMGISSAPGTVATVMFESSATPNSWRVRQQTLSISLPISLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGDGLECAVFGKLPCAA					
a681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGGFGMPSEGSVLRLPVGDGLECAVFCQFPRAA					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKN	GGFAVEEADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVR	VGVFVGLVAAEET	PAAVVFKN	GGFAVEEADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHYG	NTLGXKLTDFTTI	RALSADGGGLVV	QCAPFAAL	
a681	VLFGDGVGGDAAVE	CRGKCLCKCVHCG	NTXGGKLADFTT	ILALSADGGGLVV	QCAPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAAAT GCCGTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTG
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCCATTTCGA CAAGGCAGTC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVS YGKWRKNWDIR YCLLHLIHL SSTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY.. .EMAMPSEP DWIQTAFDMA YGFIRFPTDR
101 PIRTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

		10	20	30	40	50	60
m682.pep		MRDFTVWVSYGKWRKNWD	IRYCLHLHLHS	SSTRLRKCGRILSG	ICEPFLITPDLT	MHYC	
		:	:				
g682		MRDFAVWVPYGERRKNWD	IRYCLPHLIRLSPT	RLRKCGRILSG	ICEPFLITPDLT	MHYC	
		10	20	30	40	50	60
		70	80	90	100	110	
m682.pep		PILILIDY----	EMAMPSEPDW	IQTAFCMAYGF	FIREFPTDRPI	TRQSGVVRIS	PRTGFR
			:				
g682		PILILIDYICVNDEIK	MPSEPDW	IQTAFCM	A-GFIREFPTDR	PILTRQSGVVRIS	PRTGFR
		70	80	90	100	110	
		120	130				
m682.pep		YPTRSLPKSKKAYGX					
g682		YPTRSLPKSKKAYGX					
		120	130				

```
a682.seq
1  ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACACTGT CTATTTTGA TTTAAATTGA
201 ATAT.....
251 .....TATA TTCGGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCCGAC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA
```

```
a682.pep
  1 MRDFTVWVS Y GKWRKNWDIR YCLLHLIHL S STRLRKCGRI LSGICEPFCL
51 ITPDLTMHYC PILILIEY. . . . . . . . . . . . . . . . . .YIRFPTDR
101 PILTRPTGVV RISPRTGFR Y PTRSLPKSKK AYG*
```

		10	20	30	40	50	60
m682.pep		MRDFTVWVSYGKWRKNWDI	RYCLHLIHLSS	TLRKCGRILSGICE	PFCLITPDLTMHYC		
a682		MRDFTVWVSYGKWRKNWDI	RYCLHLIHLSS	TLRKCGRILSGICE	PFCLITPDLTMHYC		
		10	20	30	40	50	60
		70	80	90	100	110	120
m682.pep		PILILIDYEMAMPSEPDWI	QTAFCMAYGFIR	FPTDRPIRTRQSGVVRIS	PRTGFRYPTRS		
		:		:	:		
a682		PILILIEY-----	-----YIR	FPTDRPI	LTRPTGVVRIS	PRTGFRYPTRS	
				70	80	90	100
		130					
m682.pep		LPKSKKAYGX					
a682		LPKSKKAYGX					
		110					

```
g683.seq
1  ATGATTAAGG  AAACCCCTAAT  GCGCCCAATC  TTCTCATCTT  TCGTTTTACT
51  CCTATTTTG  ATAACCGCCT  GCAGCACACC  GGACAAGTCT  GCGCGATGGG
101 AAAATATCGG  CACAATCTCA  AACGGCAATA  TTCATACATA  TATTAATAAA
151 GACAGTGTTG  GAAAAACCG  AAATCTGTAT  ATTTTCCAG  ATAAAAAAGT
201 TGTTACCAAT  CTGAAACAAG  AAGCTTTTGC  CACACACGCC  CCATACAAGA
251 CTGCCATTGC  CGAGTGGGAA  ATCCACTGCA  ACAACAAAAC  ATACCGCTTA
301 AGTTCTGCAT  AGTTATTTTC  TACCAAAAAA  ACGGAAATTC  CCACACAAAA
351 CTACACAGCC  TCTTCCCTCG  GCCCGATGAG  CATCCTGTTC  GGGACATATA
```

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401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683 >:

g683.pep

```

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..

```

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTTACCAAT CTAAACAAG AACGTTTGC CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAG AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep..

```

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
g683	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMSILSGTLTEKQYETVCGKKLX					
g683	SSLRPMSILSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq

```

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
201 TGTTACCAAT CTAAACAAG AACGTTTGC CNACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AATGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep

```

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFXDKKVVTN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL
```

101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLFPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
a683	MIKETLMRPIFLSFVLFPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVTLNKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
a683	IFXDKKVVTLNKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMISLSGTLTEKQYETVCGKKLX					
a683	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

g684.seq

1	ATGCGCCTTT	TCCCATCGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACCGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCATCAACAC
201	CGCACAAAAC	CATGTTTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAC	CTTTGTTTCT
301	GCCTCAGCA	GCGGCAGTAC	CGACAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

g684.pep

1	MRLFPIAAAL	TLAACGTVQS	TOYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGGLVYQT	DPYRINTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRTFVP
101	ASRSGSTDKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	CYAAMTAALE	QGLKQAAQQM	VE*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

m684.seq

1	ATGCGCCTTT	TCCCGATTGC	CGCCGCCCTG	TCGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTTCT
301	GCCTCAGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CGATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

m684.pep

1	MRLFPIAAAL	SLAACGTVQS	TOYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGGLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD

151 GYAAMTAALE QGLKQAAQOM VE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

m684/g684 97.7% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPIAAALSLAACGTVQSTQYFVL	PDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT				
g684	MRLFPIAAALTLAACGTVQSTQYFVL	PDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT				
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGST	TEKWT	VYIDAFQGS			
g684	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGST	TEKWT	VYIDAFQGS			
	70	80	90	100	110	120
	130	140	150	160	170	
m684.pep	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
g684	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

a684.seq

1	ATGCGCCTCT	TCCCGATTGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTCTT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TGCACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTGAGATA			

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

a684.pep

1	MRLFPIAAAL	TLAACGTVQS	TQYFVL	PDSR	YIRPATQGG	TAVEVRLAEP
51	LKRGGGLVYQT	DPYRLNTAQN	HVWADTLDD	LEAALSNAFN	RLDSTRIFVP	
101	ASRSGST	TEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAALE	QGLKQAAQOM	VE*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPIAAALSLAACGTVQSTQYFVL	PDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT				
a684	MRLFPIAAALTLAACGTVQSTQYFVL	PDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT				
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGST	TEKWT	VYIDAFQGS			
a684	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGST	TEKWT	VYIDAFQGS			
	70	80	90	100	110	120
	130	140	150	160	170	

1098

```

m684.pep      YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
              |||
a684          YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
              130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

```

g685.seq
1  TTGTTTGGCC  GTATCGGGAA  TTTTGCCTTT  TCGGCGGTGG  TTTCTGCAGG
51  TTGTTTGGCTT  AATAATAAAC  ATTCTTATTC  GTATGCAAAG  GAACCGCACA
101 CCGTGAAACC  GCGTTTTTAT  TGGGCAGCCT  GCGCCGTCTT  GCCGGCCGCC
151 TGTTCCGCCG  AACCTGCCGC  CGAAAAAACT  GTATCCGCCG  CATCCCAAGC
201 CGCATCCACA  CCTGTGCCCA  CGCTGACCGT  GCCGACCGCG  CGGGCGGATG
251 CCGTTGTGCC  GAAGAATCCC  GAACGcgctcg  ccgtgtAcga  CtggtGCGGCG
301 TtggatACGC  TGACCGAGCC  GGGCGTGAAT  GTGGGCGCAA  CCACCGCGCC
351 GGTGCGCGTG  GACTATTGTC  AGCCTGCATT  TGACAAGGCG  GCAACGGTGG
401 GGACGCTGTT  TGAGCCCGAT  TGCGAATCCC  TGCACCGCCA  CAATCCGCAG
451 TTTGTCAATTA  CCGGCGGGCC  GGGTGCAGAA  GCGTATGAAC  AGTTGGCGAA
501 AAACCGCACC  ACCATAGATT  TGACGGTGGA  CAACGGCAAT  ATCCGCACCA
551 GCGGCGAGAA  GCAGATGGAG  ACCCTGTCTG  GGATTTTCGG  TAAGGAAGCG
601 CGCGTGGCGG  AATTGAATGC  GCAGATTGAC  GCGCTGTTCG  CCGAAAAGCG
651 CGAAGCCGCC  AAAGGCAAG  GACGCGGGCT  GGTGCTGTCT  GTTACAGGCA
701 ACAAGGTGTC  CGCCTTCGGC  ACGCAATCGC  GGTGGCAAG  TTGGATACAC
751 GGCGACATCG  GCCTGCCGCC  CGTGGACGAA  TCTTTACGCA  ACGAAGGGCA
801 CGGGCAGCCC  GTTTCCTTCG  AATACATCAA  AGAGAAAAAC  CCGGCTGGA
851 TTTTCATCAT  CGACCGCACC  GCCGCCATCG  GGCAGGAAGG  GCCGGCTGCC
901 GTGGAAGTGT  TGGATAACGC  GCTGGTATGC  GGCACGAACG  CTTGGAAGCG
951 CAAGCAAATC  ATCGTCATGC  CTGCCGCGAA  CTACATTGTC  GCGGGCGGCG
1001 CGCGGCAGTT  GATACAGGCG  GCGGAACAGT  TGAAGCGCGG  GTTTGAAAAA
1051 GCAGAACCCG  TTGCGGCGCA  GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685>:

```

g685.pep
1  LFCRIGNFAF  CGVVSAGCLL  NNKHSYSYAK  EPHTVKPRFY  WAACAVLPAA
51  CSPEPAEAKT  VSAASQAAST  PVATLTVPTA  RGDVAVPKNP  ERVAVYDWAA
101 LDTLTPGVN  VGATTAPVRV  DYLLQPAFDKA  ATVGLTFEPD  CESLHRHNPQ
151 FVITGGPGAE  AYEQLAKNAT  TIDLTVDNNG  IRTSGEKQME  TLSRIFGKEA
201 RVAELNAQID  ALFAQKREAA  KGKGRGLVLS  VTGNKVSAG  TQSRLASWIH
251 GDIGLPPVDE  SLRNEGHGQP  VSFYIYEKN  PGWIFIIDRT  AAIGQEGPAA
301 VEVLDNALVC  GTNAWKRKQI  IVMPAANYIV  AGGARQLIQA  AEQLKAAFEK
351 AEPVAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

```

m685.seq
1  TTGTTTGGCC  GTATCGGGAA  TTTTGCCTTT  TCGGCGGTGG  TTTCTGCAGG
51  TTGTTTGGCTT  AATAATAAAC  ATTCTTATTC  GTATGCAAAG  GAACCGCACA
101 CCGTGAAACC  GCGTTTTTAT  TGGGCAGCCT  GCGCCGTCTT  GCTGACCGCC
151 TGTTCCGCCG  AACCTGCCGC  CGAAAAAACT  GTATCCGCCG  CATCCGCATC
201 TGCCGCCACG  CTGACCGTGC  CGACCGCGCG  GGGCGATGCC  GTTGTGCCGA
251 AGAATCCCGA  ACGCGTCGCC  GTGTACGACT  GGGCGGCGTT  GGATACGCTG
301 ACCGAATTGG  GCGTGAATGT  GGGCGCAACC  ACCGCGCCGG  TGCGCGTGGA
351 TTATTTGCAG  CCTGCATTG  ACAAGGCGGC  AACGGTGGGG  ACGCTGTTTCG
401 AGCCCCGATTA  CGAAGCCCTG  CACCGCTACA  ATCCTCAGCT  TGTCATTACC
451 GCGGGGCGCG  GCGCGGAAGC  GTATGAACAG  TAGCGAAAA  ACGCGACCAC
501 CATAGATCTG  ACGGTGGACA  ACGGCAATAT  CCGCACCAAG  GCGGAAAAGC
551 AGATGGAGAC  CTTGGCGCGG  ATTTTCGGCA  AGGAAGCGCG  CGCGGCGGAA
601 TTGAAGGCGC  AGATTGACGC  GCTGTTTCGCC  CAAACGCGCG  AAGCCGCCAA
651 AGGCAAAGGA  CGCGGGCTGG  TGCTGTCTGG  TACGGGCAAC  AAGGTGTCCG
701 CCTTCGGCAC  CGAGTCGCGG  TTGGCAAGTT  GGATACACGG  CGACATCGGC
751 CTACCGCCTG  TAGACGAATC  TTTACGCAAC  GAGGGGCACG  GGCAGCCTGT
801 TTCTTTCGAA  TACATCAAAG  AGAAAAACCC  CGATTGGATT  TTCATCATCG
851 ACCGTACCGC  CGCCATCGGG  CAGGAAGGGC  CGGCGGCTGT  CGAAGTATTG
901 GATAACGCGC  TGGTACGCGG  CACGAACGCT  TGGAAAGCGCA  AGCAAATCAT
951 CGTCATGCCT  GCCGCGAATT  ACATTGTCGC  GGGCGGCGCG  CGGCAGTTGA
1001 TTCAGGCGGC  GGAGCAGTTG  AAGCGGCGCT  TTAAGGAGGC  AGAACCCGTT
1051 CCGGCGGGGA  AAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

m685.pep

1099

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKKGK RGLVLSVTGN KVSAGFTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQ LKAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

```

m685/g685    94.4% identity in 356 aa overlap

              10      20      30      40      50      60
m685.pep     LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
              |||||
g685          LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPEPAAEKT
              10      20      30      40      50      60

              70      80      90      100     110
m685.pep     VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
              ||||| :|
g685          VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTEPGVNVGATTAPVRV
              70      80      90      100     110     120

              120     130     140     150     160     170
m685.pep     DYLPAPAFDKAATVGTLEFPDYEALHRYNPQLVITGGPGAEEYQLAKNATTIDLTVDNGN
              |||||
g685          DYLPAPAFDKAATVGTLEFPDCESLHRHNPQFVITGGPGAEEYQLAKNATTIDLTVDNGN
              130     140     150     160     170     180

              180     190     200     210     220     230
m685.pep     IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKKGKRGVLVSVTGNKVSAGF
              |||||
g685          IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKKGKRGVLVSVTGNKVSAGF
              190     200     210     220     230     240

              240     250     260     270     280     290
m685.pep     TQSRLASWIHGDIGLPPVDESLRNEGHPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA
              |||||
g685          TQSRLASWIHGDIGLPPVDESLRNEGHPVSEFYIKEKNPGWIFIIDRTAAIGQEGPAA
              250     260     270     280     290     300

              300     310     320     330     340     350
m685.pep     VEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQKAAFKKAEPVAAAGKKX
              |||||
g685          VEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQKAAFEKAEPVAAQX
              310     320     330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTTGCC GTATCGGGAA TTTTGCCTTT TCGCGCTGG TTTCTGCAGG
51 TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAACCC GCGTTTATAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
351 TTATTTGCAG CCTGCATTG ACAAGGCGGC AACCGTGGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTATTACC
451 GGCGGGCCGG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCGAAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAAGG CGCGGGCTGG TGCTGTCCGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

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1100

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851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGAAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAACT ACATTGTGCG GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

a685.pep

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAGFTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSE FYIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQL KEAFKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

m685/a685 98.9% identity in 355 aa overlap

	10	20	30	40	50	60
m685.pep	LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPPEAAEKT					
a685	LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPPEAAEKT					
	10	20	30	40	50	60
m685.pep	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
a685	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
	70	80	90	100	110	120
m685.pep	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
a685	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
	70	80	90	100	110	120
m685.pep	PAFDKAATVGTLEFDPYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS					
a685	PAFDKAATVGTLEFDPYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS					
	130	140	150	160	170	180
m685.pep	PAFDKAATVGTLEFDPYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS					
a685	PAFDKAATVGTLEFDPYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS					
	130	140	150	160	170	180
m685.pep	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGFTQSR					
a685	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGFTQSR					
	190	200	210	220	230	240
m685.pep	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGFTQSR					
a685	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGFTQSR					
	190	200	210	220	230	240
m685.pep	LASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
a685	LASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
	250	260	270	280	290	300
m685.pep	LASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
a685	LASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
	250	260	270	280	290	300
m685.pep	DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAGKKX					
a685	DNALVRGTNAWKRKQIIVMPAANYIVAGGSRLIQAAEQLKAAFEKAEPVAAGKEX					
	310	320	330	340	350	
m685.pep	DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAGKKX					
a685	DNALVRGTNAWKRKQIIVMPAANYIVAGGSRLIQAAEQLKAAFEKAEPVAAGKEX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

g686.seq (partial)

```

1  ..AATTTCTCCT GCCGCGCCGA TGATGTTTT GACGATATCT GCAGTGCCGT
51  TGAAGGCTTC ggcgGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCGTCAGCA TAGCGCCGGC
151 ATTGTGGAAA CGGTCGGCAA GCCGTGTGCC GGTGCTGCGG TTGTCGGTCA
201 GGTTAGGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTG CGTATCCGTC CCAATGGATG CGGTAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686>:

```
g686.pep (partial)
1  ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
51  IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

```
m686.seq..
1  ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCGGCAT TGGTTTGGC
51  GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
201 CGCGTTTGAA TCCGTCGCCT ACTCCTTGC TACGACATACT ACCGGCATTG
251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
401 TCGGCGGGAT GGTGTTCTGA TCCGTCCCAA TGGATGCGGT AAAGGCTAAA
451 TCCGTCACCG GGACTACCGG CTCATCAGA ATCGGAATGT GA
```

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

```
m686.pep
1  MMLKKFVLGG IAALVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
51  GFGGIARSVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFV SVPMDAVKAK
151 SVNGTTGFIR IGM*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

				10	20	30
g686.pep				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKKFVLGGIAALVLAACG	SGSEGGSGAXX	XXNFSCSADDVFNDICSAVEGFGGIARSVQLG			
	10	20	30	40	50	60
		40	50	60	70	80
g686.pep		AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
m686		AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
		70	80	90	100	110
						120
		100	110	120	130	
g686.pep		GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFVRIGMX				
m686		GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFVRIGMX				
		130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

```
a686.seq (partial)
1  ..AATTTCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAAGCTTC GCGGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGCTCAGCA TACTACCGGT
151 ATTGTGGAAA CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGAGGCGG GATATTTTGG GCAACGCCCT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTG CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA
```

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

```
a686.pep (partial)
```

1102

```

1  ..NFSCRADDVF DDICSAVESF GGIARSVQLG AVSGGAFESV AYSLRQHTTG
51  IVETVDKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFSV PMDAVKAESV NGTTGFIRIG M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. meningitidis*:

```

m686/a686    96.2% identity in 131 aa overlap

              10      20      30      40      50      60
m686.pep     LKKFVLGGIAALVLAACGGSEGGSGAXXXNFSCSADDFVNDICSAVEGFGGIARSVQLG
a686          ||| ||||:|||||:|||||
              10      20      30
              70      80      90     100     110     120
m686.pep     AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
a686          |||||:|||||:|||||:|||||:|||||:|||||
              40      50      60      70      80      90
              130     140     150     160
m686.pep     GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX
a686          |||||:|||||:|||||:|||||
              100     110     120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2279>

```

g687.seq
1  ATGAAATCCA GACACCTCGC CCTCGCCCTC GCGGTGCGG CCTGTTCGC
51  CCTTGCCGGG TCGGACAGCA AAGTCCAAAC CAGCGTCCCC GCGACAGCG
101 CGCCTGCCGC TTCGGCAGCC GCCGCCCGG CAGGACTGGT CGAAGGGCAA
151 AACTACACCG TCCTTGCCAA CCGGATTCCT CAACAGCAGG CAGGCAAGGT
201 TGAAGTGCTT GAGTTTTCG GCTATTTTG TCCGCACTGC GCCCGCCTcg
251 AACCTGTTTT GAGCAAACAC GCCAAGTCTT TTAAGACGA TATGTACCTG
301 CGTACCGAAC ACGTCGTCTG GCAGAAAGAA ATGCTGCCGC TGGCACGCct
351 cGCCGCCGCC GTCGATATGG CTGCCGCCGA AAGCAAAGAT GTGGCGAACA
401 GCCATATTTT CGATGCGATG GTCAACCAAA AAATCAAGCT GCAAGAGCCG
451 GAAGTCCTCA AAAAATGGCT GGGCGAACAa ACcgcttTG ACGGCAAAAA
501 AGTCCTTGCC GCCTACGAAT CCCCCGAAAG TCAGCGCGGC GCcggcAAAA
551 TGCAGGAGCT GACCGAAACC TTCCAAATCG ACGGTACGCC CACGGTTATC
601 GTCGGCGGCA AATATAAAGT CGAATTTGCC GACTGGGAGT CCGGTATGAA
651 CACCATCGAC CTTTGGCGG ACAAAGTACG TGAAGAACAA AAAGCCGCGC
701 AGTAG

```

This corresponds to the amino acid sequence <2280 ID 724; ORF 687 >:

```

g687.pep
1  MKSRHLALAL GVAALFALAA CDSKVQTSVP ADSAPAASAA AAPAGLVEGQ
51  NYTVLANPIP QQQAGKVEVL EFFGYFCPHC ARLEPVLSKH AKSFKDDMYL
101 RTEHVWVQKE MLPLARLAAA VDMAAAESKD VANSHIFDAM VNQIKIKLQEP
151 EVLKKWLGEQ TAFDGKKVLA AYESPESQAR AGKMQELTET FQIDGTPTVI
201 VGGRYKVEFA DWESGMNTID LLADKVREEQ KAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2281>:

```

m687.seq
1  ATGAAATCCA GACACCTTGC CCTCGGCGTT GCCGCCCTGT TCGCCCTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAGCGT CCCCGCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACCGTCCTTG CCAACCCGAT TCCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAAGCA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCCTCGCCGC
351 CGCGGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAAA TCCGGAAAGT
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT

```

```

501 TGCCGCCTAC GAGTCCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGTAATATA AAGTTGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAGGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>:

```

m687.pep
1  MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVVWQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QRIKLQNPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

```

m687/g687  97.0% identity in 234 aa overlap

          10      20      30      40      50
m687.pep  MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPASAAAAAPAGLVEGQNYTVLANPIP
          |||||  |||||  |||||  |||||  |||||
g687       MKSRHLALALGV AALFALAACDSKVQTSVPADSAPASAAAAAPAGLVEGQNYTVLANPIP
          10      20      30      40      50      60

          60      70      80      90      100     110
m687.pep  QQQAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTHEVVWQKEMLTLARLAAA
          |||||  |||||  |||||  |||||  |||||  |||||
g687       QQQAGKVEVLEFFGYFCPHCARLEPVLSKHAKSFKDDMYLRTHEVVWQKEMPLARLAAA
          70      80      90      100     110     120

          120     130     140     150     160     170
m687.pep  VDMAAADSKDVANSHIFDAMVNQIKLQNPVLEVLKWLGEQTAFDGKKVLAAYESPESQAR
          |||||  |||||  |||||  |||||  |||||  |||||
g687       VDMAAAESKDVANSHIFDAMVNQIKLQEPVLEVLKWLGEQTAFDGKKVLAAYESPESQAR
          130     140     150     160     170     180

          180     190     200     210     220     230
m687.pep  ADKMQLTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          |||||  |||||  |||||  |||||  |||||  |||||
g687       AGKMQLTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

```

a687.seq
1  ATGAAATCCA AACACCTCGC CCTCGCGGTT GCCGCCCTGT TCGCACTTGC
51  CGCGTGCAGC AGCAAAGTCC AAACCAGCGT CCCC GCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAAACTAT
151 ACTGTCTCTT CCAACCCGAT TCCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCT TCTGGCAGAA AGAATGCTG ACGCTCGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAAATCA AGCTGCAAGA GCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAGTCCT
501 TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGCAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAGGCC GCGCACTAA

```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

```

a687.pep
1  MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVVWQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QRIKLQEPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

m687.pep	10	20	30	40	50	60
	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAAASAAAAPAGLVEGQNYTVLANPIPQQ					
a687	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAAASAAAAPAGLVEGQNYTVLANPIPQQ					
	10	20	30	40	50	60
m687.pep	70	80	90	100	110	120
	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVWQKEMTLARLAAAVD					
a687	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVWQKEMTLARLAAAVD					
	70	80	90	100	110	120
m687.pep	130	140	150	160	170	180
	MAAADSKDVANSHIFDAMVNQIKLQNPVLLKWLGEQTAFDGKKVLAAYESPESQARAD					
a687	MAAADSKDVANSHIFDAMVNQIKLQNPVLLKWLGEQTAFDGKKVLAAYESPESQARAD					
	130	140	150	160	170	180
m687.pep	190	200	210	220	230	
	KMQLTETTFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX					
a687	KMQLTETTFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAHX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTTGCACAG	AAAGGTTCTC	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTGTT	CAGCCTGACC	GCGTGCAGCG
101	TCGAACGCGT	CTCGCTGTT	CCCTCCTACA	AACTCAAAAT	CATCCAAGGC
151	AACGAACTCG	AACCGCGCGC	CGTTGCCGCC	CTGCGCCCGC	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688>:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DALQNAAEAL	RAKQNADKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTTGCACAG	AAAGGCATTT	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTCCT	CGGCCTTGCC	GCGTGCAGTG
101	CCGAACGCGT	TTCACGTGTC	CCCTCGTACA	AACTCAAAAT	CATACAGGGC
151	AACGAACTCG	AACCGCGCGC	CGTTGCCGCC	CTCCGCCCGC	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCATTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGTCCTGC	AAAACGCTGC	CGAAGCCCTC	AAAGACCGCC
401	AAAACACAGA	CAAACCATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHPSRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DVLQNAAEAL	KDRQNTDKP*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

m688/g688 90.6% identity in 138 aa overlap

	10	20	30	40	50	60
m688.pep	VLHYP	SRFAQGISVN	KTLLALSALL	GLAACS	SAERVS	LFPSYKLKIIQ
g688	VLHXT	SRFAQGSPVN	KTLLALSALL	GLAACS	SAERVS	LFPSYKLKIIQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m688.pep	LRPGMT	KDQVLL	LLGSPILR	DAFHTDR	WDYTFNT	SRNGI
g688	LRPGMT	KDQVLL	LLGSPILR	DAFHTDR	WDYTFNT	SRNGI
	70	80	90	100	110	120
	130	140				
m688.pep	DVLQN	AEEALKDR	QNTDKPX			
g688	DALQN	AEEALKDR	QNTDKPX			
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

a688.seq

1	GTGTT	ACTACT	ACCCAT	CCCG	ATTTGC	CACAG	AAAGGC	ATTT	CCGTGA	AACAA
51	AACCT	CATC	CTCGC	CTTT	CGGCC	CTCCT	CGGC	CTTGCC	GCGTGC	AGCG
101	TCGA	ACGCGT	TTCAC	TGTT	CCCTCG	TACA	AACTCA	AAAT	CATAC	AGGGC
151	AACGA	ACTCG	AACCT	CGCG	CGTGC	CCTCC	CGCCCG	GTATGA	ACCAA	
201	AGAC	CAAGTC	CTGCT	CCTGC	TCGGC	AGCCC	CATACT	GC	GACGC	ATTC
251	ATAC	CGACCG	CTGGG	ACTAT	ACCTT	CAACA	CCTCC	CGCAA	CGGC	ATCATC
301	AAAG	ACCGAA	GCAAT	CTGAC	CGTCT	ATTTT	GAAA	ACGGCG	TGCTCG	TCCG
351	CACG	AAGGC	AACGC	CCTGC	AAAAT	GCCGC	CGAAG	CCCTC	CGCGT	AAAC
401	AAAAC	GCAGA	CAACA	ATAA						

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

a688.pep

1	VLHYP	SRFAQ	KGISVN	KTLL	LALSALL	GLAACS	SAERVS	LFPSYKLKIIQ
51	NELEP	RAVAS	LRPGMT	KDQV	LLLGSP	ILRDAF	HTDRWDY	TFNTSRNGII
101	KDRS	NLT	VYF	ENGLV	LRTEG	NALQN	AEEAL	RVKQNA

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

m688/a688 93.5% identity in 138 aa overlap

	10	20	30	40	50	60
m688.pep	VLHYP	SRFAQGISVN	KTLLALSALL	GLAACS	SAERVS	LFPSYKLKIIQ
a688	VLHYP	SRFAQGISVN	KTLLALSALL	GLAACS	SAERVS	LFPSYKLKIIQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m688.pep	LRPGMT	KDQVLL	LLGSPILR	DAFHTDR	WDYTFNT	SRNGI
a688	LRPGMT	KDQVLL	LLGSPILR	DAFHTDR	WDYTFNT	SRNGI
	70	80	90	100	110	120
	130	140				
m688.pep	DVLQN	AEEALKDR	QNTDKPX			
a688	NALQN	AEEALRVK	QNA	DKQX		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

g689.seq (partial)

```

1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTTCCAT CGATGCCTAC CTGCCCGCGA
101  TTCCCGAAAT GGCAGCGCGG CTGAACGCGG ATATCCACCG TATCGAATAG
151  AGTCTGAGTT TGTATTATGTT CGGCACGGCG TTCCGGGCAAG TGGCCGGCGG
201  CGCGGTGTCC GACATCAAAG GCGCAAACCG CGTCGCCCTG ACCGGTTTGA
251  TTGTATATTG CCTTGGCGTT GCCGCCATCG TATTGCTTC GAGTACCGAA
301  CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCCGGCGCAG GCATGGCTGT
351  AGTCATCGTC ggtgcgatgg tgcgcgatTA TTATCCGGA CGCAAAGCCG
401  cgcAGATGTT TGCCCTTATC GGCATCATTG TGATGGTTGT GCCGCTGGCC
451  GCACCCATGG TCGGCGCATT GTTGCAAGGA TTGGGCGGAT GCGGGCGCAT
501  TTTCTTTTTC ttggcGgcgT ATTGCGCGGT GCTGCCCGGT TTGGTACAGT
551  ATTTCTTGCC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTT
601  GGGCTGGTGG CGGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCGCGAT
651  GGGTtatCTG TTTTTCAGG CATTGAGCTT CGGTTCGATG TTCGCCTTTC
701  TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACACGT TACGCCGCAC
751  CGGTACGCAT GGTGTTTGC ACTCAACATC ATCAGCATGA TGTTTTTCAG
801  CCGCGTTACC GCGTGGCGGC TTAACACCGG CGCGCATCCG CAAAGCATCC
851  TGCTGCGGGG GATTGTCTGTC CAATTGCGG CCAACCCGTC CCAACTCGCC
901  GCCGTGCTGT TTTTCGGGTT GCGCCCGTTT TGGCTGCCGG TCGCGTCCGT
951  GATGTTTTTC GTCGGTACGC AGGGCCTGGT CGGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAA GAAGAGGGCG GCAGCGCGAA CGCCGTGTCG
1051 GGTGTATTCC GGTCCCTAAT CGGCGCGGGC GTGGTCATGG CGGCAACCGT
1101 GATGGCGGCA ACCATGACCG CGTCCGCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGGAAGGAAA ACGAAAAAAA GCGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689>:

g689.pep (partial)

```

1  ..SPPLPEMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SLSLFMFQTA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101  QLLNLRAVQA FGAGMAVVIV GAMVRDYISG RKAAQMFALI GILMVVPLA
151  APMVGALLQG LGGWRAIFVF LAAYSPVLPG LVQYFLPNPA VGGKIGRDVF
201  GLVAGRFRKRV LKTRAAMGYL FFQAFSFGSM FAFLETSSFV YRQLYHVTPH
251  RYAWVFALNI ITMFFSRVT AWRLKTGAHP QSILLRGIVV QFAANPSOLA
301  AVLFFGLPPE WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351  GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKRIL

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

m689.seq

```

1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTCG CCGGGCTTTT
51  GTTGCCGCTT GTTTGTGCGG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101  GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151  CTTTCTGCCC ATTATCCTGA AATGAGCGAA AAAGTATGAG CGGTTTTGAT
201  GCGGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
251  CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301  CAGAGTTTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTTCG
351  CGGTTCCGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401  TGATTGTATA TTGCCCTGCC GTTGCCGCCA TCGTATTGTT TTCGAGTGCC
451  GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTGCGTG CCGGCATGAC
501  TGTGGTCATC GTCGGCGCAA TGGTGCGCGA TTATTATTCC GGACGCAAAG
551  CCGCCAGATG GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601  GTCGCACCCA TGGTCGGGCG ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651  GATTTTTGTT TTTCTGGCGG CGTATTGCTT GGTGCTGCTC GGTTTGGTAC
701  AGTATTTCTT GCCCAAGCCC GCCGTGCGCG GCAAAATCGG ACGGACGCTG
751  TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAAA CCCGTGCTGC
801  GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTGCGTTTC ATGTTGCGCT
851  TTCTGACCGA ATCTTCCTTC GTGTACGAGC AGCTCTACCG TGTTACGCTT
901  CATCAATACG CTTGGGCGTT TGCATCAAC ATCATACGA TGATGTTTTT
951  CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CCGCGTGCAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACTT GTCCAACTC
1051 GCCGCCGTGC TGTTTTTCGG GTTGCCCCCG TTTTGCTGCT TGGTCGCGTG
1101 CGTGATGTTT FCCGTGCGTA CGCAGGGCTT GGTGCGTGCA AACACGCGAG
1151 CGTGTGTTAT GTCCTATTTT AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTCTTTCAC GACGGTTCGG CAACCGTGAT GCGGGCAACG ATGACCGCGT
1301 CCACCTCTTG CGGCATTGCG CTCTGTGGC TCTGCTCGCA TCGTGCCTGG

```


1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA

This corresponds to the amino acid sequence <SEQ ID 2294; ORF 689>:

m689.pep
 1 LLIHYIVPVR PVLPGLLLP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
 51 PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
 101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLIVYCLA VAAIVFVSSA
 151 EQLNLNRVVO AFGAGMTVVI VGAMVRDYY SGRKAAQMFAL IGIILMVVPL
 201 VAPMVGALLQ GLGGWQAI FV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
 251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSV VYQQLYRVTP
 301 HQYAWAFALN IITMMFFNRV TAWRLKTGVH PQSILLWGIV VQFAANLSQL
 351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
 401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
 451 KENGQSEYL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

m689.pep	30	40	50	60	70	80
	CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSEKLMAVLMAMLVTLMPFSIDAY					
g689						
					SPPLPPMSGKLMAVLMAVLVALMPFSIDAY	
				10	20	30
m689.pep	90	100	110	120	130	140
	LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLAV					
g689						
	LPAIPEMAQPLNADIHRIEXSLSLFMFGTAFGQVAGGAVSDIKGRKPVALTGLIVYCLAV					
	40	50	60	70	80	90
m689.pep	150	160	170	180	190	200
	AAIVFVSSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYYSGRKAQMFALIGIILMVVPLV					
g689						
	AAIVFASSTEQLNLNRVVQAFGAGMAVVIVGAMVRDYYSGRKAQMFALIGIILMVVPLA					
	100	110	120	130	140	150
m689.pep	210	220	230	240	250	260
	APMVGALLQGLGGWQAI FV FLAAYSLVLLGLVQYFLPKPAVGGKIGRDVFGVLVAGRFRKRV					
g689						
	APMVGALLQGLGGWRAIFVFLAAYSPVLPGLVQYFLPNPAVGGKIGRDVFGVLVAGRFRKRV					
	160	170	180	190	200	210
m689.pep	270	280	290	300	310	320
	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMMFFNRVT					
g689						
	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYRQLYHVTPHRYAWVFALNIITMMFFSRVT					
	220	230	240	250	260	270
m689.pep	330	340	350	360	370	380
	AWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMF SVGTQGLVGAN					
g689						
	AWRLKTGAHPQSILLRGIVVQFAANPSQLAAVLFFGLPPFWLPVACVMF SVGTQGLVGAD					
	280	290	300	310	320	330
m689.pep	390	400	410	420	430	440
	TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDGSATVMAATMTASTSCGIAL					
g689						
	TQACFMSYFKEEGGSANAVSGVFRSLIGAGVMAAT-----VMAATMTASASCGIAL					
	340	350	360		370	380
m689.pep	450	460				
	LWLCSHRAWKENGQSEYLX					
g689						
	LWLCSHKAWKENEKKRIL					
	390	400				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

```
a689.seq
1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTCG CGGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCT CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTATATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAAGTATGAT CGGTTTGTAT
201 GGCATGCTCG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCCG
251 CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCACG GCGTTCGGAC AGGTGGTCGG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGGCCCTCTA CTGCCTTGCC GTTGCCGCCA TCGTATTTCG TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTGCGTG CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCSCGA TTATTATTCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTGTGT TTTCTGGCGG CGTATTGCGT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG CAGGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCCGTGCCCG
801 GATGGGTAT CTGTTTTC AGGCATTGAG CTTGCGTTCG ATGTTGCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCA CGTTACGCCG
901 CACCAGTACG CTTGGGCGTT TGCACCAAC ATCATCACGA TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAAC CGGCGTGCAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGCGTT GGTGCGTGCA AACACGCAGG
1151 CGTGTTTAT GTCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGCGCAC
1251 CTTCTGTCAC GACGGTTCGG CAACCGTGAT GCGGCAACC ATGACCGCGT
1301 CTACCTCTTG CGGCATTGCG CTTTGTGGC TCTGCTCGCA TCGTGGCTGG
1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

```
a689.pep
1  LLIHYIVPVR PVLPGLLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLLNLRVVQ AFGAGMTVVI VGAMVRDYSY GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAIFV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSV VYQQLYHVT
301 HQYAWAFALN IITMEFFNRI TAWRLKTGVH PQSILWGVIV VQFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

m689/a689 99.1% identity in 459 aa overlap

```

          10      20      30      40      50      60
m689.pep  LLIHYIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
          |||
a689      LLIHYIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
          10      20      30      40      50      60

          70      80      90      100     110     120
m689.pep  KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
          |||
a689      KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
          70      80      90      100     110     120

          130     140     150     160     170     180
m689.pep  SDIKGRKPVALTGLIVYCLAVAAIVFVSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYS
          |||
a689      SDIKGRKPVALTGLAVYCLAVAAIVFASSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYS
          130     140     150     160     170     180

          190     200     210     220     230     240
m689.pep  GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIFVFLAAYSLVLLGLVQYFLPKP
```

1109

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|||||
a689  GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWOAIFVFLAAYSLLVLLGLVQYFLPKP
      190      200      210      220      230      240

      250      260      270      280      290      300
m689.pep  AVGGKIGRDVFGVLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP
      |||||
a689  AVGGKIGRDVFGVLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYHVT
      250      260      270      280      290      300

      310      320      330      340      350      360
m689.pep  HQYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFFGLPP
      |||||
a689  HQYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFFGLPP
      310      320      330      340      350      360

      370      380      390      400      410      420
m689.pep  FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLH
      |||||
a689  FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLH
      370      380      390      400      410      420

      430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEYLX
      |||||
a689  DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEYLX
      430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

g690.seq (partial)

```

1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTCCCAAAC CGATTGCAA
151 CCGGCCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCCTGC ACCCGGCCGC CGGCATTGGC GATCTCATAC
251 AGCAAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 AACGAACTGG AAACCCGTTT CGGCTTACCC GGCGGCGGCT ATGACAACAT
351 ACAGCGGCTG CTgtttCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACCCGC GgCAAGGCG
551 AGGAACCGAA ACGCGCACGT TATTTGAAG TTTCGGCAAC ATctgCctaT
601 TTgaaccgGC ACAaacaacGG ACTTggcgGC AATTTCaAT ACATCGGCCA
651 ATTGCCCGGC TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTtagAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

g690.pep (partial)

```

1  MKNKTS LPL WLAAILAAR SPSKEDKKE NGASAASSSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQQIAEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSQKTR GQGEPPKRAR YFEVSATSAY
201 LNRHNNGLGG NFQYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPDKPF LD
251 IHFDENGKIT RIVVYEKN IY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

m690.seq .

```

1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCCGGTCAT
101 CCGCTGTCTC GTCCTCCGCG TCATCAGCTC CTCCCAAAC CGATTGCAA
151 CCGACCCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATTGC ACCAGCCTGC ACCCGGCCAC CGGCATTGAC GATCTCATGC
251 AGCAAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 CACGAACTGG AAACCCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCGC GGACAAGGCG

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1110

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551 AGGAGCCGAA ACGCACGCGT TATTTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTTCCAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTGTAGAC
751 ATCCATTGTT ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCAATCCAA ACACGGGGCG AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
1  MKNKTSLLLL WLTAIMLTAC SPSKDDKTKE VGASAASSA SSAPSQTDLQ
51 PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQQIAEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQKIILAI EDLRYGKRTI
151 SRQAQNALME QERRLREATL LLIQGSQETR GQGEPEPKRTR YFEVSATPAY
201 SSRHNNGLGG NFQYISQLPG YLKIHGEMLE NQSLFRLSNR ERNPDKPFLL
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

m690/g690 89.3% identity in 408 aa overlap

	10	20	30	40	50	60
m690.pep	MKNKTSLLLLWLTAIMLTAC	SPSKDDKTKEVGASAASSA	SSAPSQTDLQ	PTASAPDNVK		
g690	MKNKTSLLPLWLAAILAAR	SPSKEDKTKENGASAASSA	SSQTDLQPAASAPDNVK			
	10	20	30	40	50	60
	70	80	90	100	110	120
m690.pep	QAESAPPSNCTSLHPATGID	DLMQQIAEHIDSDCLFALSH	HELETRFGLPDGGYDNIQRL			
g690	QAESAPLXNCTGLHPAAGIGD	LIQIAEHIDSDCLFALSH	NELETRFGLPGGYDNIQRL			
	70	80	90	100	110	120
	130	140	150	160	170	180
m690.pep	LFPDIRPEDPDYHQKIILAI	EDLRYGKRTISRQAQNALME	QERRLREATLLLIQGSQETR			
g690	LFPDIRPEDPDYHQKIMLAIE	DLRYGTRTISRQAQDAIME	QERRLREATLMLTQGSQKTR			
	130	140	150	160	170	180
	190	200	210	220	230	240
m690.pep	GQGEPEPKRTRYFEVSATPAY	SSRHNNGLGGNFQYISQLPG	YLKIHGEMLENQSLFRLSNR			
g690	GQGEPEPKRTRYFEVSATPAY	LNRRHNNGLGGNFQYISQLPG	YLMKHGEMLENQSLFRLSNR			
	190	200	210	220	230	240
	250	260	270	279		
m690.pep	ERNPDKPFLLIHFDENGKIT	RIVVYEKNIYFNPNTGRI				
g690	ERNPDKPFLLIHFDENGKIT	RIVVYEKNIY				
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
51  GACCGCGTGT TCCCGGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTC GTCCACGGCA TCCCGCGCTT CGTCTCCGC GCCCCAAACC
151 GATTTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCGC TCAAAATTGCA CCGACCTGCA CCCC GCCACC GGCATTGACG
251 ATCTCATGCA GCAAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCTGTTT GGCTTACCCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTTCCCGA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGCAATTG AAGACTTGCG TTACGGAAAG
451 CGCACGATCA GCCGGCAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
551 GACAAGGCGA GGAGCCGAAA CGCACGCGTT ATTTTGAAGT TTCGGCAACC
601 CTGCCTATT CGAGCCGGCA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGCCAA TTGCCCGGCT ATCTGAAAAT ACACGGAGAA ATGCTTGAAA

```

1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTATAGACA TCCATTTTGA CGAAAATGGC AAAATCACGC GTATTGTCGT
 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep

1 MKNKTSSLLL WLAAMMLTAC SPSKEDKKE NGASAASSTA SAASSAPQT
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDPDYHOKII LAIEDLRYGK
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRQGQEEP K RTRYFEVSAT
 201 PAYSSRHNNG LGGNFYIYQ LPGYLKIHE MLENQSLFRL SNRERNPDKP
 251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

	10	20	30	40	50	
m690.pep	MKNKTSSLLWLTAIMLTACSPSKDDKTKEVGASAASSSASSAPS---	QTDLOPTASAPD				
a690	MKNKTSSLLWLAAAMMLTACSPSKEDKTKENGASAASSTASAPQTDLQPAASAPD					
	10	20	30	40	50	60
	60	70	80	90	100	110
m690.pep	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI					
a690	NVKQAESVPPSNCTDLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPGGGYDNI					
	70	80	90	100	110	120
	120	130	140	150	160	170
m690.pep	QRLFPDIRPEDPDYHOKIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ					
a690	QRLFPDIRPEDPDYHOKIILAIEDLRYGKRTISRQAQDALMEQERRLREATLLLIQGSQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m690.pep	ETRGQGEPEPKRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHEMLENQSLFRL					
a690	ETRGQGEPEPKRTRYFEVSATPAYSSRHNNGLGGNFQYIGQLPGYLKIHEMLENQSLFRL					
	190	200	210	220	230	240
	240	250	260	270	279	
m690.pep	SNRERNPDKPFLLDIHFDENGKITRIVVYEKNIYFNPNTGRIX					
a690	SNRERNPDKPFLLDIHFDENGKITRIVVYEKNIYFNPNLGRRX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq

1 GTGCCGCTGC CTGCTCCCTG CCGTTTGTCC AAACCTGCCG CCTCTTTTTT
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCGGAA CGATTTCCTAA CCGAACTGCG ACATACGCCG GCTCGGGCTG
 151 ACACAGGGTC AGCACAATGA GCTGCGTAAA ATCCGCGCCG CCTTCAAAT
 201 GCGGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATCCGAA CACAGCCGCC
 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG
 301 GCGCGCGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTGCGGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
 401 AGCAGCAAAT GTGGCTTCTC TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep

1 VLPAPPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TQGOHNELRK IRAAFKMGD RARLKVHSE HSRRSVVEI ISSDVFNRE
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAAATGA GCTGCGTAA ATCCGCACCG CCTTCAAAT
201 GGCGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
251 GCCGGTCTGT CGTCGAAATC ATTTCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTTGCAGT
351 GGACGAATTG GAAATCCAAC ACCGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNENE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691  97.2% identity in 144 aa overlap

          10      20      30      40      50      60
m691.pep  VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFOPNCDIRRLGLTQSQHNELRK
          |||
g691       VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFOPNCDIRRLGLTQSQHNELRK
          10      20      30      40      50      60

          70      80      90      100     110     120
m691.pep  IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNENEARDYVESRYLSGMDFAVDEL
          |||
g691       IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNENEARDYVESRYLSGMDFAVDEL
          70      80      90      100     110     120

          130     140
m691.pep  EIQRFFHILTPQQQMWLSCLKX
          |||
g691       EIQRFFHILTPQQQMWLSCLKX
          130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAAATGA ACTGCGTAA ATCCGCACCG CCTTCAAAT
201 GGCGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTTCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTTGCAGT
351 GGACGAATTG GAAATCCAAC ACCGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQSQHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNENE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

m691/a691 97.2% identity in 144 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2309>

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692 >:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

```
m692.seq
1  GTGTTGCACA  CGCTTTGTCG  CTGTTCGGAA  TCGATACGCC  GGATTGCGCG
51  GAATGCGCAGG  GAATGGCGGA  TTAAGGACAA  AAAATGCGGT  CTGAACACGG
101 ATACAGTTCA  GACGGCATCA  TTTTATACGA  CTGCCTTATT  TGGCTGCGCC
151 TTCATTCCAT  CGCGGACGGG  ATTATGAGCC  CTCGAAGCGT  TTGTGCGCGT
201 AGGCTTTGAA  CGCTCTGGAG  TTTATAGGCT  CGGTTACGTC  TTTAAGCATT
251 TGGCTGTCTT  TGTCGGCGGT  CTTGACGGCA  GACCAAGTTGA  CATAGGCCAA
301 GCTCGGTTCT  TGGAAACAGG  CTTTCGGTCAG  CTTCATGCGC  CTGCTTTATG
351 CGTAGTTGCC  GTTGACGACG  GCAAAATCCA  CGTCGCGCGC  GCTACGCGGG
```

1114

```

401 AGTTGCGCGG CTTCAGCTC GACGATTTTG ATGTTTTTCA GGTTCCTCGGC
451 GATGTCCGCT TTGGATGCGG TCAACGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTGAGC ATCACCAGA CGCGGCGGAA GTTGGACGGG
551 TCGTTGGCGG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTCCGCACT TGGAAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGTACATAG TCGGTAAACT CGACCAAGTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGC TTGGATTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTGTG CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGCGC CGCTGTCTT TTGACGCGC CAGGCGGCGA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>:

```

m692.pep
1 VLHTLCRCSE SIRRIRRNGR EWRIKGQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGFE RVGVIGLVY FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVFGVLG
151 DVRFQCGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVGGRYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AYIVGKLDQF DGVAFFLQLG LDLFDDHIAE VADGRAEDDF FFRAVVG
301 RSGCGGRAVF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

m692/g692 91.1% identity in 338 aa overlap

	10	20	30	40	50	60
m692.pep	VLHTLCRCSE	SIRRIRRNGR	EWRIKGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
g692	VSHTRCRCSE	SIRRIWRNGR	EWRIKGQKCR	LNTDAVQTAS	FYTTALFGCA	FIPCGRVFVA
	10	20	30	40	50	60
	70	80	90	100	110	120
m692.pep	LEAFVRVGFE	RVGVIGLVY	FKPLAVFVGG	FDGRPVDIGK	ARFLEQGFQ	LHAAAYGVVA
g692	LEAFVRVGFE	RVGVIGLVY	FKPLAVFVGG	FDGRPVDIGK	ARLLEQGFQ	LHAAAYGVVA
	70	80	90	100	110	120
	130	140	150	160	170	180
m692.pep	VDDGKIHVGA	ATRQLRGFKL	DDFDVFGVLG	DVRFQCGQRI	DAVFEFDPTQ	FVEHHQDAGE
g692	VDDGKIHVGA	AARQLCGFKL	DDFDVFGVFR	DVFGCGQRI	DAVFEFDPTQ	FVQHHQGACE
	130	140	150	160	170	180
	190	200	210	220	230	240
m692.pep	VGRVVGGRYG	AAVDFDFQRF	QLARVQSQR	GRHLEDFGDV	QIVFFFEVVK	IGFVLEDVDV
g692	VGRVVGGRYG	AAVDFDFQRF	QFARIQSQR	GRHLEGFQV	VFFFEIVK	IGFVLEDVDV
	190	200	210	220	230	240
	250	260	270	280	290	
m692.pep	QLALSQCQIR	AYIVGKLDQF	DGVAFFLQLG	LDLFDDHIAE	VADGRAEDDF	FFRAVVG--
g692	QLALRQCQIR	AHIVGKFDQF	DGVAFFLQLG	LDLFDDHIAE	VAHGRAEDDF	FFRAVIGRR
	250	260	270	280	290	300
	300	310	320	330		
m692.pep	GGRSGCGRAV	FLTAAGGEDER	ECGGKGFE	EGFHIFS		
g692	GGGRGCG-RA	VFLTAAGCEDER	ECGGKGFE	EGFHIFS		
	310	320	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2313>

```

a692.seq
1 GTGTTGCACA CGCTTTGTCG CTGTTGCGAA TCGATACGCC GGATTCGGCG

```


1115

```

51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTCGGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTCGA GGTTTTCGGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAAGA CGCGGCGCAA GTTGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCC GGGTACAGTC CCAAGGCGC GGTCGGCACT TGGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTGTGA AGTCGTCAAG ATAGGGTTTG
701 TGTTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGCACATAG TCGGTAAACT CGACCAAGTT GACGGGTGAG CCTTTTCTCT
801 CCAGCTCGGG TTGATTTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCGGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTATCTTT TTGACCGCGC CAGGCGCGCA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

a692.pep

```

1  VLHTLCRCSE SIRRIIRNGR EWRIKGQKCR LNTDTVQTAS FYTTALFGCA
51  FIPCGRGFVA LEAFVRVGFV RVGVIGLGYV FKPLAVFVGG FDGRFPVDIGK
101 ARFLEQGFQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVFQVFG
151 NVRFGCGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVRGGRG AAVFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDDVDV QLALSQCQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRAVVG
301 RSGCGGRAIF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

m692/a692 98.8% identity in 336 aa overlap

	10	20	30	40	50	60
m692.pep	VLHTLCRCSE	SIRRIIRNGR	EWRIKGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
a692	VLHTLCRCSE	SIRRIIRNGR	EWRIKGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
	10	20	30	40	50	60
	70	80	90	100	110	120
m692.pep	LEAFVRVGF	FERVGVIGL	GYVFKPLA	VFVGFDGR	PVDIGKAR	FLEQGFQ
a692	LEAFVRVGF	FERVGVIGL	GYVFKPLA	VFVGFDGR	PVDIGKAR	FLEQGFQ
	70	80	90	100	110	120
	130	140	150	160	170	180
m692.pep	VDDGKIHV	GAATRQLR	GFKLDDF	VDVFGV	FCGQRI	DAVFEFD
a692	VDDGKIHV	GAATRQLR	GFKLDDF	VDVFGV	FCGQRI	DAVFEFD
	130	140	150	160	170	180
	190	200	210	220	230	240
m692.pep	VGRVVRG	RGYGA	AVFDFQ	RFLARV	QSQRGR	HLEDFG
a692	VGRVVRG	RGYGA	AVFDFQ	RFLARV	QSQRGR	HLEDFG
	190	200	210	220	230	240
	250	260	270	280	290	300
m692.pep	QLALSQC	QIRAYI	VGKLDQ	FDGVA	FFLQLG	LDLFFD
a692	QLALSQC	QIRAYI	VGKLDQ	FDGVA	FFLQLG	LDLFFD
	250	260	270	280	290	300
	310	320	330			
m692.pep	RSGCGGR	AVFLTA	AGGEDER	ECGGKG	FEEGFH	IFSX
a692	RSGCGGR	AVFLTA	AGGEDER	ECGGKG	FEEGFH	IFSX

310 320 330

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

```
g694.seq
1   TCGGCATTTG TGTTGCCCAA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
51  AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
151 TTCATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCGCG ACCAACACTT
201 CGGGCGCGGA CGCGCTGCC GTTACGCCGA CTTTGCTTTT GCCTTCAAAC
251 CACGTGCGTT GCaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATTGGGCG
351 AACCGACCAC AATCACGATG TCGCACTGTT CCGCCAGCTC TTGACGGCG
401 GTTTCGGGT TGGTCGTGCG ATAGCAGATG TCTTCCTTGT GCGGATTGCG
451 GATATTGGGG AAACGCGCGT TCAGCGCGCG GATGATGTCT TTGGTTTCAT
501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTG GGGGTTTCTG
551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
601 CCGTGCAAGC TGCCCCATCG TGCCCTTCGAC CTCGGCGTGC CCCTTATGCC
651 CGATCATGAT GATTTCACAG TCTTGGGCAT CCAGTCGGGC GACTTCCTTA
701 TGCACTTTCG TCACCAGCGG GCAAGTCGCA TCAAATACCC GGAAACCGCG
751 CTCCGCGGCT TCCTGCTGCA CCGCCTTCGA TACGCCGTGT GCCGAATAAA
801 CCAGTGTCGC GCCCGCGCGC ACTTCCGCCA AGTCTTCGAT AAACACCGCG
851 CCTTTTTCGC GCAGGTTGTC CACGACGAAT TTGTTGTGGA CGACTTCGTG
901 GCGCACATAA ACCGCGCGCG CGAATTCTTC CAAAGCACGT TCGACAATAC
951 TGATTGCCCC ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTCG CGTTCATAAG TTTTGCATTC CGTGTTCAGA CGGCATTAC
1051 GTTTTTTTGC TNNATCTTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
1101 ACCGCACCGA CGCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

```
g694.pep (partial)
1   SAFVLPHKPM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPFAHG
51  FMPPSAYGCQ YFPHQHFGRG RACRYADFAF AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
151 DIGETRVQRG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHFRHQR ASRIKYPETA
251 LRRFLHLRLR YAVCRINQCR ARRHFRQVFD KHRAFFAQV V HDEFVVDVDFV
301 AHINRAAEFF QSTFDNTDCP IHTGAEEARI GKDDGFSVHK FCIPCSDGIH
351 VFLLXLCDGR YCQAPPTPHR RR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

```
m694.seq
1   TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTC
51  GACGGCATTT GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTGTCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCTGCGG TTACGCCGAC TTTGTTTTCG CCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGCATGT CGCACTGTTC TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTCGTCGCA TAGCAGATAT CTTCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GGCGCAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CTTATGCCC GATCATGATG
701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCG TCCGCGCTT
801 CTTGCCGCG CGCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTCGCG
851 CCGCGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATT GCCCGA
1001 TCCACACCA GCGAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTCTC
1051 GTTCATAAGC CCGGTATTTT GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTTCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

```
m694.pep
1   LVSASGTRQK CRLKPVOTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFKLPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNHDVALF CQLFDGGLPV
```

```

151 GRRADIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 HSRISDRFDQK HFARKRLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLYRYACVRN QCRARRHRFRQ VFNKHRTFFT
301 QVVHDEFVFN DFWAHINRRA ELFCSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPT PHRRR*

```

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

		10	20	30	40	50
m694 .pep	LVSASGTRQKCRCLKPVQTAFVLPKHS----	TPASTFAQIGFGFALAAQLFGQDEHNAFFR				
		:				
g694		SAFVLPKHPMPALTPASTFAQIGFGFALAAQLLGQDEHDAFFR				
		10	20	30	40	
	60	70	80	90	100	110
m694 .pep	TLAFAYGFVPPSAYGCGQYFPHQHFGRRGRACRYADFVFALKPCALQVACIIHHIRIDSARC					
	:					
g694	APPPFAHGFMPPSAYGCGQYFPHQHFGRRGRACRYADFAFAFKPRALQVGRVGVHHIRIDSARC					
	50	60	70	80	90	100
	120	130	140	150	160	170
m694 .pep	RHFAQAVAVGRIGRTDHNHDVALFCQLFDGGGLPVGRRRIADIFLVRIADIGETRVQRGDDV					
g694	RHFAQAVAVGRIGRTDHNHDVALFCQLFDGGGLPVGRRRIADVFLVRIADIGETRVQRGDDV					
	110	120	130	140	150	160
	180	190	200	210	220	230
m694 .pep	FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPHRSFDLDVPLMPDHDDFT					
g694	FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARCKLPHRAFDLGVPLMPDHDDFT					
	170	180	190	200	210	220
	240	250	260	270	280	290
m694 .pep	VLGIQSGDFLMMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFQVFNKHR					
g694	VLGIQSGDFLMMHFRHQRASRIKYPETALRRFLLHRLRYAVCRINQCRARRHFQVFDKHR					
	230	240	250	260	270	280
	300	310	320	330	340	350
m694 .pep	TFETQVVHDEFVVDFFVAHINRRAELEFQSTFDNTDCPIHTSAEAAARIGKDDGFLVHKPGI					
g694	AFFAQVVHDEFVVDFFVAHINRRAEFFQSTFDNTDCPIHTGAEAAARIGKDDGFSVHKFCI					
	290	300	310	320	330	340
	360	370	380			
m694 .pep	SFSDGINIFLLGFYGGRCCTPPTPHRRRX					
g694	PCSDGIHVFLXXLCDGRYCQAPPTPHRRRX					
	350	360	370			

a694.seq

1	TTGGTTTCCG	TACCCGGCAC	ACGGCAAAAA	TGCCGTCTGA	AGCCTGTTC
51	GACGCGCATT	GTGTTGCCCA	AACATTCAAC	GCGTCGCTCA	ACGTTTGCAC
101	AAATCGGGTT	TGGTTTCGCC	CTCGCGGCGC	AACTCTTTGG	GCAGGACGAA
151	CACAATGCTT	TCCTCCGCAG	CCTCGCCTTC	CGGTACGGTT	TCGTCGCCCC
201	ATCCGCGTAT	GGTTGCCAGT	ACTTCCCGCA	CCAACACTTC	GGCGCGCGAC
251	GCGCCTGCCG	TTACGCCGAC	TTTGTTTTTG	CCCTCAAACC	ATGCGCGTTG
301	CAGGTAGCCT	GCATTATCCA	CCATATAACG	ATGCATTCGG	CGCGATCCGG
351	CCACTTTCGC	CAAGCGGTTG	CTGTTGGACG	AATTGGGGCA	ACCGACACA
401	ATGCAGATGT	CGCACTGTTC	TGCCAACTCT	TTGACGGCGG	TTTGCCGGTT
451	GTCGCTGCGA	TAGCAGATAT	CTTCTCTTGT	CGGATTCGGG	ATATTGGGGA
501	AACGCGCGTT	CAGCGCGGGC	ATGATGCTTT	TGTTTTCATC	ACCGGAGAGC
551	GTGGTTTGCG	TGACATAGGC	GAGTTTGTCT	GGGTTTCTGA	CTTCGAGTTT
601	TGCCACATCT	CCGACCGTTT	TCGACAAAAG	CATTTTGGCC	GCGCGAAGCT
651	GCCCCATCGT	TCCTTCGACC	TCGACGTGCC	CCTTATGCCC	GATCATGATG

1118

```

701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTGTGTC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACCTCTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAATC CCGGTATTTT GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

a694.pep

```

1  LVSASGTRQK CRLKPVQTAFL VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDHVALF CQLFDGGLPV
151 GRRADIIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPFR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVNV DVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

m694/a694 100.0% identity in 385 aa overlap

	10	20	30	40	50	60
m694.pep	LVSASGTRQK CRLKPVQTAFL VLPKHSTPAS TFAQIGFGFALAAQLFGQDEHNAFFRTLAF					
a694	LVSASGTRQK CRLKPVQTAFL VLPKHSTPAS TFAQIGFGFALAAQLFGQDEHNAFFRTLAF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m694.pep	AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL QVACIIHHIR IDSARCRHFA					
a694	AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL QVACIIHHIR IDSARCRHFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m694.pep	QAVAVGRIGR TDHNDHVALFCQLFDGGLPV GRRADIIFLV RIADIGETRV QRGDDVFGFI					
a694	QAVAVGRIGR TDHNDHVALFCQLFDGGLPV GRRADIIFLV RIADIGETRV QRGDDVFGFI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m694.pep	DRERGLADIG EFVGVSDFEF CHISDRFDQKH FARRKLPFRSFDLDVPLMP DHDDFTVLGI					
a694	DRERGLADIG EFVGVSDFEF CHISDRFDQKH FARRKLPFRSFDLDVPLMP DHDDFTVLGI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m694.pep	QSGDFLMHFR HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT					
a694	QSGDFLMHFR HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m694.pep	QVVHDEFVNV DVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL VHKPGISFSD					
a694	QVVHDEFVNV DVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL VHKPGISFSD					
	310	320	330	340	350	360
	370	380				
m694.pep	GINIFLLGFY GGRCCPTPPT PHRRRX					
a694	GINIFLLGFY GGRCCPTPPT PHRRRX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695.seq
1  TTGCTCAAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGAACGG AAGGGTGATG CGCGAAGCGG CTTTGTATGC GCCGCCCAGT
101  GTCAAAATTC TCAAAGATTT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151  TGTCCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCCTG CTTCTGAAAA
201  AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGTCTG
251  CCTCTGTGC TTCCGTTTTC CCGTTCCGG AGGCGAGCCG AACCGAAATG
301  CCGACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351  GCAAGACCGT TTGGACTATC TGAAGGCAA AATCGTCCGG CTGTGGAACG
401  AAGTGGAAT GTTAAACGGG AAAGTCAAAG CATGGAGCA TACGAAAATA
451  CACCCTTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501  AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551  AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACTA TCAAAACGGC
601  AGGTTTCTG CCGCAGCCGC CTGTGTAAG GGGCGGACG GCGGAGACGG
651  CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGTGCAA AGCAGGGCGC
701  GTATGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751  CGTTTCAAAG ACAGCCCAAC CGCGCCGAA GTCATATTCA AAATCGGCGA
801  ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851  GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCGCCGCA
901  GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```
g695.pep
1  LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCNSQRF QSKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIWL SVSASCASVL PVPEGSRTM
101  PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151  HPSGRITYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLY NQALKHYQNG
201  RFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251  RFKDSPTAPE VIFKIGECQY RLQKDIARA TWRSLIQTYP GSPAARKRAA
301  AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695.seq
1  TTGCTCAAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGCTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101  GTCGGCATCC TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151  CGTCCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCCTG CTTCTGAAAA
201  AATAATGAAG ATCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGTCCG
251  CCTCCTGTGC TTCCGTTTCA CCGTTCCGG CAGGCGACCA AACCGAAATG
301  TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351  GCAAGACCGT TTGGACTATC TGAAGGCAA AATCGTCCGG CTGTGGAACG
401  AAGTGGAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451  CATTCTTCCG GCAGGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501  AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCTG
551  AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACTA TAAAAGCGGC
601  AAGTTTCTG CCGCTGCCTC CCGTTGAAA GCGCGGACG GAGGCGACGG
651  CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGTGCAA AGCAGGGCGC
701  GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751  CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801  ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851  GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCGCCGCA
901  GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695.pep
1  LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRRHPQRF QSKPAERPAAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIWL SVSASCASVS PVPAGSQTEM
101  STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151  HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLY NQALKHYKSG
201  KFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251  RFKDSPTAPE AMFKIGECQY RLQKDIARA TWRSLIQTYP GSPAARKRAA
301  AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

m695/g695 90.8% identity in 305 aa overlap

	10	20	30	40	50	60
m695.pep	LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR					
	: :			:		
g695	LPQTRPARRHHRQYFVERKGDARSGFXCAAQCNSQRFQSKPAERYADCPHHPARRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m695.pep	LDPASEKIMKIKLPLFIWLSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
	:				:	
g695	FDPASEKIMKTKLPLFIWLSVSASCASVLPVPEGSRTemptQENASDGIPYPVPTLQDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m695.pep	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDRLKEHYLNTEGGSASA					
			:			
g695	LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDRLKEHYLNTEGGSASA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m695.pep	HTVETAQNLNQALKHYKSGKFSAAASLLKGADGGDGGGIAQRSMYLLQLSRARMGNCS					
		:				
g695	HTVETAQNLNQALKHYQNGRFSAAAALLKGADGGDGGGIAQRSMYLLQLSRARMGNCS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m695.pep	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
		:				
g695	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
	250	260	270	280	290	300
m695.pep	AVRKRKX					
g695	AVRKRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

1	TTGCCTCAAG	CTTGTCGGGC	AAGGCGGCAT	CATTGCCATC	GACAATATTT
51	TGTTGAACGG	AAGGGTGATG	CGCGAAGCGG	CTTCCGATGC	GCCGCCCAGC
101	GTCGGGCATCC	TCAAAGATTT	TAATCAAAC	CTGCCGAACG	ATACGCGGAT
151	TGTCCCCATC	ACCCTGCCCG	TCGGCGACGG	TTTGACCTG	CTTCTGAAAA
201	AATAATGAAG	ACCAAATTAC	CGCTTTTAT	CATTTGGCTG	TCCGTATCCG
251	CCGCCTGTTT	TTCCCTGTT	TCCGCAATA	TTCAGGATAT	GCGGCTCGAA
301	CCGCAGGCAG	AGGCAGGTAG	TTCGGACGCT	ATTCCCTATC	CCGTTCCAC
351	TCTGCAAGAC	CGTTTGATT	ATCTGGAAGG	CACACTCGTC	CGCTGTGCA
401	ACGAAGTGGA	AACCTTAAAC	GGCAAAGTCA	AAGCACTGGA	GCATGCGAAA
451	ACACACCTT	CCAGCAGGGC	ATACGTCCAA	AAACTCGACG	ACCGCAAGTT
501	GAAAGAGCAT	TACCTCAATA	CCGAAGGCGG	CAGCGCATCC	GCACATACCG
551	TCGAAACCGC	ACAAAACCTC	TACAATCAGG	CACTCAAACA	CTATAAAGC
601	GGCAGGTTT	CTGCCGCTGC	CTCCCTGTTG	AAAGGCGCGG	ACGGAGGCGA
651	CGGCGGCAGC	ATCGCGCAAC	GCAGTATGTA	CCTGTTGCTG	CAAAGCAGGG
701	CGCGTATGGG	CAACTGCGAA	TCCGTCATCG	AAATCGGAGG	GCGTTACGCC
751	AACCGTTTCA	AAGACAGCCC	AACCGCGCCT	GAAGCCATGT	TCAAAATCGG
801	CGAATGCCAA	TACAGGCTTC	AGCAAAAAGA	CATTGCAAGG	GCGACTTGGC
851	GCAGCCTGAT	ACAGACCTAT	CCCGGCAGCC	CGCGGCAGAA	ACGCGCGGCC
901	GCAGCCGTGC	GCAAACGATA	G		

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

1	LPQACPARRH	HCHRQYFVER	KGDARSGFRC	AAQRRHPQRF	*SKPAERYAD
51	CPHHPARRRR	FDPASEKIMK	TKLPLFIWL	SVSAACSSPV	SRNIQDMRLE
101	PQAEAGSSDA	IPYPVPTLQD	RLDYLEGLTV	RLSNEVETLN	GKVKALEHAK
151	THPSSRAYVQ	KLDDRKLKEH	YLNTEGGSAS	AHTVETAQNL	YNQALKHYKS
201	GRFSAAASLL	KGADGGDGGG	IAQRSMYLLL	QSRARMGNCE	SVIEIGGRYA
251	NRFKDSPTAP	EAMFKIGECQ	YRLQKDIAR	ATWRSLIQTY	PGSPAAKRAA
301	AAVRKR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

```

      10      20      30      40      50      60
m695.pep  LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAPHRPHHPARRRR
          |||: |::||| ||||:||||||| ||||| ||||| | |||||
a695      LPQACPARRHCHRQYFVERKGDARSGFRCAAQRRHPQRFQSKPAERYADCPHHPARRRR
          10      20      30      40      50      60

      70      80      90      100     110
m695.pep  LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQT--EMSTRENASDGIPYPVPTL
          :||||| :||||| ||||:| | | : | | : : :|||:|||||
a695      FDPASEKIMKTKLPLFIIWLSVSAACSS--PVSRIQDMRLEPQAEAGSSDAIPYPVPTL
          70      80      90      100     110

      120     130     140     150     160     170
m695.pep  QDRLDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYLNTEGGS
          ||||| :||||| ||||| ||||| ||||| ||||| ||||| |||||
a695      QDRLDYLEGLVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLD DRKLKEHYLNTEGGS
      120     130     140     150     160     170

      180     190     200     210     220     230
m695.pep  ASAHTVETAQONLYNQALKHYKSGKFSAAASLLKGADGGDGGGSIQRSMYLLQLSRARMGN
          ||||| :||||| ||||| ||||| ||||| ||||| ||||| |||||
a695      ASAHTVETAQONLYNQALKHYKSGRFSAAASLLKGADGGDGGGSIQRSMYLLQLSRARMGN
      180     190     200     210     220     230

      240     250     260     270     280     290
m695.pep  CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAGR
          ||||| :||||| ||||| ||||| ||||| ||||| ||||| |||||
a695      CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAGR
      240     250     260     270     280     290

      300
m695.pep  AAAAVRKRX
          |||||
a695      AAAAVRKRX
      300

```

The following partial DNA sequence was identified in *N. gonorrhoeae*

g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>:

g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

```

m696.seq
1  TTGGGTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GGCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTTG GCTTCTTTCG AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

```

m696.pep
1  LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFNLN
101 LLFGFLRTSC QGSRHHCNGQ *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:

a696.seq

1122

```

1   TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGCTGCGC CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GCGGCAGAA
251 GCCGCAAGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCTGTTTG GCTTCTTGGC AACAAGCTGC CAAGGCAGCC GCCATCATG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

```

a696.pep
1   LGCROAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRVFNI GLNGLNRFLN
101 LLFGFLRTSC QGSRHHCGNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

```

m696/a696    100.0% identity in 120 aa overlap

          10      20      30      40      50      60
m696.pep    LGCROAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
a696         LGCROAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
          10      20      30      40      50      60

          70      80      90     100     110     120
m696.pep    ISRSIFDLVFRFFDGRSGRLGGRSRVFNI GLNGLNRFLNLLFGFLRTSCQGSRRHHCGNQ
a696         ISRSIFDLVFRFFDGRSGRLGGRSRVFNI GLNGLNRFLNLLFGFLRTSCQGSRRHHCGNQ
          70      80      90     100     110     120

m696.pep    X
            |
a696         X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

```

g700.seq
1   ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTTCCTA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTCG
151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGGC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTC CTTAACGGCG GGGGCATCCG
501 GCTGTCGGTT TGGTTTATAT TGTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTAATGACCG AGGCTTACCG
651 GGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTTC GGATGCGGCG
751 GTGGGGGTTC GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTTTC CACGCTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

```

g700.pep
1   MSSLMTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSLS
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKGKGV
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMPS ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```


1123

201 GFGWYSLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPIQGAG GLEVVPVAVS FGVVVNIAAP FLMVVFSTLG
 301 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2333>:

m700.seq

1 ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
 51 ATTTTATATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
 101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCTG
 151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGAC GATATGGCGT TGACGGTTCT
 201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
 251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
 301 GTCGGCGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
 351 TGCATTCGGC AACTGATGC GCGATATTG GATGCCGTCT GAAAGCGCGG
 401 GCATGTATTG TCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAAA
 451 AGCAGCGCGC TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTTCG
 501 GTTGTCCGTC TGGTTTATGC TTTTATCTCT TTCGGGCGGG CTGCTGTTTG
 551 CCGCATCGAC AGACGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
 601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTCATGACCG AGGCTTACGG
 651 CGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGGCA CGAGAGCTGT
 701 TTGCACTGGC ATTTATCCCG CTGCTGATGA AGCGTTTTC AGATGCGGCG
 751 GTGGGGGTTG GCGGTGCGAC CAGTATGGAT TTTACATTGC CCGTGATTCA
 801 GGGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
 851 TGGTCAATAT CGCCGCCCG TTTCTGATGG TGGTGTTCG CGCTTTGGGT
 901 TGA

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

m700.pep

1 MD~~SL~~MTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLIGVSL
 51 RVEDLGSRLD DMALT~~VL~~WLF VCTVGANLLA LAVLGKLFPP RIKGKGVSV
 101 VGVSGSVGQL GCVLLGFAFG KLMRDIWMPES ESAGMYCLML LVFLIGVQLK
 151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASTDGV SWTKGLAMAS
 201 GFGWYSLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPIQGAG GLEVVPVAVS FGVVVNIAAP FLMVVFSALG
 301 *

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

	10	20	30	40	50	60
m700.pep	MD SL MTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLIGVSLSRVEDLGSRLD					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
m700.pep	DMALT VL WLFVCTVGANLLALAVLGKLFPPRIKGKGVSVGVSGSVGQLGCVLLGFAFG					
g700	DMALT VL WLFVCTVGANLLALAVLGKLSPPWRIGGKGVSVGVSGSVRQLGCVLLGFVSG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGVSLRQVLNRRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYSLSGLVMT EAY GAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASADGVSWTKGLAMASGFGWYSLSGLVMT EAY GAVWGSIMLLNDLARELFALAFIP					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
g700	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
g700	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```

a700.seq
  1  ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
 51  ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101  TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTGTGCG
151  CGCGTGGAGG ATTTGGGTTT CCGGTTGGAC GATATGGCGT TGACGGTTCT
201  GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251  TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301  GTCGGTGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351  TGCATCCGGC AAAGTATGTC GCGATATTTG GATGCCGTCT GAAAACGCGG
401  GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451  AGCAGCGGCG TATCGTTGCG GCAGGTTTTG GTCAACCGCA GGGGTATTCT
501  GTTGTGCGTC TGGTTTATGC TTTTATCTCT TTCAGGCGGG CTGCTGTTTG
551  CCGCATCGGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601  GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTGATGACCG AGGCTTACGG
651  CGCGGTATGG GGCAGTATCG CGCTTTTGAA CGATTTGGCA CGAGAGCTGT
701  TCGCGCTGGC ATTTATTCCG CTGCTGATGA AGCGTTTCC CGATGCGGCA
751  GTGGGGGTCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTCT
801  GGGTGCGGGC GGCTTGAAG CCGTACCGGT AGCGGTCAGC TTCGGCGTGG
851  TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTCCT CGCTTTGGGC
901  TGA

```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```

a700.pep
  1  MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSL
 51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLPW RIKGKGV
101  VGVSGSVGQL GCVLLGFASG KLMRDIWMP ENAGMYCLML LVLXIGVQL
151  SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201  GFGWYSLSL VMTEAYGAVW GSIALNDLA RELFALAFIP LLMKRFPDAA
251  VGVGGATSMDF TLPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSALG
301  *

```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
a700	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKGKGVSVGVSGSVGQLGCVLLGFASG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKGKGVSVGVSGSVGQLGCVLLGFASG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180

q701.seq

1	ATGTCTTGGC	ACATATTCCA	AGTTGCAGGG	ATACCGACCG	CTTCGATGGC
51	ACAATCTACG	CCGTCTTCGC	CGACGATGGC	GAAAAC TTGT	TTGGAGACGT
101	CGCCGGAAGC	GGGGCTGATG	GTATGGGTCTG	CGCCCAACTC	TTTCGCCGGT
151	TTCAAACGGT	TTTCGTCCAT	ATCGCACACG	ATAATGGCGG	CAGGGCTATA
201	CAGTTGGGCG	GTCAACAAGG	CGGACATACC	GACAGGGCCG	GCACCTGCGA
251	TGAATACGGT	ATCGCCGGGT	TTCACATCGC	CGTATTGCAC	GCCGATTTTCG
301	TGGGCGGTCTG	GTAAGCGCTC	GCTCAACAGC	AGGGCGATTTC	CTTCGTTGAC
351	GTTGTCTGTC	GGCGGCACGA	GGCTGTTGTC	GGCATAA	

q701.ppt

1 MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VVWAPNSFAG
51 FKRFSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISSLTLSC GGTRLLSA*

m701.seq

1	ATGTCTTGGC	ACATATTCCA	TGTAGCAGGG	ATACCGACGG	CTTCGATGGC
51	GCAATCCACG	CCGTCTTCGC	CGACGATGGC	AAAGACTTGT	TTGGATACTT
101	CGCCGGAAGC	AGGGTTAATG	GTATGGGTGC	CACCCAATTG	TTTCGCCAGT
151	TTCAAACGGT	TTTCGTTCAT	ATCGCAAACG	ATGATGGCGG	CGGGACTGTA
201	CAGTTGGGCG	GTCAACAGGG	CGGACATACC	GACAGGGCCT	GCCCCAGCGA
251	TGAATACGGT	GTCGCCGGGT	TTGACATCGC	CGTATTGCAC	GCCGATTTCG
301	TGGGCGGTTCG	GCAAAGCGTC	GCTCAACACG	AGGGCGGATT	CTTCGTTGAC
351	ATTATCGGGC	AGCGAACACG	GGCTGTTGTC	GGCATAA	

m701.ppt

1 MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPEAGLM VVVPNSFAS
51 FKRFFSISQT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISSLTSLG SGTRLLSA*

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

m701/q701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSISQT					
	: : : : :					
g701	MSWHIFQVAGIPTASMAQSTPSSPTMAKTCLETSPHGLMVWVAPNSFAGFKRESSISHT					

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	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG					
	: : : : : :					
g701	IMAAGLYSWAVNKADIPTGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISLTLSC					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
	:
g701	GGTRLLSAX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTTCGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTG CGCCCACTC TTTCCGCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTTCG
301 TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351 GTTGTGCGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
51  FKRFSSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTLTG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASF					
	: : : : :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPEAGLMVWVAPNSFASF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG					
	: : : : :					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTLTG					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
a701	SGTRLLSAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGTt ccaAAGCCAG TTGGACTTCG CCCGGAGtgg cAACGCCGGG
51  AATCAGGGGA ATGCCGCTGT TGCGGCCGGC TCTGGCGAGG GATTCGTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTGAGGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAAC TG CGCCGGCGGT
351 CAGGATTTTCG cgggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

```

1  MPCSKASWTS PGVATPGIRG MPLLRLPALAR DSCKPGLMAK TAPASSTALS
51  CSQLVTVPAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

m702.seq

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACG CGCCGGCGGT
351 CAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

m702.pep

```

1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSQLVTVPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

m702/g702

	10	20	30	40	50	60
m702.pep	MPCSKASWISPGVATPGIRGMPLLWPALAR DSCSPGLMAK TAPASSTALS CSQLVTVPAP					
	:					
g702	MPCSKASWTS PGVATPGIRGMPLLRLPALARDSCKPGLMAK TAPASSTALS CSQLVTVPAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m702.pep	TMALGTSIAIRRMASRPTGVRVISRVGMPPSTRAWDKSMAVLKSSIAIT GTTAPAVKIS					
	:					
g702	MMALGISLAI RRMASPTGVRKVISRVGMPPSTRARDKSTAVLKSSIAIT GTTAPAVRIS					
	70	80	90	100	110	120
	130	140				
m702.pep	RGVSLDISVL RVEWGILLRW DRLX					
g702	RGVSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

a702.seq

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACG CGCCGGCGGT
351 CAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

a702.pep

```

1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSQLVTVPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

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```

m702.pep      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVLPAP
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702          MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVLPAP
               10      20      30      40      50      60

               70      80      90      100     110     120
m702.pep      TMLAGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702          TMLAGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
               70      80      90      100     110     120

               130     140
m702.pep      RGVSLDISVLRVEWGILLRWDR LX
               ||||||||||||||||||||||||
a702          RGVSLDISVLRVEWGILLRWDR LX
               130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

g703.seq

```

1   ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTTAA CCGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CCGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GTTTACGACA ATATCAGCGG TTTTATATAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAACA AACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTGGGAA CAGGGTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCTT CTTTGTACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GGCGGAACGG ATTGACCGTG CCGTctgTgc gcTGTtggt aaggCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

g703.pep

```

1   MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTRKTGAP
201 DGYVPLKDLE QGVPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
251 KVPSFDEMKG QIAGNLQAER IDRAVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

m703.seq

```

1   ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CCGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CCGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGGAA CAGGGTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGCA ACGCCGCTGA

```

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

```

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51 EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGYVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSDREV
251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

```

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

	10	20	30	40	50	60
m703.pep	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m703.pep	LENEVVNTVVAAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVVNTVVAAQEVKRLKLDRAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m703.pep	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDKEENAKKAVADLKAKKG					
g703	EAYALHIAKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTDKEENAKKAVADLKAKKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m703.pep	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
	250	260	270	280	289	
m703.pep	VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703	VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

```

1 ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT
101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAGAAC AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

1130

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

```

a703.pep
  1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGYVPLKDLE QGVPPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

m703/a703    100.0% identity in 288 aa overlap

      10      20      30      40      50      60
m703.pep    MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL
a703         MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL
      10      20      30      40      50      60

      70      80      90     100     110     120
m703.pep    LENEVVNTVVAQEVKRLKLDRSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG
a703         LENEVVNTVVAQEVKRLKLDRSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG
      70      80      90     100     110     120

      130     140     150     160     170     180
m703.pep    EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG
a703         EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG
      130     140     150     160     170     180

      190     200     210     220     230     240
m703.pep    FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG
a703         FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG
      190     200     210     220     230     240

      250     260     270     280     289
m703.pep    VYYVNSREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX
a703         VYYVNSREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX
      250     260     270     280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

```

a704.seq
  1 ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
 51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
151 AAACAACGCA CCGCCGACGC GCAAAAAACC GAGCTGCCGC CCAAGAAAT
201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
251 TGGAACCCCA CGGCGGCACG CGCGAGGCGG TTTTAATGCT CGGCGGCATC
301 ACCTGCGCCG CCTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCGTACAGA
351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG
401 TCTGGGACGA CGGCAAAATC CGCCTTCCG ACATTCTGTT GAAAATCAGG
451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCGC
501 CAACCAAAAA GAACGCAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
551 TGGGGATGAT GCAGACGATG ATGTTTCGCG TGCCGACCTA CCTTTACGGC
601 GGCACATCGA AATCCGATTT CCTGCAAATC CTCCATTGGG GCGGCTTTTT
651 AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGGCG
701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA

```


1131

```

801  TGCAGGGGAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851  TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901  GCCGCCGAGA GGCTGGTGAA GCTGATTCCT GCGTTTTGCC ATCATATGCC
951  CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCCTTGAC
1051 GGCACGGTGC TGGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGCGGGC
1201 GGCACGCGAC TGTGCGACAT CGTCCGCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCCGTCT TCATCGGCTG GACGCTGTAC
1351 GCCGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCCTGC GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGTTCTA
1451 CCGGTACGCT GCGCGCGGAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCTCG CCCAAACAC CGACATCATC TTCGACAAA CCGGCACGCT
1551 GACCCAAGGC AAACCCGCCG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTCTCGCG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCCTTG CCCGCGCCAT CCTCAACTGC CGCATTCAG ACGGCAGCGT
1701 CCCCACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GCGGAAACAC AGGTTTGGGC ATTGGGCAGG
1801 GCATCCTATG TCGCGGAAAT TTCAGGTAAA GAACCGCAA CAGAAGCGCG
1851 CGGCAGCGCG GTTACCTCG GCAGTCAAAG CGGTTTCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCG CGGAGGCGGT GCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CCGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCG CCGTTTGGC
2151 GCAGGCAGAC GTATCCGCCG CCGCAGCGGG CGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCCGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```

a704.pep
1  MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAQS IIDAGLSYY
51  KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLIE QQLLRDTGIV RIDLNYSTHR CRVWDDGKI RLSDILLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMMQTM MFALPTYLYG
201 GDIEPDLFI LHWGGFLMVL PVVFCAPVF YQALRLDKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAEALAEQYAS SFIFGELLTA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTTDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSQSGFQ AVFYLDPLK DSAAEAVRQL
651 AGKNLTLHIL SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIKDI NDAPVLAQAD VSAAAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRONLIWAG AYNIIAVPLA VLGYPQFWIA ALGMSFSSLA
801 VLGNALRLHK RGMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep  MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVAQSIIDAGLSYYKQRTADAQKT
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a704      MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVAQSIIDAGLSYYKQRTADAQKT
          10      20      30      40      50      60

          70      80      90     100     110     120
m704.pep  ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLLRDTGIV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a704      ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLLRDTGIV

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1132

	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	RIDLNYSTHRCRVVDDGKIRLS	DILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA				
	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	VAGLGMMQTMFALPTYLYGGDIEP	DFLQILHWGGFLMVLPPVVFYCAVPFYQGALRDLKN				
	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	RRVGMDDPITVAIIMTFIAGVYSLATNAGQGM	FESIAMLLFFLLGGRFMEHIARRKAGD				
	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	AAERLVKLIPAFCHHMPDYPDTQETCEAAVVKL	KAGDIVLVKPGETIPVDGTVLEGSSAV				
	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	NESMLTGESLPVAKMPSEKVTAGTLNTQSPLI	IRTDRTGGGTRLSHIVRLLDRALAQKPR				
	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	TAELEQYASSFIFGELLAVPVFIGWTLYADAHTALWITVALLVITCPCALSLATPTAL					
	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	AASTGTLAREGILIGGKQAIETLAQTTDII	FDKTGTLTQGKPAVRRISLLRGTDFAFVLA				
	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	VAQALEQQSEHPLARAILNCRISDGSVPDIAIKQRLNRIGEGVGAQLTVNGETQVWALGR					
	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	ASYVAEISGKEPQTEGGGSAVYLGSGSGFQAVFYLT	DPLKDSAAEAVRQLAGKNLTLHIL				
	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	SGDRETAVAETARALGVHYRAQAMPEDKLEYVKALQKEGKKVLMIGDGINDAPVLAQAD					
	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	VSAAAAGGTDIARDGADIVLLNEDLRTVAHLLDQARRTRHI	IRONLIWAGAYNIIAVPLA				
	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	VLGYVQPWIAALGMSFSSLA	VLGNALRLHKGKMQSEKMPSEQX				
	790	800	810	820		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2357>:

```

g705.seq
1  GTGTTCAATA ATTTCCttgC CTCTCTGCCG TTTATGACGG AAACACGCGC
51  TGATATGCTC ATCAGCGCGT TTTGGCCCAT GGTAAAGCC GGCTTTACAG
101 TGTCTTtgcC TTTGGCGATC GCTTCTTTCG TTATCGGCAT GATTATTGCC
151 GTAGCCGTTG CTTTGGTAAG AATCATGCCT TCCGGCGGTA TTTTCCAAAA
201 ATGCTTGTtG AAGCTGGTGG AATTTTATAT TTCCGTCGTT CGCGGTACGC
251 CGCTGTtGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC GTCCGTCGGC
301 ATCTATATCA ATCCGATTCC CGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGCGGCATAC GCTTCCGAAA CCATACGCGC GGCGATTTTG TCCGTGCCGA
401 AAGGGCAGTG GGAAGCAGGT TTCTCCATCG GTATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCACC GCAGGCATTG CGCGTCGCCG TTCCGCCGTT
501 GAGCAACGAG TTTATCGGCT TGTTCAAAAA CACCTCGCTT GCCGCCGTGG
551 TAACGGTAAC GGAGCTTTTC CGTGTGCGAC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCTGTCTA TATCGAAGCT GCATTGGTTT ATTGGTGTtT
651 CTGTAAAGTG CTGTTTTTGA TTCAGGCGCG TTTGGAAAAA CGTTTCGACC
701 GTTATGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

```

g705.pep
1  VFNNFLASLP FMTETRADML ISAFWPMVKA GFTVSLPLAI ASFVIGMIIA
51  VAVALVRIMP SGGIFQKCLL KLVEFYISVV RGTPLLVLQV IVFYGLPSVG
101 IYINPIPAAI IGFSNLVGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVKV LFLIQARLEK RFDRYVAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

```

m705.seq
1  GTGTTCAATA ATTTCTTtGC TTCGCTGCCG TTTATGACGG AAACACGCGC
51  CGATATGATT GTCAGCGCGT TTTTGCCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTTG CTTTGGTtGC GATTATGCCG GCCGGCGGCA TCGTGCGGAA
201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTtGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGCGGCATAC GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCTA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TTGTGCGGCC GCAGGCATTG CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGCTCA TATCGAAGCC GCTTTGTTTT ACTGGTGTtT
651 TTGTAAAGTG CTGTTCTCTA TTCAGGCGCG TTTGGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

```

m705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLQV IVFYGLPSVG
101 IYIDPIPAAI IGFSNLVGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVKV LFLIQARLEK RFDRYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

```

m705/g705    95.0% identity in 238 aa overlap

              10      20      30      40      50      60
m705.pep    VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g705         VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIASFVIGMIIAVALVRIMP
              10      20      30      40      50      60

              70      80      90      100     110     120
m705.pep    AGGIVRKILLKLVEFYISVIRGTPLLVLQVIVFYGLPSVGIYIDPIPAAIIGFSNLVGAY
              :||| :| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1134

```

g705      SGGIFQKCLLKLVEFYISVVRGTPLLVLVIVFYGLPSVGIYINPIAAIIGFSLNVGAY
           70      80      90      100     110     120

           130     140     150     160     170     180
m705.pep  ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
g705      ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180

           190     200     210     220     230     239
m705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
           |||
g705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTTCAATA  ATTTCCCTTGC  TTCGCTGCCG  TTTATGACGG  AAACACGCGC
51 CGATATGATT  GTCAGCGCGT  TTTTGCCTAT  GGTCAAAGCC  GGCTTCGCGG
101 TCTCTCTGCC  TTTGGCGGCA  GCTTCTTTTC  TTATCGGTAT  GATGATTGCG
151 GTAGCCGTGG  CTTTGGTGCG  GATTATGCCC  GCCGGCGGCA  TCGTGCGGAA
201 AATCCTGCTG  AAATTGGTGG  AATTTTATAT  TTCCGTCATT  CGCGGTACGC
251 CGCTGTTGGT  TCAGCTTGTG  ATTGTGTTTT  ACGGGCTGCC  TTCCGTCGGC
301 ATCTATATCG  ACCCGATTCC  TGCCGCCATC  ATCGGCTTTT  CGCTCAATGT
351 CGGCGCATAT  GCTTCCGAAA  CCATACGCGC  GGCAATTTTG  TCCGTACCGA
401 AAGGCCAATG  GGAAGCAGGT  TTCTCCATCG  GCATGACCTA  TATGCAGACG
451 TTCCGCCGCA  TCGTCGCGCC  GCAGGCATTT  CGCGTTGCCG  TGCCGCCTTT
501 GAGCAACGAG  TTTATCGGTT  TGTTAAAAA  CACCTCGCTC  GCGGCAGTCG
551 TGACGGTAAC  GGAATTATTC  CGCGTCGCGC  AGGAAACGGC  AAACCGCACT
601 TATGACTTTT  TGCCCGTCTA  TATCGAAGCC  GCTTTGGTTT  ACTGGTGTTC
651 TTGTAAAGTG  CTGTTCTCTG  TTCAGGCGCG  TTTGGAAAAA  CGTTTCGACC
701 GCTACGTCGC  CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP  FMTETRADMI  VSAFLPMVKA  GFAVSLPLAA  ASEVIGMMIA
51 VAVALVRIMP  AGGIVRKILL  KLVEFYISVI  RGTPLLVLV  IVFYGLPSVG
101 IYIDPIPAAI  IGFSLVNGAY  ASETIRAAIL  SVPKGQWEAG  FSIGMTYMQT
151 FRRIVAPQAF  RVAVPPLSNE  FIGLFKNTSL  AAVVTVTELF  RVAQETANRT
201 YDFLPVYIEA  ALVYWCFCVK  VFLFIQARLE  KRFDRYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

           10      20      30      40      50      60
a705.pep  VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           |||
m705      VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           10      20      30      40      50      60

           70      80      90      100     110     120
a705.pep  AGGIVRKILLKLVEFYISVIRGTPLLVLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
           |||
m705      AGGIVRKILLKLVEFYISVIRGTPLLVLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
           70      80      90      100     110     120

           130     140     150     160     170     180
a705.pep  ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
m705      ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180

           190     200     210     220     230     239
a705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLFIQARLEKRFDRYVAKX
           |||
m705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLFIQARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq

```

1  ATGAACCTCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
51  CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCggaa
101 ccgtCCTGTT CGCCACCGCA CTCGCCCGgc tACTCCACCT CCAacacggc
151 gAATGGATAG GGAtgaCCGT CTTCTGTCGT CTCGGCATGC TCCAGTTCCA
201 AGGCGcgatt tActccaacg cgggtGAacg taTGctcggg acgggtcatcg
251 ggctgGGCGC GGGTTTGGgc gTTTTATGGC TGAACCAGCA TTAttccac
301 ggcaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
351 ctGGGCGGCG GTCGGCAAAA acggctacgt ccctatgctg GCGGGGctgA
401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGCGCGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AACTCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCCGCCCT CATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep

```

1  MNSSQRKRLS GRWLNSYERY RHRRLIHAVR LGGTVLFATA LARLLHLQHG
51  EWIGMTVFVV LGMLQFQGA IYNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWLDSG
151 LMRAMNVLIG AAIATAAAL LPLKSTLMWR FMLADNLAD SKMIAEISNG
201 RRMTRERLEQ NMVKMRQINA RMVKSRSHLA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE ROHLRQSLLE TREHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq

```

1  ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51  CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCTGTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTCTGTCGT CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CCGTGGAACG TATGCTCGGC ACGGTTCATCG
251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACCAGCA TTATTTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AACTCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep

```

1  MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51  EWIGMTVFVV LGMLQFQGA IYKAVRMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWLDSG
151 LMRAMNVLIG AAIATAAAL LPLKSTLMWR FMLADNLAD SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSHLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTVALING

```

1136

301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
 351 TRRKWLDAHE RQHLRQSLLE TREHG*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQRNRLVSRWLSYERYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
g706	MNSSQRKRLSGRWLSYERYRRLIHAVRLGGTVLFATALARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m706.pep	LGMLQFQGAIYSKAVERMLGTVIGLGAGLVWLNLQHYFHGNLLFYLTVGTSALAGWAA					
g706	LGMLQFQGAIYSNAVERMLGTVIGLGAGLVWLNLQHYFHGNLLFYLTIGTSALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m706.pep	VGKNGYVPMLAGLTMCLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
g706	VGKNGYVPMLAGLTMCLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m706.pep	FMLADNLADCSKMI AEISNGRRMTREERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
g706	FMLADNLADCSKMI AEISNGRRMTREERLEQNMVKMRQINARMVKSRSHLAATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m706.pep	AMMEAMQHAHRKIVNTELLTTAAKLQSPKNGSEIRLLDRHFTLLQTDLQQTVALING					
g706	SMMEAMQHAHRKIVNTELLTTAAKLQSPKNGSEIRLLDRHFTLLQTDLQQTAAALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
m706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRKWLDAHE					
g706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRKWLDAHE					
	310	320	330	340	350	360
	370					
m706.pep	RQHLRQSLLETREHGX					
g706	RQHLRQSLLETREHGX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

```

1  ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51  CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCCTGTT CGCCACCGCC TCCGCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATACCGT CTTCGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CGGTGGAACG TATGCTCGGC ACGGTCATCG
251 GGCTGGGCGC GGGTTGGGC GTTTTATGGC TGAACCAGCA TTATTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCGGGGCTGA
401 CGATGTGCAT GCTCATCGGC GACAACGGCA GCGAATGGTT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
501 CGCCAACTG CTGCCGCTGA AATCCACACT GATGTGCGCT TTCATGCTTG
551 CCGACAACCT GACCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCCGGAACG CCTCGAAGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGAG CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAAATTG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAACCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC

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1137

```

901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAG
1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
  1 MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
 51 EWIGMTVFVV LGMLQFQGA IYSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWFD SG
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLDC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSHLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLE TREHS*

```

a706/m706 99.5% identity in 374 aa overlap

	10	20	30	40	50	60
a706.pep	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
m706	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a706.pep	LGMLQFQGA IYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVGTASALAGWAA					
m706	LGMLQFQGA IYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVGTASALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a706.pep	VGKNGYVPM LAGLTMCLIGDNGSEWFD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
m706	VGKNGYVPM LAGLTMCLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
a706.pep	FMLADNLDC SKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
m706	FMLADNLDC SKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a706.pep	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
m706	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
a706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
	310	320	330	340	350	360
	370					
a706.pep	RQHLRQSLE TREHSX					
m706	RQHLRQSLE TREHGX					
	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

m707.seq

```

1   ATGGAAATTA TTAACGATGC AGAACTTATC CGTTCCATGC AGCGTCAGCA
51  GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTGGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTTCTTT
201 TCTTCCTTCT GTGCTCATGA AAGAAACAGC TTTTAAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCGTGGCTG GCTACCTCAC TTCCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTCGGGA ATTCGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTCC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGCCG AGTGTTAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTTACAG
601 ATCAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
651 TGCGGGCGGC AAAACGACCG GCAAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTTGT TTTATGTTTC ATATGGACGC
751 GGTTTGGCGC ACAAACCGGA CTTGACTGAT GCCACCGGTA CGGAAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCAATTA TTCGGTGCCG GTAAAAAAT
851 GGCTGTTTTT TTTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGCATTCCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCGCGCGAG CGCATGCTTT GCGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCCG CTCTGCAGGC TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAC
1151 GCGGGACCGG CATGCGCCAA AGTATGCCCTG CACCGGAAGA AAACGGCGGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGA
1251 CGCAGCCGCC CCATTTATTT TAGGCAAAAC GCAGTTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCCA AGATAAATTG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
1401 TTTCCGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCGG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCCG
1551 CTTCAGAGGA GGGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTTG
1601 CCGGCAAGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```

1   MEIINDAELI RSMQRQOHID AELLTDANVR FEQPLEKNNY VLSEDETPTCT
51  RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 IVRGYLTSQA IIQPNMDSG ILKLRVSAGE IGDRIYEEKR DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRLRP SVKTDIQUIP SEEEGKSDLQ
201 IKWQONKPIR FSIQIDDAGG KTTGKYQGNV ALSFDNPLGL SDFYVVSYGR
251 GLAHRDLDLD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGHRYHEATE
301 GYSVNYDYNG KQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAE LRHRAY LNRWQLDGKL SYKRGTGMRQ SMPAPEENG
401 DILPGTSRMK IITASLDAAA PFILGKQOFF YATAIQAWN KPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGKQ LMGAVVGFGR GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```

1   NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51  GAGCAGGCTA CAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTC GGGAAATTCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCATTC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGAAAACC TGCGTCGTTT GCCGAGTGTT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATT TACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTTCA GTATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAA ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NNTAAGCGAT TNGTTTTATG TTTCATATGG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNCCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

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1139

```

751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTG AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTCG CGGATTTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
  1 XKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
 51 KLRVSAGEIG DIRYEEKRDY KSAEGSISAF NNKXPLYRNK ILNLRDVEQG
101 LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ YQSSLAER
251 LWXXFXXTS VXMKLWTRQT KYIDDAEIE VQRRSAGWE AELRHAYLX
301 RWQLDGKLSY KRGTGMRQSM PAPEENGGGT IPXXSRMKII TAGLDAAAPX
351 MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

a707/m707 95.3% identity in 486 aa overlap

```

a707.pep                                10      20      30
                                     XKETAFTKGMCLGSNNLSRLQKAAQQILIVR
                                     |||
m707      EDETPCTRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIVR
              50      60      70      80      90      100

a707.pep              40      50      60      70      80      90
GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEEKRDYKSAEGSISAFNNKXPLYRNKI
|||
m707      GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEEKRDGKSAEGSISAFNNKXPLYRNKI
              110     120     130     140     150     160

a707.pep              100     110     120     130     140     150
LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
|||
m707      LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
              170     180     190     200     210     220

a707.pep              160     170     180     190     200     210
GKYQGNVALSXDNPGLGLSDXFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
|||
m707      GKYYQGNVALSFDNPGLGLSDLFYVSYGRGLAHKTDLTDATGTETESGSRYSVHYSVPVKK
              230     240     250     260     270     280

a707.pep              220     230     240     250     260     270
WLFNFHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWXXFXXTSVXMKLWTRQTY
|||
m707      WLFNFHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWRNRLHKT'SVGMKLWTRQTY
              290     300     310     320     330     340

a707.pep              280     290     300     310     320     330
KYIDDAEIEVQRRRSAGWEAELRHAYLXRWQLDGKLSYKRGTGMRQSMPEPEENGGGTI
|||
m707      KYIDDAEIEVQRRRSAGWEAELRHAYLNRWQLDGKLSYKRGTGMRQSMPEPEENGGDIL
              350     360     370     380     390     400

```

	340	350	360	370	380	390
a707.pep	PXXSRMKIITAGLDAAAPXMLGKQQFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG					
	: : :					
m707	PGTSRMKIITASLDAAAPFILGKQQFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG					
	410	420	430	440	450	460
	400	410	420	430	440	450
a707.pep	EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK					
m707	EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK					
	470	480	490	500	510	520
	460	470	480			
a707.pep	VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX					
m707	VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX					
	530	540	550	560		

```
g708.seq
1  ATGCCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCCT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC CGCGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTTGCTCGAG TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCGC GAAAGTTTCC GGAAGCCCTT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACATA GGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCGCTTGGCCG
401 ACCCCACCTA CCGACCCCTT TATATTGCCA ACCTGAATAA AGCTTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCGCGC CAGCCGCGAT TCCCACCCGC ATTTAAAGAA CTGGCGGCCA
551 CCAAAATGCT GCGCGGGCAG TTGGCGGATG CCGATTACTA CTTTAAAAAT
601 TACCAAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTGC TGTAGGCTT
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCTC
751 ACCGGTCAAT AA
```

g708.pep

1	MPFKPSKRIS	LLLVLALGAC	STSYRPSRAE	KANQVSNIKT	QLAMEYMRGQ
51	PYRQATASIE	DALKSNPKNE	LAWLVRAEII	QYLKVNDKAQ	ESFRQALSII
101	PDSAEINNNY	GWFLCGRLNR	PAESMAYFDK	ALADPTYPTP	YIANLNKGIC
151	SAKQGQFGLA	EAYLKRSIAA	QPQFPFAFKE	LARTKMLAGQ	LGADADYYFKK
201	YQSRVEVLQA	DDLLLGWKIA	KALGNVQAAY	EYEAQLQANF	PYSEELQTVL
251	TGQ*				

```
m708.seq
1  ATGCGCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCCTT
51  GGGCGCGTGC AGCACTTCTT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGAAGCCCTT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAAC TAC GGT TGGTTCC TATCGGCGAG
351 GCTCAACCGC CTTGCCGAAT CTATGGCATA TTTGCAATAA GCTCTGGCCG
401 ACCCCACCTA CCGACCCCTT TATATTGCCA ACCTGAATAA AGGACATATG
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCGGCC CAGCCGCGAT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAATGCTT GCGCCGGCAG TTGGGCGATG CCGATTACTA CTTAAAAAAA
601 TACAAAGCA GGGTAGAAGT CTTACAGGCC GATGATTTGC TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GCGGCGATAC GAATATGAAG
701 CACAATTGCA GCGCAATTTC CCCTACTCGG AAGAATTGCA AACCGTCTCT
751 ACCGGTCAAT AA
```

m708.per

1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLKVNDKAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSALAA QPQFPAPFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

          10      20      30      40      50      60
m708.pep  MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
          |||
g708      MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
          10      20      30      40      50      60

          70      80      90     100     110     120
m708.pep  DALKSDPKNELAWLVRAEIYQYLKVNDKAQESFRQALSIKPDSDAEINNNYGWFLCGRLNR
          |||
g708      DALKSNPKNELAWLVRAEIYQYLKVNDKAQESFRQALSIKPDSDAEINNNYGWFLCGRLNR
          70      80      90     100     110     120

          130     140     150     160     170     180
m708.pep  PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPAPFKE
          |||
g708      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPAPFKE
          130     140     150     160     170     180

          190     200     210     220     230     240
m708.pep  LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF
          |||
g708      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNVQAAYEYEAQLQANF
          190     200     210     220     230     240

          250
m708.pep  PYSEELQTVLTGQX
          |||
g708      PYSEELQTVLTGQX
          250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACACT NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLKVNDKAQ ESFRQXLSIK
101 PDSAEINNNY XWFLCGRLNR PAESMAYFDK ALADPTYXPX YIANLNKGIC
151 SAKQGQFGLA EAYLKRSALAA QPQFPAPFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIQYLKVNDKAQESFRQXLSIKPDSAEINNNYXWFLCGRLNR					
m708	DALKSDPKNELAWLVRAEIQYLKVNDKAQESFRQALSIPKPSAEINNNYXWFLCGRLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
m708	PAESMAYFDKALADPTYTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

```

1  ATGTTTGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51  CGTCGCTCGT GCTCTGATTG CCGCAATGGG CTATACCATC ATTTCAATTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CCGCGGTTT GAAATACAAC GATATGCAGG CAGGGATGAT
201 AGGCGCGTTG AATCAGGGTA TGGCGCGCGT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGGCTGAT TTCCCGACTT TATTTTATT TTCCGCCTT
351 CCGCTGTGTT TCCGTCATCG GCGTGTCCAT CCGCAGCAGC CTGACCGCCT
401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
451 GATATGGCGA TGACGgcggg cgcgattgTT tccggTGTGT TTTTCGGCGA
501 TAAATGTCC CCGCTTTCCG ACACCACGGG CATTTCCGCG TCCATCGTCG
551 GTATCGACCT GTTTGAACAC ATCAAAAACA TGATGTACAC CACCATCCCT
601 GCGTGGCTTA TCAGCGCGGC ACTGATGCTT TGGCTTCTC CCAGCGTCGC
651 CCGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCAT GTTGGTCGTT
751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCCATGCTCT TTACCGTCAT
801 TCCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTATGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA
901 GACATTGCCA AACTGATTTT CCGCGGCGGC TTGGAGAGTA TGTCTTTAC
951 GCAGACCATC GTTATCCTCG GTATGAGTTT GGGCGGGCTG CTGTTTGGCG
1001 TCGGTGTGAT TCCTTCCTTG CTGGAGGCGG TCCGTACCTT CTGACGAAT
1051 GCCGGACGCG CGACGTCAG CGTTGCCATG ACTTCGGTCG GGGTCAATTT
1101 CCTGATTGGA GAGCAATATT TGAGCATCCT GCTTTCGGGA GAAACGTTCA
1151 AACCCGTTTA CGACAACTC GGCCTGCATT CGTGCAACCT GTCGCGGACT
1201 CTGGAAGATG CGGGACCGT GATTAACCCG CTCGTGCCGT GGAGCGTGTG
1251 CGGCGTATTT ATCAGCCACG CCCTTGGCGT ACCCGTTTGG GAATATCTGC
1301 CTTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTAACCTT GTTATTCGGC
1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

```

1  MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQAGMIGAL NQGMGAVYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGGISPT YFYFSAFALC SVIGVSISS LTACATVGVA FMGMAAFQA
151 DMAMTAGAIV SGVFFGDKMS PLSDTTGISA SIVGIDLFEH IKNNMYTTIP
201 AWLISAALML WLLPSVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVV
251 LALMRVNAV V AMLFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DIAKLISRGG LESMFFTQTI VILGMSLGLL LFALGVIPSL LEAVRTFLTN

```

1143

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLFLG
 451 WTGLTSLKK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq

```

1 ATGTTTCGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTTCATTGG
101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CCGCGCGGTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACTTGTTC TTCTTCATCG
251 GCGTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCCGACT TATTTTATT TTTCTCCTT
351 CCGCGCTGTG TCCGTTCATG CCGTGTCCAT CCGCAGCAGC CTGACCACCT
401 CGGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
451 GATATGGCGA TGACGGCGGG CCGGATTGTT TCGGGCGCAT TTTTGGCGA
501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCCGCG TCCATCGTCG
551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTCGC
651 CCGCGAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCCTG GTTGGTCATT
751 TTGGCATTGA TGCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT
801 GGTGTCCGTT GCTGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGTGCGTG GTTTACGGC GGCTACAAAC TCGAAGCGA AGCGTTTAAA
901 GATGTTGTCA AACTGATTTC GCGCGGCGGT TTGGAAAGTA TGTTTTTCAC
951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTTGCCT
1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT
1051 GCCGGACGCG CGACGTTTCA CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCGGGT GAAACGTTCA
1151 AACCCGTTTA CGATAAGCTC GGTCTGCATT CCGCAATCT GTGCGGACG
1201 CTGGAAGATG CGGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTT ATCAGCCACG CGCTGGCGCT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep

```

1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51 YGLARGLKYN DMQOGMIGAL NOGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGLISPT YFYFSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAFQA
151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFH IKNMYYTIP
201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DVVKLISRGG LESMFFTQTI VILGMSLGL LFALGVIPSL LEAIRTFLTN
351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLFLG
451 WTGLTSLKK*

```

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLDDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	DMQOGMIGALNOGMGAIYLF FFIGLMVSALMMSGAIPTLMYYGFGLISPTYFYFSSFALC					
g709	DMQAGMIGALNOGMGAVYLF FFIGLMVSALMMSGAIPTLMYYGFGLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	SVIGVSIGSSLTTCATVGVA FMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVA FMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SIVGIDLFH IKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFH IKNMYYTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
m709.pep	SIVGIDLFH IKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFH IKNMYYTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLFTVMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
g709	SLIPFALLVVLALMRVNAVVMFLFTVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMFFTQTIVILGMSLGGLLFALGVIPSLLEAIRTFTLNAGRATFSVAM					
g709	DIAKLISRGGLESMFFTQTIVILGMSLGGLLFALGVIPSLLEAVRTFTLNAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEYQLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPSVCGVF					
g709	TSVGVNFLIGEYQLSILLSGETFKPVYDKLGLHSCNLSRTLEDAGTVINPLVPSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKXX					
g709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKXX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTTCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTNGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTNTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCCGACT TATTTTATTT TTTCCGCCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCACCT
401 GCGCCACTGT CGGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGGN CNNGATTGTN NNGNCGCAT TNTTNGGCGN
501 CAAAATGTCN CCGCTTCCG ATACGNCGGG CATNTCCGCG TCCATTGTCG
551 GTATCGACCT GTTTGAACAC ATCAAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACACCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGCGCT GTTGGTCGTT
751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCTATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTNTANA
901 GACATTGCCA AACTCATTTT TCGCGGCGGT TTGGAAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATTCTTG GGATGAGCCT TGGCGGGCTG CTGTTTGCAC
1001 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTGAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTGNGGT GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTC ATCANCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDM PRGEALAVVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQQGMIGAL NQMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGLISPT YFYFSAFALC SVIGVSISS LTTTCATVGVA XMGXXXAFXA
151 XMXXXXXXIV XXAXXGXKMS PLSDTXGXSA SIVGIDLFH IKNMMYTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLVV
251 LALMRVNAV VAMLFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMFFTQTI VILGMSLGG L FALGAIPSL LDAVRSTFTN
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST

```

1145

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

a709/m709 91.1% identity in 459 aa overlap

	10	20	30	40	50	60
a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTIIXLEWLPHMSIIAAIVVLILYGLARGLKYN					
m709	MFAFXSLDMPRGEALAVVVALIAAMGYTIIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a709.pep	DMQQGMIGALNQGMGAIYLFFFIGLMVSALMMSGAIPTLMYYGFGGLISPTYFYFSAFALC					
m709	DMQQGMIGALNQGMGAIYLFFFIGLMVSALMMSGAIPTLMYYGFGGLISPTYFYFSSFALC					
	70	80	90	100	110	120
	130	140	150	160	170	180
a709.pep	SVIGVSIGSSLTTCATVGVAIXXAFAXMXXXXXIVXXAXXGXKMSPLSDTXGXA					
m709	SVIGVSIGSSLTTCATVGVAIFMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a709.pep	SIVGIDLFEHIKNMMYTTIPAWLISXXLMLXLLPSVAAQDLNSVESFRSQLEATGLVHCY					
m709	SIVGIDLFEHIKNMMYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
	250	260	270	280	290	300
a709.pep	SLIPFALLVVLALMRVNAVVAFLFTVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAXX					
m709	SLIPFALLVILALMRINAVVAFLFTVMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a709.pep	DIAKLISRGGLSMFFTQTIVILGMSLGGLLFALGAIPSLDDAVRSFLTNAAGRXTFSVAM					
m709	DVVKLISRGGLSMFFTQTIVILGMSLGGLLFALGVIPSLLEAIRFTLTNAAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
a709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
m709	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
a709.pep	IXHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTLSKKX					
m709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTLSKKX					
	430	440	450	460		

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq

1	ATGGAACCC	ACGAAAAAAT	CCGCCTGATG	CGCGAATTGA	ATAAATGGTC
51	CCAGGAGGAT	ATGCGCGAAA	AGCTGGCGAT	GTCCGCAGGC	GGGTATGCCA
101	AAATCGAACG	GGGCGAAACG	CAGTTAAATA	TCCCGCGTTT	GGAGCAGTTG
151	GCTCAGATTT	TCAAAATCGA	TATGTGGGAC	TTGCTCAAAT	CGGGCGGTGG
201	TGGGATGGTG	TTTCAGATTA	ATGAAGGTGA	TAGTGGTGGC	GATATTGCGT
251	TGTATGCGTC	GGGTGATGTT	TCGATGAAAA	TAGAATTTTT	AAAAATGGAG

```
m710.pep
  1  METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
 51  AQIFKIDMWD LLKSGGGGMV FQINEGDSGG DIALYASGDV SMKIEFLKME
101  LKHCKEMLEQ KDKEIELLRK LTETV*
```

```
a710.seq
1  ATGGAAACCC  ACGAAAAAAT  CCGCCTGATG  CGCGAATTGA  ATAAATGGTC
51  CCAGGAGGAT  ATGGCGGAAA  AGCTGGCGAT  GTCGCGAGGC  GGGTATGCCA
101 AAATCGAACG  AAGCGAAACG  CAGTTGAATA  TCCCGCGTTT  GGAGCAGTTG
151 GCGCAGATTT  TCAAATTGA  TATGTGGGAC  TTGCTCAAAT  CGGCGGCGGG
201 CGGGATGGTG  TTGCAGATTA  ACGATGTGGA  TACCAACAGC  GGGGAATTTG
251 CAATCTATAC  CGCTCAGGAT  GCATCNGGTA  AAGCTGGATT  TGTTAAATAG
301 GAATTAAAC  ACTGTAAAGA  ATAGTTGGAA  CACAAGACA  AAGAAATCGA
351 GCTGCTCCGC  AAGCTGACCG  AAACCGTTTA  A
```

```
a710.pep
  1  METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
 51  AQIFKIDMWD LLKSGGGGMV LQINDVDTNS GEFAIYTAQD ASGKAGFVKM
101  ELKHCKEMLE HKDKIEILLR KLTETV*
```

```

      10          20          30          40          50          60
a710.pep    METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLQLAQIFKIDMWD
             |||||
m710        METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLQLAQIFKIDMWD
             |||||

      70          80          90         100         110         120
a710.pep    LLKSGGGGMVLQINDVDTNSTGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKKEIELLR
             |||||::||: |: : |:::||: |:| | :|||:|||||:|:|||||
m710        LLKSGGGGMVFQINEGDSTG-DIALYASGDVSMKIEFLKMELKHCKEMLEQKDKEIELLR
             70          80          90         100         110

a710.pep    KLTETVX
             |||||
m710        KLTETVX
             120

```


1147

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
1  ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACCTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACGCTA
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACCAGC TTAAACAGC
851 TTGAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAE YRNLTASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFDDYNAGRM
251 NYRPDLKYD RALAHQFAKA EMGGADFSTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
1  ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACCTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACGCTA
551 GTTGTCTGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACCAGC TTAAACAGC
851 TTGAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
```

1148

```

901   CCGGATAAAG AGCAGAAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951   TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001  TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051  GACAGCCGTG AAGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101  GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151  TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201  ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251  CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

a711.pep

```

1   MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSlyTTD RGFdYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

	10	20	30	40	50	60
a711.pep	MPAPDLGFALS LPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLMLNDIKTS					
m711	MPAPDLGFALS LPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLMLNDIKTS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a711.pep	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
	130	140	150	160	170	180
a711.pep	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a711.pep	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSlyTTD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSlyTTD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a711.pep	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEVKQRLDIDGK					
m711	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEVKQRLDIDGK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a711.pep	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
m711	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
	310	320	330	340	350	360
	370	380	390	400	410	420
a711.pep	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420

a711.pep	AKFMAKKKVLKX
m711	AKFMAKKKVLKX
	430

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```

m712.seq
  1  ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
 51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTTTGCCGC
101  AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
151  CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGCGGGCCGA
201  TTTGTTCCGA CAAGGCTCGC TGGCGCATT TATGGTGCAG CAAGCATTTG
251  CCAACAACCC TTATTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301  GCAGGCGTGC AGGCAACCGC AACC GTTACC CTTTCCGGCA CGGCCACCGC
351  GCCGGGCGTG GTGGAATCA CGATTGGCGG CAAGCAGGTA AGCAGGCCG
401  TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451  ATCACTGCCG CCGATGTAAC CGTTACC GCA TCCGGCAGCG GCGCAGCCGT
501  TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551  CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601  GCGGTGCGCA AAAATGCGGA CATTGCCACG GCCTTGTTCA AAGTGGCGGG
651  CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701  AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751  GGCTGTATCG GCGTATTGGG TATGAGTGCG GCCTTGAGCA CGGCCACGAC
801  CGCTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851  GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GCGGTGTTG
901  GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951  GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA CTACTCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTAAAGAGC GAGATTTTGG ACGTGCTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GCGCGGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCGCCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GCGCATTGA
1401 TTTGATTTTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

```

m712.pep
  1  MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPQKVL MVAPMLTAGI
 51  QPALEPVQLF SDAEAADLFG QGSLAHL MVR QAFANNPYLD LTVIGIADHS
101  AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151  ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201  GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNIEQR
251  GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301  AFEEDPAKPL NTLEIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
351  QIMRAVSTYT KSNNTDDPA LLDITTIRTL DYVRRSVKER IALRFPRDKL
401  SDRLLPKVKS EILDVLIKLD QAEIENAEA NKGKLVVARA QNDPNRVNAI
451  IPADV VNG LH VFAGRIDLIL *

```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```

m713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACC GC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTCGATTTT GTCATCGGCA GGTTGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCGCTTTG GGCAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAACCCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCCTTTT CCGAGGTAC
651 TTTTTTGGCG CAATCGCACG GCCGCAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTACTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```

m713.pep
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VQALATHIAN SVGLHPWLEP DGTLVVGGAD YSSPPVATLC WSRTDSRCNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDWKWYKD PTMTLHREPKT
251 VVVSADADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWLWQPLR
301 VHVIDDEHGI DAVFFLMGRR FMLSRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGGK GKKQAETAVF E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```

a713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACC GC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTCGATTTT GTCATCGGCA GGTTGGGGCC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCGCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAACCCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCCTTTT CTGAGGTAC
651 TTTTTTGGCG CAATCGCACG GCCGCAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTACTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGCATGGA TGGCACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG

```

1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep

```

1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLLVVGVD YSSPPVATLC WSRTDSRRNI
201 ERMDIEWDTD NRFSEVTF LA QSHGRSGDSA KHD LKWVYKD PTMTLHRPKT
251 VVVSADNLA ALQKQAKQL ADWRLEGFTL TITVGGHKTR DGV LWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FMLS RMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGKKG GKKQAETAVF E*

```

a713/m713 98.4% identity in 381 aa overlap

	10	20	30	40	50	60
a713.pep	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLSGESCE					
m713	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLSGESCE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a713.pep	VVIDGQIVMTGIIGSQRHGKSKGGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
m713	VVIDGQIVMTGIIGSQRHGKSKGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a713.pep	AAPWPQIKAVVLKVENNPALDKIDIEPGETVWQALTHIAN SVGLHPWLEPDGTLLVVGVD					
m713	AAPWPQIKAVVLKAENNPALGKIDIEPGETVWQALTHIAN SVGLHPWLEPDGTLLVVGAD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a713.pep	YSSPPVATLCWSRTDSRRNIERMDIEWDTNRFSEVTF LAQSHGRSGDSAKHDLKWVYKD					
m713	YSSPPVATLCWSRTDSRCNIERMDIEWDTNRFSEVTF LAQSHGRSGDSAKHDLKWVYKD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a713.pep	PTMTLHRPKTVVVSADNLAALQKQAKQLADWRLEGFTLTITVGGHKTRDGV LWQPGQR					
m713	PTMTLHRPKTVVVSADNLAALQKQAKQLADWRLEGFTLTITVGGHKTRDGV LWQPGLR					
	250	260	270	280	290	300
	310	320	330	340	350	360
a713.pep	VHVIDDEHGI DAVFFLMGRRFMLS RMDGTQ TELRLKEDGI WTPDAYPKKAE AARKRKGR					
m713	VHVIDDEHGI DAVFFLMGRRFMLS RMDGTQ TELRLKEDGI WTPDAYPKKAE AARKRKGR					
	310	320	330	340	350	360
	370	380				
a713.pep	KGVSHKGKKGKKQAETAVFEX					
m713	KGVSHKGKKGKKQAETAVFEX					
	370	380				

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```
m714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGCTG TTGCCCCCG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGA
201 CCGTACGGGC AAAAACC GCCGCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATCCGCGCC
451 GGTATCTCGG CCGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGCTA A
```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```
m714.pep
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  RSAGQMLADW ERVLGLDGTG KNRQHRVLAV MAKNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```
a714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGTCTG TTGCCCCCG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGA
201 CCGTACGGGC AAAAACC GCCGCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATCCGCGCC
451 GGTATCTCGG CCGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGATA A
```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```
a714.pep
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  SSAGQMLADW ERVLGLDGTG KNRQRRVLAV MAKNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPRSAGQMLADW					
	10	20	30	40	50	60
	70 80 90 100 110 120					
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
	70	80	90	100	110	120
	130 140 150 160 170 180					
a714.pep	AGDRLAPQEI MWVWHVNVRG GNNRITRFRAGISAAGDRLTDYSDAVIESL FNRLKPAHTA					

1154

m714 AGDRLAPQEIMVWVHVNVVRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
130 140 150 160 170 180

a714.pep IRFTYRX
|||||||
m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq
1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
51 GCGGCTTGCG AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
201 GGGTCGCTCG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep
1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGNTIV YAAIHNFGGM
101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGSLIP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq
1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
51 GCGGCTTGCG AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
201 GGGTCGCTCG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep
1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
51 PKWLGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGNTIV YAAIHNFGGM
101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGSLIP*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq
1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCGGC GCCGTGCGC CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep
1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

m716.seq
 1 ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
 201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
 301 TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

m716.pep
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHNSAHG SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
 101 SK*

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHNSAHGSCGASKSAEGSCGA-----				
g716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQGSAGASKSAEGSCGASKSAEG				
	10	20	30	40	50
	60	70	80	90	100
m716.pep	----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX				
g716	SCGAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

a716.seq
 1 ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
 201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
 301 TCTAAATAA

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

a716.pep
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHNSAHG SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
 101 SK*

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHNSAHGSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHNSAHGSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

g717.seq
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC

```

51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTTCAAAC  CCTGTTCTCG  CCGCCGCTGC
251  TGTTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTGC
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAACACC  TCCGTCTGTA  CGCCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CCGCGCCCGT  TTTGCCCCGC  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTCCCGTGC  AATCGAAGAA  AACGCCACGC
851  CGGCCCGCCT  CTCGGCAACG  GCAGAAATCC  CCGCCGCCCT  GCTTGCCCTC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCCCTCC  TCCTGCTGCC
951  GGAAACTAC  GCCGCCGTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGccgc
1001  cgtgTTTTA  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CTTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCACG  CGCGGCGCGG
1151  CGGTGTCCTG  TGCCGCCTCA  TTCTGGTGTG  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAAA  CGCCTGCCGC  TTTATATGCA
1251  CACATTGTTC  TGCCGTGCC  CCTCGGCGCG  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCcctgttt  gccggcgtAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCTGCG  GCCACCGGAA  AAATTTGCAC  AAATGTTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```

1  MDTKEILGYA  AGSIGSAVLA  VIILPLLSWY  FPADDIGRIV  LMQTAAGLTV
51  SVLCLGLDQA  YVREYYAAAD  KDTLKFKTLF  PPLIFSAAIA  ALLLSRPSLP
101  SEILFSLDDA  AAGIGLVLFE  LSELPPIRFL  LVLRMGRAL  AFSSAQLVPK
151  LAILLLLELT  VGLLHFPANT  SVLTAVYALA  NLAAAFLLF  QNRCLKAVR
201  RAPFSPAVLH  RGLRYGIPLA  LSSLAYWGLA  SADRLFLKXY  AGLEQLGVYS
251  MGISFGGAAL  LLOSIFSTVW  TPYIFRAIEE  NATPARLSAT  AESAAALLAS
301  ALCLTGFESP  LASLLLPENY  AAVRFTVWSC  MLPLFLYTLT  EISGIGLNVV
351  RKTRPIALAT  LGALAAANLLL  LGLAVPSGGT  RGAAVACAAS  FWLFFVFKTE
401  SSCRLWQPLK  RLPLYMHTLF  CLASSAAYTC  FGTPANYPLF  AGVWAAAYLAG
451  CILRHRKNLH  KLFHYLKKQG  FPL*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

m717.seq

```

1  ATGGACACAA  AAGAAATCCT  CGGCTACGCG  GCAGGCTCGA  TCGGCAGCGC
51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCCGCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  GCTGACGGTG
151  TCGGTGTTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACTT  TGTTCAAAC  CCTGTTCTCG  CCGCCGCTGC
251  TGTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTGC
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCCGTCTGTA  CGCCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CACGCACCGT  TTTGCCCCGC  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGTTCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGCGC  AATCGAAGAA  AACGCCCCGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAAATCC  CCGCCGCCCT  GCTTGCCCTC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCCCTCC  TCCTGCTGCC
951  GGAAACTAC  GCCGCCGTCC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTTG  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCGATCGC  GCTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CTTGCTGCTG  CTGGGGCTTG  CCGTGCCGTC  CGGCGGCGCG  CGCGGCGCGG
1151  CGGTGTCCTG  TGCCGCCTCA  TTCTGGCTGT  TTTTGCCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAAA  CGCCTGCCGC  TTTATCTGCA
1251  CACATTGTCT  TGCTGACCT  CCTCGGCGCG  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCCTGTTT  GCCGGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCTGCG  GCCACCGGAA  AGATTTGCAC  AAATGTTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep
 1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
 51 SVLCLGLDQA YVREYYATAD KDTLFTLFL PPLLSAAAIA ALLSRPSLP
 101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLMEGRAL AFSSAQLVVK
 151 LAIIIIPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
 201 HAPFSPAVLH RGLRYGIPIA LSSIAYWGLA SADRLFLKKY AGLEQLGVYS
 251 MGISFGGAAL LFQSFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
 301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
 351 RKTRPIALAT LGALAANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
 401 SSCRLWQPLK RPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAAYLAG
 451 CILRHRKDLH KLFHYLKKQG FPL*

m717/g717 96.4% identity in 473 aa overlap

	10	20	30	40	50	60
m717.pep	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
g717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m717.pep	YVREYYATADKDTLFTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE					
g717	YVREYYAADKDTLFTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m717.pep	LSFLPIRFLLLVLRMEGRALAFSSAQLVVKLAIIIIPLTVGLLHFPANTAVLTAVYALA					
g717	LSFLPIRFLLLVLRMEGRALAFSSAQLVVKLAIIIIPLTVGLLHFPANTSVLTAVYALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m717.pep	NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAIWGLASADRLFLKKY					
g717	NLAAAFLLFQNRCLKAVRRAPFSPAVLHRLRYGIPIALSSIAIWGLASADRLFLKKY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m717.pep	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
g717	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENATPARLSATAESAAALLAS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m717.pep	ALCLTGIFSPPLASLLPENYA AAVRFIVVSCMLPPLFCTLA EISGIGLNVVRKTRPIALAT					
g717	ALCLTGIFSPPLASLLPENYA AAVRFIVVSCMLPPLFCTLA EISGIGLNVVRKTRPIALAT					
	310	320	330	340	350	360
	370	380	390	400	410	420
m717.pep	LGALAANLLLGLAVPSGGARGA AAVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
g717	LGALAANLLLGLAVPSGGTRGA AAVACAASFWLFFAFKTESSCRLWQPLKRLPLYMHTLF					
	370	380	390	400	410	420
	430	440	450	460	470	
m717.pep	CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLHLYLKKQGFPLX					
g717	CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLHLYLKKQGFPLX					
	430	440	450	460	470	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
 51 GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
 101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGGG GCTGACGGTG
 151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
 201 CGCCGCCGAC AAAGACACTT TGTTCAAAC CCTGTTCTCG CCGCCGCTGC

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251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTCGCT CGACGATGCC GCCGCCGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTGC
401 GTATGGAAGG ACGCGCCTT GCCTTTTCGT CCGCGCAACT CGTGTCCAAG
451 CTCGCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACTTTCC
501 GGCGAACACC GCCGTCCTGA CCGCGGTTTA CGCGCTGGCA AACCTTGCCG
551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGTCTGAA GGCCGTCCGG
601 CGCGCACCGT TTTTCATCCG CGTCCTGCAT CGCGGCCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTTTCT GAAAAAATAT GCCGGCCTAG AACAGCTCGG CGTTTATTTCG
751 ATGGGTATTT CGTTCGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTTCCGCGC AATCGAAGCA AACGCCCCGC
851 CCGCCCGCCT CTCGGCAACG GCAGAAATCCG CCGCCGCCCT GCTTGCCCTC
901 GCCCTCTGCC TGACCGGCAT TTTCTCGCCC CTCGCCTCCC TCCTGCTGCC
951 GGAAACTAC GCCGCCGTCC GGTTCATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTG CACGCTGTA GAAATCAGCG GCATCGGTTT GAACGTGCTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCTGCTGCTG CTGGGCTTG CCGTACCGTC CGGCGGCGCG CGCGGCGCGG
1151 CGGTTGCTG TGCCGCTCA TTTTGGCTGT TTTTGTGTTT CAAGACCGAA
1201 AGCTCCTGCC GCCTGTGGCA GCCGCTCAA CGCCTGCCGC TTTATATGCA
1251 CACATGTTC TGCCTGCCT CCTCGCGGC CTACACCTGC TTCGGCAGTC
1301 CGGCAACTA CCCCCTGTTT GCCGGCGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCCTGC GCCACCGAA AGATTTGCAC AAAGTGTTC ATTATTTGAA
1401 AAAACAAGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYAAAD KDTLFKTLFL PPLLSAAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLRMERAL AFSSAQLVSK
151 LAILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPFSSAVLH RGLRYGPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPPLFCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGA RGAAVACAAS FWLFFVFKTE
401 SSCRLWQPLK RLPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLAG
451 CILHRKDLH KLFHYLKKQG FPL*

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a717/m717 97.9% identity in 473 aa overlap

```

          10      20      30      40      50      60
a717.pep  MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
          |||
m717      MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
          10      20      30      40      50      60

          70      80      90      100     110     120
a717.pep  YVREYAAADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE
          |||
m717      YVREYYATADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE
          70      80      90      100     110     120

          130     140     150     160     170     180
a717.pep  LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA
          |||
m717      LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA
          130     140     150     160     170     180

          190     200     210     220     230     240
a717.pep  NLAAAFLLFQNRCLKAVRRAPFSSAVLHRLRYGPIALSSIAWGLASADRLFLKKY
          |||
m717      NLAAAFLLFQNRCLKAVRRAPFSPAVLHRLRYGPIALSSIAWGLASADRLFLKKY
          190     200     210     220     230     240

          250     260     270     280     290     300
a717.pep  AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEANAPPARLSATAESAAALLAS

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|||||
m717      AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
           250      260      270      280      290      300

           310      320      330      340      350      360
a717.pep  ALCLTGIFSPLASLLLPENYA AVR FIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
|||||
m717      ALCLTGIFSPLASLLLPENYA AVR FIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
           310      320      330      340      350      360

           370      380      390      400      410      420
a717.pep  LGALAANLLLLGLAVPSGGARGA AVACAASFVWFFVFKTESSCRLWQPLKRLPLYMHTLF
|||||
m717      LGALAANLLLLGLAVPSGGARGA AVACAASFVWFFAFKTESSCRLWQPLKRLPLYLHTLF
           370      380      390      400      410      420

           430      440      450      460      470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKLHFHYLKKQGFFPLX
|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLHFHYLKKQGFFPLX
           430      440      450      460      470

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g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1  TCAGACGGCC TTTACGTACC CCGAACTTT ATCCACCGCC CGCAAAGCTG
51 GTTCAAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTC TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTTTGG
251 AGCTGTACGG CATGCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCTT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGCAGAT GGCCGACTGG
451 TGCGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTTGA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGGCGTACAA
751 ATCCCCGAAA GCTGGGTGCG CGACAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGGTTGAGCC
951 CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

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This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1  SDGLYVPRNF IHRPQSWFKW DKDNGLLLRT RENPEGEALW PLGVVHTQK
51 SRSVQQARNG LFRTLSWLYM FKHYAVHDFE EFLELYGMPI RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLLQADW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRRDLLV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKFEFDTRE PKDIAVFADA IPKLVDVGVO
251 IPESWVRDKL VIPDVQEGEA VLVQRQPDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

a718.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTCATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCTGC TTCGAGCGGT GCGGAAATC GGTCAACAAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAT TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCCGG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGACAC AACCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAA CAACTATCCC CATGCCGACC CAAACGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGCTTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTGA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

a718.pep

```

1  MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDS DIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEKLSD QAYEMMDSL P TLEDLIMDL M DAVGHGFSAL EVIEWFSDGL
151 YLPRNFIHRP QSWFKWDKDN G LLLRTREN P EGEALWPLGW VVHTQKSRSV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMDWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRPVKF EFDTREPKDI AVFADAI PKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPNVRT ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDENSQLN PMVRQVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEWVFS					
m718	SDGLYLPRNFIHRPQSWFKWDKDNGLLLRT					
					10	20
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
m718	RENPEGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLLQMDW					
m718	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTATSNPFLQMDW					

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
m718	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLO					
	160	170	180	190	200	210
a718.pep	360	370	380	390	400	410
m718	INYPHADPNRPVKFEFDTREPKDIAVFADAIPKLVDVGVQIPESWVRDKLVIPDVQEGEA					
	220	230	240	250	260	270
a718.pep	420	430	440	450	460	470
m718	VLVRQVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
	280	290	300	310	320	330
a718.pep	480	490	500	510	520	
m718	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	340	350	360	370	380	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATGCGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGCGCACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGTCGAGT GGTATTTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACGCCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAAATCCG GAAGGGCAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTCTAT CCAAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCTTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGGAATC GGTCACAACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCAG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGGCGCGC TGATTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCGGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCGA GCATCAGGAA
1351 ATATTGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQKEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDSIDIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEKLSLD QAYENMMSLP TLEDLIMDLN DAVGHGFSAL EWEVVFSDGL
151 YLPNRFIHRP QSWFKWDKDN GLLLRTRNRP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRICK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGTTATSNPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

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351 IGPFLOINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq

```

1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCC CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGTGTC TGCCTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC CGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGACAG CTTTCTGCGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGTGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCCTG TTCGAGCGGT GCGGGAATC GGTCAACAAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAA CAACTATCCC CATGCGGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCACGCTAT CCCGAAATG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACCTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGGCG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGCGCGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep

```

1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHELFDI EERDSIAAN MGRKRALLT LNWRVAPPRN
101 ATPEEKLSD QAYEMMDSL TLEDLMDLM DAVGHGFSAL EVEWVFSGL
151 YLPRNFIHRP QSWFKWDKDN GLLRLTREN EGEALWPLGW VVHTQKRSV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIG YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQADWCEKS
301 AARLILGQTL TSGADGKST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLOINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
m718-1	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
	10	20	30	40	50	60
a718.pep	RAQHELFDIEERDSIAANMGRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSL					
m718-1	RAQHELFDIEERDSIAANMGRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSL					
	70	80	90	100	110	120
a718.pep	TLEDLMDLMDAVGHGFSALEVEWVFSGLYLPRNFIHRPQSWFKWDKDNGLLRLTREN					
m718-1	TLEDLMDLMDAVGHGFSALEVEWVFSGLYLPRNFIHRPQSWFKWDKDNGLLRLTREN					
	130	140	150	160	170	180
a718.pep	TLEDLMDLMDAVGHGFSALEVEWVFSGLYLPRNFIHRPQSWFKWDKDNGLLRLTREN					
m718-1	TLEDLMDLMDAVGHGFSALEVEWVFSGLYLPRNFIHRPQSWFKWDKDNGLLRLTREN					

a718.pep	190	200	210	220	230	240
	EGEALWPLGWVHTQKSRSVQQARNGLFRTLWLYMFKHYAVHDFAEFLELYGMPIRIGK					
m718-1	EGEALWPLGWVHTQKSRSVQQARNGLFRTLWLYMFKHYAVHDFAEFLELYGMPIRIGK					
	190	200	210	220	230	240
a718.pep	250	260	270	280	290	300
	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQMADWCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMADWCEKS					
	250	260	270	280	290	300
a718.pep	310	320	330	340	350	360
	AARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
a718.pep	370	380	390	400	410	420
	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDVGVIQIPESWVRDKLVI PDVQEGEAVLVR					
m718-1	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDVGVIQIPESWVRDKLVI PDVQEGEAVLVR					
	370	380	390	400	410	420
a718.pep	430	440	450	460	470	480
	QVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAL					
m718-1	QVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAL					
	430	440	450	460	470	480
a718.pep	490	500	510	520		
	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

1	ATGGCAAACG	GGAACATGAA	ACTGTCGTTG	GTGTTAACCG	CCCGAGATGA
51	CGGAGCGAGA	CGGCTACTGG	CTGATACTCA	ACGACAATTA	GATCGTACCG
101	CGAAATCGCG	GGCGCAACTT	GAACGGCAAA	GCCATACTTA	TGCGTTGACC
151	GGCATCCGCT	CAGAAAAACA	GATTCAACGC	GAAATCATGC	TGACACAGGC
201	TGCGTTTAAC	CGTTTGCGGC	GCAGCGGCAA	GGCATCACAA	AATGATTTGG
251	CACGGGCGGC	GGTCGCTACG	CGTAACCGAA	TTCCGCGAGCT	GAACGCGGAA
301	CTGAAACAGG	GCACGGGATT	TGCGGACAAG	ATGGGAAAAA	TCGGAAGATT
351	CGGTGCAGCT	GCGGTGGCTG	GTGGCGCGGC	AGCGTATACG	GTGCTTAAGC
401	CTGCTATGGA	CAACAGAAAG	CAGCTTGATG	AGAACATCAA	CCGCGTGTCC
451	AGACAGGCAT	TTATTGAGGA	TAACAGTAAA	TCGGCAGCGT	GGATTGCAAC
501	TGAAGGTGCG	CAACAGATCA	AGGATTTGGC	ACTTGAACCT	GTGAGAAAAA
551	ATGGCGGGAC	CCACGATAAG	GCTTTGGATT	TAATCAGCGG	CATGATGACC
601	ACCGGTCTGA	ATTTTGCCCA	AAACCAAGAA	GAAGCGCAGG	CGGCATATGC
651	TTTTGCACTT	GCCTCAGAAG	GCAGTGGCGA	GGATACGGCA	AAACTGATTA
701	AAACCCTGAA	AGATGGCGGC	ATGAGCGGTA	AAGACCTGCA	ACTCGGGCTT
751	GAGCACGTCT	TGCAATCGGG	TTAGACGGC	ACTTTCGAGG	TGCGGGATAT
801	GGTTCCGGAG	CTGCCGAGCC	TGCTCTCTGC	CGCGCAACAG	GCAGGGATGA
851	ATGGTGTCCG	CGGTTTGGAC	TACCTGCTCT	CACTCTTACA	ATCTGCGGCG
901	AATAAATCGG	GCAGTCCTGC	CGAAGCGGCG	ACTAATGTGC	AAAATCTTTT
951	GAGTAAAACT	CTGTCGCCTG	ACACGATAGG	TCGTCTGAAG	AAGATGGCAA
1001	ATCCGAATGA	CCCGAAGAAA	GGTGTGCGAT	GGATAGGCTC	GGTTGTGCAA
1051	GGCAAGCAAA	ACGGCGAAAA	CGCAGTGCGA	GTGTTGTCCC	GTCTTGCCGA
1101	TGCCATGCTA	GTAAAGGATA	AGCAATACCA	AGATTATAAG	AAACGCGCGG
1151	CTGCAGGCGA	TAAGACGGCG	GCGGAGCAGG	CAAATATGCT	TAAGGGCGCG
1201	CTTTTGGCGC	AACTGCTGCC	TGATTTGCAG	GCAAAACAAG	GTTTGCTGGC
1251	TGCAACGGAT	ATGACGCAAA	TCCGTGAATA	TATGGCTTCG	TTGGCTGGCG

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1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCGAG CGGCGTGGCA GCAGGTGCCA CAGCGGCAGG CCGTAAGTTG
1651 CTGTCATGGG GAAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAGC GGTTTGCGTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAA CAACGGTATC CGATTTGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTTTCAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GCGCGAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151 CGGCCGTGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

```

m719.pep
  1 MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
 51 GIRSEKQIQE EIMLTQAAFN RLARSGKASQ NDLARAAVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPADNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAYAFAL ASEGSGEDTA KLIKTLKDGG MSGKDLQLGL
251 EHVLSGLDG TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLLQSAA
301 NKSGPSAEAA TNVQNLLSKT LSPDTIGRLK KMANPNPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLDNGK IAKNNEARML
451 SAAQQEQQE SLAMLRESLT GTLVDMETSF KKLAAYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKR AGLLGMLLYS ESLGDGTLPK GLRGTKTTPPE
601 MINRLKNGI RFEPAPKREQ ARGGVPOYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQQQT AAYQAALAQD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVS RYQVAMFGRG AGQ*

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a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

```

m720.seq
  1 ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCGG
 51 CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTGTGTCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCAGG TGCAGATTAA TCGGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGTGC
251 TGGTGCACCC TGTTTGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTTT GAAAACGCCT
401 TTTTGGTCGA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTGTA TCGGTGTTG GCGGTGGATG CCGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGCAGCA TCGGGTACGT
551 TTGGCGCGGT GCGCCGTTG TTTGATTTG ACAAATTGC CTTTCCCGAT
601 CCGGGCGGAT ACAGTGCAGC GCGCTTTAAA AACGGCTCGG CCAAGCTGTT
651 TGCGGATATA TCGGTCATGG TAGATACTGG CATACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGTT GGTGCGCCGC ACAGCGGTTT
751 GACGGGGCTG CCGCTGTTGC CGACCGCGCC GCGGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGGCCTGCA AAACCGCCTG AACCAGTTAA

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1165

```

851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CGGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTGCGGTGGC AACGGCATTG ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTGTA TTGAGGTTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTTAC GGCGATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

m720.pep

```

1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
51 GROVQINAVF WKGKYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AEAQEIFVF ENAFLVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAAAVADRA AAI PDNLLTG RFS DGLQNLRL NRLTAKQVQP VAQAVRLLST
301 SLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGGLTANAVY TEAYQTAE SL RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

a720.seq (partial)

```

1 GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTGATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGCGGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGATATC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGGCA
301 GGCGTCTGA ATGCGTTGGT TCGGCGGCTC ATCAACCAA AGCCGCGGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGCG GCTCAATCCC
451 CATATCCACC ACCCGCGGTT TATCAAGCGC GGCACTTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

a720.pep (partial)

```

1 GLQNLRLNLT AKQVQPVQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRAMRRRM QAEIAALRAV QTAAAESGGL TANAVYTEAY QTAE SLRAAA
101 GRLNALVA AV INQKPLIVR QAPIDGTI HQ IAHEFYGDIA RAAELVRLNP
151 HIHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

                250      260      270      280      290      300
m720.pep      SPRQRF DGAAAVADRAAAIPDNLLTGRFSDGLQNLRLNRLTAKQVQPVAQAVRLLSTSSLL
                |||||||
a720           GLQNLRLNLTAKQVQPVAQAVRLLSTSSLL
                10      20      30

                310      320      330      340      350      360
m720.pep      SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAAESGGLTANAVYTEAY
                |||||||
a720           SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAAESGGLTANAVYTEAY
                40      50      60      70      80      90

                370      380      390      400      410      420
m720.pep      QTAESLRAAGRLNALVA AVINQKPLIVRQAPIDGTI HQIAHEFYGDIA RAAELVRLNP
                |||||||
a720           QTAESLRAAGRLNALVA AVINQKPLIVRQAPIDGTI HQIAHEFYGDIA RAAELVRLNP
                100      110      120      130      140      150

                430      440
m720.pep      HIHHPAFIKRGT LVNSYAKX

```

a720 |||||
 HIHHPAFIKRGTLVNSYAKX
 160 170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGCGGCGAT TGTCCGCGCT CGTGGAAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTGCGCG AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTTGAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTTCG TGCCTGGCA GGCTCGCAA CGGGCGGCAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG
1001 CAAAATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC
1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pep
1 MSKNAQKTL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
51 NGHADVALL SSRNQLVVYD EHOTLYKEKN GOPAPAAGWM RWLEFTPKGM
101 FAEVETDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQOLF DLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAKGVLKQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGCGGCGAT TGTCCGCGCT CGTGGAAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTGCGCG AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCA
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTTGAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTTCG TGCCTGGCA GGCTCGCAA CGGGCGGTAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG
1001 CAAAATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

```

a721.pep
1  MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
51  NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQQLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAALA GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

	10	20	30	40	50	60
a721.pep	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPWYLTEENGHDVALLAN					
m721	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPWYLTEENGHDVALLAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a721.pep	SSRNQLVVDYEHXTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
m721	SSRNQLVVDYEHQTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a721.pep	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
m721	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
	130	140	150	160	170	180
	190	200	210	220	230	240
a721.pep	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a721.pep	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLKQPPGGLAFLTGFI					
m721	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLKQPPGGLAFLTGFI					
	250	260	270	280	290	300
	310	320	330	340	350	
a721.pep	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAMKLGMSGEEFVKIKESGKX					
m721	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAMKLGMSGEEFVKIKESGKX					
	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
1  GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51  TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCCTCA TGC GCGGCTT GAGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGACCTGC AAGTGCATAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGCGCGA AATACCGGCA ATCGCCGACG

```

1168

```

401 AGCCGGGCGC GCGGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGCGGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCGGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAACGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

m722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPPTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRPPAGG NRYDYKNWAL
201 SVDGVT SAYV YPLRRGLGTV DIAITSADGV SSETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

a722.seq

```

1 GTGTTTGAAA CGCCGACATT TGAGCAAATC GCGGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CGGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GCGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GCGGCCAAT GTGCGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGCGGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCGGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAACGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

a722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPPTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRPPAGG NRYDYKNWAL
201 SVDGVT SAYV YPLRRGLGTV DIAITSADGV PSETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

1169

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```

m723.seq
1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCCGAACACC TTATTTTAC CGTTTACAAA CACAATACCG
101 TCTTCGCCCC CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTCGGGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTTC GCAGTGGCGT
351 CCACCAGCGC GGTGTGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTA CTGACC GCCTTGCGTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTTCGCGCCA GCCGCCGTCA AACAGCAGGC CGCCGCGCCA AAATTCCTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTTT CCAAGGCTGT GGTTCAGCATT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGCGGC GGTTCGCGG GTTTCGTGTT
851 TGTTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```

m723.pep
1  MRPKPRFRRS VIACISIVIT PEHLIFTVYK HNTVFARGHF FAALHAQLH
51  FAFGHSTQQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHQR GLCDLAVNQP LVVAVGELQD FQLTETRNI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGAAVSA VSGLLLVFAM MTPCFRRRRI
301 RI*

```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```

m724.map
1  ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAAACTGCTAAAAATATCGGCGAAACC
-----+-----+-----+-----+-----+-----+ 60
TACTCAAACCTCATTTAACCCTTTTGGCGGTGTTGACGATTTTATAGCCGCTTTGG
a  M S L S K L A K K T A Q T A K N I G E T -
61  CTGCGCGCGGCTTTTCGGGAAAAATCACGCTGGTGGTGTGTCGTCGAGCCGATACAGCGC
-----+-----+-----+-----+-----+ 120
GACGCGCGCCGGAAGCCCTTTTGTGCGACCAACAGCAGGCTCGGCTATGTCGCG
a  L R A A F R G K I T L V V S S E P I Q R -
121  GTGCAGTTGAGCGGCTTGCGCGACGAAACCTGCAAGACCTTGAACATTTGCAGGAATAC
-----+-----+-----+-----+-----+ 180
CACGTCAAACCTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a  V Q L S G L A D E T L Q D L E H L Q E Y -
181  GGCTTTGCCAGCCATCCGCCCCACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
-----+-----+-----+-----+-----+ 240
CCGAAACGGTCGGTAGCGGGCTGCCGTCGCTTCGCCATCACTATGGCGACCCGCGCTTA
a  G F A S H P P D G S E A V V I P L G G N -

```

1170

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241  -----+-----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTCGGTCGTGCCGTCGATGGCGTAGTTTTTGGAAATTC
a    T S H G V I V C S Q H G S Y R I K N L K -

      CCCGGCGAGACGGCGATTTTTTAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301  -----+-----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCCACGTTTTTAGCACTAATTCGTTCCGTTT
a    P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGCCGATTGCGACGTGTACCGGGTTAACTGCAACAATACGAGGTTAATGCG
361  -----+-----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a    I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAAGTGCAGTGTTGACGGCGCAA
421  -----+-----+-----+-----+-----+-----+ 480
      CGGTGCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACGCGCGGTT
a    A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGGCCGTCGAGGGCGGCGACGGAGCCACCTTTAGC
481  -----+-----+-----+-----+-----+-----+ 540
      CCGGTTTGTAGTTGCCGTTGCCGCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAATCG
a    G Q I N G N G G M A V E G G D G A T F S -

      GGCGATGTTAACCAAACGGGGCGGAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541  -----+-----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGCCCGCGTCAAAATTGTGGCTGCCGCTGCACCACCGCCGCTTA
a    G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCGCCAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
601  -----+-----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCTGTGGGCGTATGGCTGTCTAGCCGCGTTTGAATGGCCGCGCTT
a    I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661  ----- 669
      GGCCGTATC
a    P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI
SalI SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

m724.pep

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQKG IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

a724.seq

```

1  ATGAGTTTGA GTAAATTGGC GAAAAAAACG GCACAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAAA TCGTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGTAACCG GTTAAGTGCA
401 AACAATACGA GGTAAATGCG GCCACGGATG CCAAATTTAA CGCTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```


1171

```

501  CGGCATGGCC  GTCGAGGGCG  GCGACGGAGC  CACCTTTAGC  GGCGATGTTA
551  ACCAAACGGG  CGGCAGCTTT  AACACCGACG  GCGACGTGGT  GGCCGGCAAT
601  ATATCGTTGC  GCCAGACCCC  GCATACCGAC  AGCATCGGCG  GCAAAACCTT
651  ACCGGCGGAA  CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

```

a724.pep
1   MSLSKLAKKT  AQTAKNIGET  LRAAFRGKIT  LVVSSEPIQR  VQLSGLADET
51  LQDLEHLQEY  GFASHPPDGS  EAVVIPLGGN  TSHGVIVCSQ  HGSYRIKNLK
101 PGETAIFNHE  GAKIVIKQ GK  IIEADCDVYR  VNCKQYEVNA  ATDAKFNA PL
151 VETSAVLTAQ  GQINGNGGMA  VEGGDGATFS  GDVNQTGGSF  NTDGDVVAGN
201 ISLRQHPHTD  SIGGKTLPAE  PA*

```

a724/m724 100.0% identity in 222 aa overlap

```

              10      20      30      40      50      60
a724.pep    MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADET LQDLEHLQEY
              |||||
m724         MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADET LQDLEHLQEY
              10      20      30      40      50      60

              70      80      90     100     110     120
a724.pep    GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQ GK
              |||||
m724         GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQ GK
              70      80      90     100     110     120

              130     140     150     160     170     180
a724.pep    IIEADCDVYRVNCKQYEVNAATDAKFNA PLVETSAVLTAQ GQINGNGGMAVEGGDGATFS
              |||||
m724         IIEADCDVYRVNCKQYEVNAATDAKFNA PLVETSAVLTAQ GQINGNGGMAVEGGDGATFS
              130     140     150     160     170     180

              190     200     210     220
a724.pep    GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX
              |||||
m724         GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX
              190     200     210     220

```

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

```

m725.seq
1   ATGGTGCGCA  CGGTTAAAAG  CTACAACGGC  GAGGCCGACG  ATTTGGCGGG
51  GCAAATCCAT  ACGCTGCCTG  CGGTTTGGGT  AACGTATGGC  GGCAGCAAAG
101 TTGAGCCTGC  CAGCACCGGC  GGCGTATGCG  GACGTTATCA  GGATACCGCC
151 GAATTTGTGG  TGATGGTGGC  GGCCCGCAAT  CTGCGCAACG  AGCAGGCGCA
201 GCGGCAAGGC  GGCATCGACA  GCCGCGAAAT  CGGCAGCAAC  GATTTAATCC
251 GCGCTGTTTC  CCGCTGCTT  GACGGCCAGC  GGCTCGGTTT  TGCCGATAGC
301 CGCGGCTTGG  TGCCCAAAGC  GGTGCGCGCG  ATTGCCAATC  ATGTGCTGGT
351 GCAAAACGCC  GCAGTAAGCA  TATATGCGGT  TGAGTATGCC  ATCCGCTTTA
401 ACACCTGCGG  GTTGGAATAT  GACCGTACC  CCGAACGCAC  CGACAATCCC
451 GACGACCCCA  ACCATATCTT  TACCAAGTAT  CAGGGTACAT  TGAGCGAGCC
501 GTGGCCTGAT  TTCGAGGGGT  TGGACGGCAA  AATTACGAC  CCGCAATCCG
551 CCGATGAAAT  ACCTGTAAAC  CTAACCCTTA  AGGATAAGCA  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

```

m725.pep
1   MVRTVKS YNG  EADDLAQI H  TLPVWV TYG  GSKVEPAS TG  GVCGRYQDTA
51  EFVVMVA ARN  LRNEQAQR QG  GIDSREIG SN  DLIRAVRR LL  DGQRLGFADS
101 RGLVPKAV RA  IANHVLVQ NA  AVSIYAVE YA  IRFNTCGL EN  DRYPERTDNP
151 DDPNHIFT KY  QGTLSEPW PD  FEGLDGKI YD  PQSADEIP VN  LTLKDKQ*

```

1172

a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

```
m726.seq
  1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
 51  CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101  CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151  GTTTTAACCC CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201  ATGGAAAATC AGCAAAGCCG CCGCCGCGGC CCGTTTCGCC AAACAAAAAA
251  CCGCCTTGGC ATTCGCCTC GCGGAAAAGG CGGACGAAC CAAAAACAGC
301  CTCTTGCGCG GCTATCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351  AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401  TGGCGCAAAT CGCCGCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451  AAAGTTATCG AAAAATCCGC CCGCCTGGCT GTTGCCGCGC GCGCGATTAT
501  CGGAAAGCGT CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551  CCGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601  GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

```
m726.pep
  1  MTIYFKNGFY DDTLGGIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
 51  VLTTPRPSPDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101  LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVLE
151  KVIEKSARLA VAAGAIIGKR QQLEDKLNTI ETAPGLDALE KEIEEWTLNI
201  G*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

```
a726.seq
  1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCAGCAT
 51  CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101  CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151  GTTTTAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201  ATGGGAAATC GGCGAAGCCG CTGCCGCGGC CCGTTTCGCC GAACAAAAAA
251  CCGCCACGGC ATTCGCCTC GCGGCAAAGG CGGACGAAC CAAAAACAGC
301  CTCTTGCGCG GCTATCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351  AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401  TGGCGCAAAT CGCCGCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451  AAAGTTGTCTG AAAAATCCGC CCGCCTGGCC GTTGCCGCGC GCGCGATTAT
501  CGGAAAGCGG CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551  CAGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601  GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

```
a726.pep
  1  MTIYFKNGFY DDTLGSIEPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
 51  VLTTPRPSEY HEWDGKKWEI GEAAAAAREFA EQKTATAFRL AAKADELKNS
101  LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVLE
151  KVVEKSARLA VAAGAIIGKR QQLEDKLNTI ETAPGLDALE KEIEEWTLNI
201  G*
```

a726/m726 95.5% identity in 201 aa overlap

```

              10      20      30      40      50      60
a726.pep      MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPRPSEY
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m726           MTIYFKNGFYDDTLGGIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPRPSPDY
              10      20      30      40      50      60
```

1173

```

              70      80      90      100      110      120
a726.pep      HEWDGKKWEIGEAAAAARFAEQKTATAFRLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
              |||||||:|:|:|||||||:|||| ||||| ||||||| ||||||| |||||||
m726          HEWDGKKWKISKAAAAARFAKQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep      LARQADNNAPTMLAQIAAARGVELDVLIEKVVEKSARLAVAAGAIIGKRQOLEDKLNIT
              ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
m726          LARQADNNAPTMLAQIAAARGVELDVLIEKVIEKSARLAVAAGAIIGKRQOLEDKLNIT
              130      140      150      160      170      180

              190      200
a726.pep      ETAPGLDALEKEIEEWTLNIGX
              ||||||| ||||||| ||||||| |||||||
m726          ETAPGLDALEKEIEEWTLNIGX
              190      200

g727.seq      not found yet
g727.pep      not found yet

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1  ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTGTC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAACT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPPD SRNPNTGFRL FSPQIPPNT QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1  ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCAGC AACTGGAAACA
201 GGCAGCGTGC GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCTGAA
251 TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DGFHHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
              ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

```

1174

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN
           10          20          30          40          50          60

           70          80          90          100         110         119
a727.pep  YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m727      YARELELARAFAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPDPSRNPNTGF
           70          80          90          100         110

           120         130         140
a727.pep  IDGFGHHGLQLYKRALGYGNX

m727      RLFSPQIPPNFTQIPPX
           120         130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

g728.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGG ATTTGATGCG GCGGGGCGCG GGAAATTCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCCG GGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGCTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACCG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCAACAT CTTGACGCGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCGAGCC TATCATGCGC AACAGACGTG GTATTTGGAT GGCGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCTTGATTT TCCTTTGAAC
1051 TTGGAAGATT TGGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

g728.pep

```

1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGCMQ AOVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGV TADMOT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

m728.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACCG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCT TGCCGGAACT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

```

1175

```

501 CCGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGT TTGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGA AAAACGG AAATCTTTT
901 ATTGCACAAT CTTCGACGGT AGCATTGAAA GCGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GCGGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGGAAAATT TGGAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

m728.pep

```

1 MFKKFKPVLL SFFALVF AFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51 AKLARLFRNA DRVVIVKES IRTEENLAGT VDDGPLQSEK DYLALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHLCLGCMQ AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNLNF
301 IAQSSTVALK ADGVTADMQT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

m728.pep	10	20	30	40	50	60
	MFKKFKPVLLSFFALVF AFW LGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA					
g728	MFKKFKPVLLSFFALVF AFW LGTGIAYEINPRWFLSDTATEVPEPNPNAFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	70	80	90	100	110	120
	DRVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	130	140	150	160	170	180
	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVN VYGGTVHGENYETTGEYRVV					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVN VYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	190	200	210	220	230	240
	WQPDGSVFDAAGRGKIGEDVYEHLCLGCMQ AQVYLAKYRDVANDEQKVWDFRKNESNRIAS					
g728	WQPDGSVFDAAGRGKIGEDVYEHLCLGCMQ AQVYLAKYRDVANDEQKVWDFRKNESNRIAS					
	190	200	210	220	230	240
m728.pep	250	260	270	280	290	300
	DSRNSVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EYYLKNLNF					
g728	DSRDYVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EYYLKNLNF					
	250	260	270	280	290	300
m728.pep	310	320	330	340	350	360
	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
g728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

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```

g728      IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
           310      320      330      340      350      360

           370
m728.pep  YAEAAAARRSGGRRDLSHX
           |||||
g728      YAEAAAARRSGGRRGLSHX
           370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

```

a728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTC TCATTTTTCG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCGAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAAATCG GGAAGATGT TTATGAGCAT
601 TGCCTCGGGT GTTATCAGAT GGCCAGGTA TATTTGCGCA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
701 GGATTGCGTC GGAATCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAAG TCTATTGGAG TTTTCGACAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCGCGC
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

```

a728.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLRYN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL POKVYWSFDN GKQRQSFYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

a728 / m728 96.3% identity in 377 aa overlap

```

           10      20      30      40      50
a728.pep  MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE--NPNFAFVAKLARLFRNA
           |||||
m728      MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
           10      20      30      40      50      60

           60      70      80      90      100     110
a728.pep  DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAVRLSRLKEKAKWFHVTEQEHGEEV
           |||||
m728      DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV
           70      80      90      100     110     120

           120     130     140     150     160     170
a728.pep  WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLRYNDRPFSVNVYGGTVHGENYETTGEYRVV
           |||||
m728      WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLRYNDRPFSVNVYGGTVHGENYETTGEYRVV
           130     140     150     160     170     180

```

1177

	180	190	200	210	220	230
a728.pep	WQPDGSVFDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSLVVGVDADGLPQKVYWSFDNGKKRQSFYYLKNLGNLF					
m728	DSRNSVFYQNMRELMPRGMKANSLVVGVDADGLPQKVYWSFDNGKKRQSFYYLKNLGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDLEKEVSR					
m728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAARRSGGRRDLSHX					
m728	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA CATTGAAAAC TACCTTGACC TCTGTTGCAG CAGCCTTTGC
51  ATTGTCGTCC TGCACCATGA TTCCTCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCGGAAAC CTTCAAAAAC GACACATCGG TTTCTTCCAT CCGCGCGGTT
151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACAGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATCG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGGCTCGCGC CAAGGCAGCT TGAGCGGCg
351 caaTGTCAGC AGCAGCTACA ATGTCGGA CTGGTGcGGca tCTTACGAAC
401 TCGATCTGTT CgGGCGCGTG CGCagcaaca GcgaagcAGC ACTGcaggGC
451 tATTTTGCCA GCGTTGCCAA CcgCGATGCG GCACATTTGa ttCtGATTGC
501 CACCGTTGCC AAAGCCTATT TCAAcgaGcG TTATGCCGAA AAAGcgatgT
551 CTTTGCGCGCa gcGTGTCTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTGCGGT ACAAGGCAGG CGTGATTTC GCGTGCGCC TGCGCCAGCA
651 GGAAGCCTTG ATTGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCa
701 gcCGCGAACA GGCGCGCAAT GCCTTGCAA CCTTGATTAA ccGTCCGATA
751 CCCGAagaCC TGCCCGCCGG TTTGCCGTTG GACaagcAGT TTTTGTGTTGA
801 AAAACTGCCT GCCGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGACA
851 TCCGCGCGCG CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 gcgCGCGCCg ccTTTTTCCC GTCCATCCGC CTGACCGGAA GCGTCGGTAC
951 GGGTTCTGTC GAATTGGGCG GGCTGTTCAA AAGCGGCACG GGCGTTTGGG
1001 CGTTCGCTCC GTCTATTACC CTGCCGATTT TTACTTGGGG AACGAACAAG
1051 GCGAACCTTG ATGTGGCAAA ACTGCGCCAA CAGGCACAAA TTGTTGCCTA
1101 TGAATCCGCG GTCCAATCCG CTTTCAAGA CGTGGCAAAC GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCGGA CTGCGTTACA AACACGGCGT
1251 ATCCGCGCGC CTCGATTTGC TCGATCGGGA ACGCATCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTCGGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CGCTCgacGG CGGATTGAAA CGGGATACCC AAACCGGCAA
1401 ATAA

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This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFQN DTSVSSIRAV
51  DLGWHDYFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNNLLP
101 TLAANANGSR QGSLSGGNVS SSYNVGLGAA SYELDLFGRV RSNSEAAALQ
151 YFASVANRDA AHLILIAIVA KAYFNERYAE KAMSLAQRVL KTREETYKLS

```

m729.seq

m729.pcp

m729.pep MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDYFAD

g729 MNTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFQNDTSVSSIRAVDLGWHDYFAD

1179

	70	80	90	100	110	120
m729.pep	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNV					
g729	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANGSRQGSLSGGNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m729.pep	SSYKVGLGAASYELDLFGRVRSSEALQGYFASTANRDAHLSLIATVAKAYFNERYAE					
g729	SSYNVGLGAASYELDLFGRVRSNSEALQGYFASVANRDAHLILIATVAKAYFNERYAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m729.pep	EAMSLAQRVLKTREETYKLSSELYKAGVISAVLRQOEALIESAKADYAHAAARSREQARN					
g729	KAMSLAQRVLKTREETYKLSSELYKAGVISAVLRQOEALIESAKADYAHAAARSREQARN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m729.pep	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m729.pep	ARAAFFPSIRLTGTGTGSAELGGLEKSGTGVWSFAPSITLPIFTWGTNKANLVDVAKLRQ					
g729	ARAAFFPSIRLTGSGVTGSELGGLEKSGTGVWAFAPSITLPIFTWGTNKANLVDVAKLRQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
m729.pep	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA					
g729	QAQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA					
	370	380	390	400	410	420
	430	440	450	460		
m729.pep	LDLLDAERSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	LDLLDAERISYAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQGX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

```

1  ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTCGC
51  ATTATCCGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGTGC GGTC
151 GATTGGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCC
301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAGC AGCAGCTACA AAGTCGGACT GGGTGC GGCA TCTTACGAAC
401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTGCGCA GCACCGCCAA CCGCGATGCG GCACATTTGA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTATGCCGAA GAAGCGATGT
551 CTTTGGCGCA ACGTGT TTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTACGTT ACAAGGCAGG CGTGATTTC GCGTGC GCCC TACGTACGCA
651 GGAAGCCCTA ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GCGCGCAAT GCCTTG GCAA CCCTGATTAA CCAACCGATA
751 CCCGACGACC TGCCCGCCGG TTTGCCGTTG GACAAGCAGT TTTTGTGTA
801 GAAGCTGCCG GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCCG CCTTTTCC C ATCCATCCGC CTGACCGGAA GCGTCGATAC
951 GCATTCTGCC GAATTGGGCG GGCTGTTCAA AAGCGGCACC GGCGTTTGT
1001 TGTTCCGACC TTCCATTACC CTGCCGATT TTACTG GGGG TACGAACAAG

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1180

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1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTCAAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGCGCGC CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCCGCGG
1301 AAGGTGCGGC TTTGTCGGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

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This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

```

a729.pep
  1 MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
  51 DLGWHDYFAD PRLQKLIDIA LERNLSLRTA VLNSEIYRKQ YMIERNLLP
 101 TLAANANDSR QGSLSGGNVS SSKVGLGAA SYELDLFGRV RRSSEALQOG
 151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
 201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
 251 PDDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
 301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
 351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
 401 ASKEALRLVG LRYKHGVSQA LDLLDAERSS YSAEGAALSA QLTRAENLAD
 451 LYKALGGGLK RDTQTDK*

```

a729 / m729 98.1% identity in 467 aa overlap

	10	20	30	40	50	60
a729.pep	MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDYFAD					
m729	MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDYFAD					
	10	20	30	40	50	60
a729.pep	PRLQKLIDIALERNLSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQSLSGGNVS					
m729	PRLQKLIDIALERNLSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQSLSGGNVS					
	70	80	90	100	110	120
a729.pep	PRLQKLIDIALERNLSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQSLSGGNVS					
m729	PRLQKLIDIALERNLSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQSLSGGNVS					
	70	80	90	100	110	120
a729.pep	SSKVGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE					
m729	SSKVGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE					
	130	140	150	160	170	180
a729.pep	SSKVGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE					
m729	SSKVGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE					
	130	140	150	160	170	180
a729.pep	EAMSLAQRVLK TREETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN					
m729	EAMSLAQRVLK TREETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN					
	190	200	210	220	230	240
a729.pep	EAMSLAQRVLK TREETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN					
m729	EAMSLAQRVLK TREETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN					
	190	200	210	220	230	240
a729.pep	ALATLINQPI PDDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
m729	ALATLINQPI PDDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
a729.pep	ALATLINQPI PDDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
m729	ALATLINQPI PDDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
a729.pep	ARAAFFPSIRLTGSVDTHSAELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ					
m729	ARAAFFPSIRLTGSVDTHSAELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
a729.pep	ARAAFFPSIRLTGSVDTHSAELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ					
m729	ARAAFFPSIRLTGSVDTHSAELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
a729.pep	QAQIVAYEAAVQSAFQDVANALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
m729	QAQIVAYEAAVQSAFQDVANALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
	370	380	390	400	410	420
a729.pep	QAQIVAYEAAVQSAFQDVANALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
m729	QAQIVAYEAAVQSAFQDVANALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
	370	380	390	400	410	420

1181

	430	440	450	460
a729.pep	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
m729	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
	430	440	450	460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

g730.seq

1	GTGAAACCGC	TGCGCAGACT	GACAAACCTC	CTTGCCGCCT	GCGCCGTAGC
51	GGCGGTCGCA	CTCATACAGC	CCGCCCTCGC	GGCGGACTTG	GCGCAAGACC
101	CGTTCATTAC	CGATAACACC	CAACGGCAGC	ACTACGAACC	CGCGGGCAAA
151	TACCACCTCT	TCGGGgaCCC	GCGCGGCAGC	GTTTCCGACC	GCACCGGCAA
201	AATCAACGTC	ATCCAAGACT	ATACCCACCA	GATGGGCAAC	CTGCTCATCC
251	AACAGGCGGC	AATCCAAGGC	AATCTTGGTT	ACACCGTCCG	CTTTTCCGGA
301	CACGGACACG	AAGAACACGC	CCCCTTCGAC	AACCACGCCG	CCGACAGCGC
351	AAGCGAAGAA	AAAGGCAACG	TTGACGACGG	CTTTACCGTG	TACCGGCTCA
401	ACTGGGAAGG	ACACGAACAT	CATCCC GCCG	ATGCCTACGA	CGGCCCGAAG
451	GGCGGCAATT	ACCCCAAAACC	TACGGGCGCA	CGAGACGAAT	ACACCTATCA
501	CGTCAACGGC	ACAGCCC GCA	GTATCAA ACT	CAATCCGACC	GACACCCGCA
551	GCATCCGGCA	ACGCATATTC	GACA ACTACA	ACAACCTCGG	CAGCAATTTT
601	TCCGACCGCG	CCGATGAAGC	CAACAGAAAA	ATGTTCCGAGC	ACAATGCCAA
651	GCTCGACCGC	TGGGGCAACA	GCATGGAGTT	TGTCAACGGC	GTCGCCGCCG
701	GCGCGCTCAA	CCCCTTTATC	AGCGCGGGCG	AAGCCTTGGG	CATAGGCGAC
751	ATACTGTACG	GAACGCGCTA	TGCCATAGAC	AAAGCCGCGA	TGCGCAACAT
801	CGCCCCCTTA	CCCGCCGAGG	GCAAATTTCG	CGCCATCGGC	GGCTTGGGCA
851	GCGCGGCGGG	CTTTGAAAAA	AATACGCGCG	AAGCCGTTGA	CCGGTGGATA
901	CAGGAAAACC	CCAATGCCGC	CGAAACCGTC	GAAGCCCTGG	TCAACGTCCT
951	GCCGTTTGCC	AAAGTCAAAA	ACCTGACAAA	GGCGGCAAAA	CCGGGGAAGG
1001	CTGCGGTTAG	TGGGGATTTT	TCTAAATCCT	ACACCTGCTC	CTTCCACGGC
1051	AGCACCTTGG	TCAAAAACGC	AGACGGCTAC	AAAGCCATTG	CCCATATTCA
1101	AGCCGGAGAC	CGCGTCCCTT	CCAAGGACGA	GGCAAGCGGA	GAAACGGGAT
1151	ACAAACCCGT	TACCGCCCGA	TACGGCAATC	CGTATCAAGA	AACCGTTTAC
1201	ATTGAAGTTT	CAGACGGCAT	CGGCAACAGC	CAAACCCTGA	TTTCCAACCG
1251	TATCCACCCG	TTTTATTTCG	ACGGCAAATG	GATTAAGGCG	GAAGATTTAA
1301	AAGCGGGAAG	CCGGCTGTTA	TCCGAAAGCG	GCAAAACCCA	AACCGTCCGC
1351	AACATCGTTG	TCAAACCAAA	ACCGCTCAA	GCCTACAATC	TGACCGTTGC
1401	CGATTGGCAT	ACCTACTTCG	TCAAGGGTAA	TCAGGCGGAA	ACGGAAGGGG
1451	TTTGGGTTCA	TAATGATTGT	CCGCCTAAAC	CAAAACCAAC	CAATCATGCC
1501	CAACAAAGAA	AAGAAGAAGC	TAAAAACGAT	TCTCATCGAA	GTGTGGGAGA
1551	TTCCAATCGT	GTCGTTTCGC	AAGGAAAGCA	ATATTTAGAT	TCCGACACAG
1601	GAAACCATGT	TTATGTAAAA	GGAGATAAAG	TGGTTATTCT	AACTCCTGAT
1651	GGAAGACAGG	TAACTCAATT	TAAGAACTCG	AAAGCCAATA	CGTCAAAAAG
1701	GGTAAAAAAT	GGGAAATGGA	CACCAAAATA	A	

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

g730.pep

1	VKPLRRLTNL	LAACAVAAVA	LIQPALAADL	AQDPFITDNT	QRQHYEPGGK
51	YHLFGDPRGS	VSDRTGKINV	IQDYTHQMG	LLIQQAAIQG	NLGYTVRFSG
101	HGHEEHAPFD	NHAADSASEE	KGNVDDGFTV	YRLNWEHGEH	HPADAYDGP
151	GGNYPKPTGA	RDEYTYHVNG	TARSIKLNPT	DTRSIRQRIF	DNYNNLGSNF
201	SDRADEANRK	MFEHNAKLDR	WGNSMEFVNG	VAAGALNPFI	SAGEALGIGD
251	ILYGTRYAID	KAAMRNIAPL	PAEGKFAAIG	GLGSAAGFEK	NTREAVDRWI
301	QENPNAETV	EALVNVLPFA	KVKNLTAAK	PGKAAVSGDF	SKSYTCSFHG
351	STLVKTADGY	KAIHAIQAGD	RVLSKDEASG	ETGYKPV TAR	YGNPYQETVY
401	IEVSDGIGNS	QTLISNRIHP	FYSDGKWIK	EDLKAGSRL	SESGKTQTVR
451	NIVVKPKPLK	AYNLTVADWH	TYFVKGNQAE	TEGVVWHNDC	PPKPKPTNHA
501	QQRKEEAKND	SHRSVGDSNR	VVREGKQYLD	SDTGNHVYVK	GDKVVILT
551	GRQVTQFKNS	KANTSKRVKN	GKWT	PK*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

m730.seq

1	GTGAAACCGC	TGCGCAGACT	GACAAACCTC	CTTGCCGCCT	GCGCCGTAGC
51	GGCGGCCGCA	CTCATACAGC	CCGCCCTCGC	GGCGGACTTG	GCGCAAGACC

1182

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101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTTCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCGGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCCGAAG
451 GGCGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAACCT CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTTC
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAATC CCAATGCCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAA GCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAAGTAT GGTTCATCA
1151 AATTTATTAA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAAA GAACAATTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAA TTAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAAAACG TGCAGAATTT TGGTTAAAT ACGGTGTTCA TTCACAAGTT
1351 AAGTCATATA TTGAATCAA AGGCGGCATT GTAAAAACAG GTTTAGGAGA
1401 TTAA

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This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
1 VKPLRRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51 YHLFGDPRGS VSDRTGKINV IQDYTHOMGN LLIQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEHGEH HPADAYDGP
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYSNLGSNF
201 SDRADANRKM FEHNAKLDR WGNMSEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPNFLNQKN RKQIKATIEA ANQQGKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

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          10      20      30      40      50      60
g730.pep  VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      VKPLRRLTNLLAACAVAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS
          10      20      30      40      50      60

          70      80      90     100     110     120
g730.pep  VSDRTGKINVIQDYTHQMGNLLIQAAIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      VSDRTGKINVIQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE
          70      80      90     100     110     120

          130     140     150     160     170     180
g730.pep  KGNVDDGFTVYRLNWEHGEHHPADAYDGPKGNNYPKPTGARDEYTYHVNGTARSIKLNPT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      KGNVDEGFTVYRLNWEHGEHHPADAYDGPKGNNYPKPTGARDEYTYHVNGTARSIKLNPT
          130     140     150     160     170     180

          190     200     210     220     230     240
g730.pep  DTRSIRQRIFDNNYNLGSNFSRDEANRKMFEHNAKLDRWGNMSEFVNGVAAGALNPFI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNMSEFINGVAAGALNPFI
          190     200     210     220     230     240

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	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTKAAPGKAAVSGDFSYSYTCFSHGSTLVKTADGY					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVRTARYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRKRTDSSKFINGREIDAVTNDALIQAKRTISAIKPKNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1  GTGAAACCGC  TCGAAGACT  CATCAAGCTC  CTTGCCGCCT  GTGCCGTAGC
51  GGCGGCCGCA  CTCATACAGC  CCGCCCTCGC  GGCGGACTTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACGCC  CAACGGCAGC  ACTACGAACC  CGGAGGCAAA
151 TACCACCTCT  TCGGCGACCC  GCGCGGCAGC  GTCTCCGACC  GCACCGGTCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCG  GATGGGCAAC  CTGCTCATCC
251 AGCAGGCAAA  CATCAACGGC  ACAATCGGCT  ACCACACCCG  CTTTTCGGGA
301 CACGGATACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 GAGCGAAGAA  AAAGGCAACG  TTGACGAAGG  CTTTACCCTA  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCCGCCG  ATGCCTACGA  CGGCCCGAAG
451 GGCGGCAATT  ACCCCAAACC  TACGGGTGCA  CGCGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCACGCA  GCATCAAAT  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATCC  GACAATTACA  GCAACCTCGG  CAGCAATTTC
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTTCGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TATCAACGGC  GTCGCCGCCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCAA  TGCGCAACAT
801 CGCCCCCTTG  CCCGCCGAGG  GCAAATTTCG  CGTCATCGGC  GGCTTGGGCA
851 GCGTGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTTGA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 CCGGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  CGGGGATTTT  TCTGCTGCAT  ACAATACAAG  AACAACCTAG
1051 AAAGTTACTA  CAGAAACAGA  GGGGTTAAAT  AGAATCAGAC  AGAACAGGAA
1101 AAATAGTAAT  ATACATGAGA  AAAATTATGG  AAGAGATAAT  CCTAATCATA
1151 TTAATGTTT  ATCTGGAAAT  TCTATACAAC  ATATACTGTA  TGGAGATGAA
1201 GCAGGAGGTG  GGCATCTTTT  TCCTGGCAAA  CCTGGTAAGA  CAACATTCCT
1251 CCAACATTGG  TCAGCCAGTA  AAATAACTCA  TGAAATTAGT  GATATCGTTA
1301 CATCCCCAAA  AACGCAATGG  TATGCACAGA  CTGGAACAGG  CGGCAATAT
1351 ATTGCTAAAG  GAAGACCAGC  TAGGTGGGTA  TCATATGAAA  CGAGAGATGG
1401 AATTCTGATC  AGAACAGTTT  ATGAACCTGC  AACAGGAAAA  GTGGTAACGT
1451 CATTCCCCGA  TAGAACCTCT  AATCCCAAAT  ATAACCCTGT  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1  VKPLRRLIKL  LAACAVAAAA  LIOPALAADL  AQDPFITDNA  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGQINV  IQDYTHRMGN  LLIQQANING  TIGYHTRFSG
101 HGYEEHAPFD  NHAADSASEE  KGNVDEGFTV  YRLNWEGHEH  HPADAYDGP
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIS  DNYSNLGSNF
201 SDRADEANRK  MFEHNAKLDR  WGNMSEFING  VAAGALNPF  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAVIG  GLGSVAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVNLTKAAP  PGKAAVSGDF  SAAYNTRTTR
351 KVTTETEGLN  RIRQNQNSN  IHEKNYGRDN  PNHINVLSGN  SIQHILYGDE
401 AGGGHLFPGK  PGKTTFPQHW  SASKITHEIS  DIVTSPKTQW  YAQTGTGGKY
451 IAKGRPARWV  SYETRDGIRI  RTVYEPATGK  VVTAFPDRTS  NPKYNPVK*

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a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRLRIKLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRLTNLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a730.pep	DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNSEFINGVAAGALNPFI					
m730	DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNSEFINGVAAGALNPFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a730.pep	QENPNAAETVEALVNLPFAKVKNLTKAAKPGKAAVSGDFSAAYNTRTTTRKVTTEGLN					
m730	QENPNAAETVEAVFNAAAQVAKLAKAAKPGKAAVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	
	370	380	390	400	410	420
a730.pep	RIRQNQKNSNIHEKNYGRDNPNIHINVLSGNSIQHILYGDEAGGGHLPFGKPGKTTTFQHW					
m730	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731.seq
1  gatttttcgag cgttttcatG CGAGAACGGT TTGTCTGTGC GCGTCCGCAA
51  TTTGGACGGC GGCAAAATCG CGTTGCGGCT GGACGGCAGG CGTGCCGTCC
101 TCTCTTCCGA CGTTGCCGCA TCCGGCGAAC GCTATACCGC CGAACACGGT
151 TTGTTCGGAA ACGGAACCGA GTGGCACCAG AAAGGCGGCG AAGCCTTTTT
201 CGGCTTTACC GATGCCTACG GCAATTCGGT CGAAACTTCC TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2476; ORF 731.ng>:

```

g731.pep
1  DFRAFSCENG LSVRVRLDG GKIALRLDGR RAVLSSDVAA SGERYTAEHG
51  LFGNGTEWHQ KGGEAFFGFT DAYGNSVETS CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731.seq
1  ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTGT CTTTGCGGCG
51  CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGCGGG CATATGCCGC
101 CCGTTCAAAA CCAAGCCGGC ACGGACGATT TTCGGGCGTT TTCCTGCGAG
151 AACGGTTTGT CTGTGCGCGT CCGCCATTG GACAGCGGCA AAGTCGCGTT
201 GCGGCTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG

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251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CACCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

m731.pep
 1 MNIRFFALT VLVSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE
 51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

g731/m731 95.2% identity in 84 aa overlap

				10	20	30
g731.pep				DFRAFSCE	NGLSVRVRNL	DGGKIALRLDGR
m731	LSLAACAV	PEAYDDGGRG	HMPPVQNQAG	DDFRAFSCE	NGLSVRVRHL	DSGKVALRLDGR
	20	30	40	50	60	70

		40	50	60	70	80
g731.pep	RAVLSSDV	AASGERYTAE	HGLFGNGTE	WHQKGGEAFFG	FTDAYGNSVET	TSCRARX
m731	RAVLSSDV	AASGERYTAE	HGLFGNATE	WHQKGGEAFFG	FTDAYGNSVET	TSCRARX
	80	90	100	110	120	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

a731.seq
 1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTGT CTTTGGCGGC
 51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGAGGG CATATGCCGC
 101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCGAG
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CATCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

a731.pep
 1 MNIRFFALT VLVSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE
 51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

a731/m731 94.4% identity in 126 aa overlap

		10	20	30	40	50	60
a731.pep	MNIRFFALT	VLVSLAACAV	PEAYDDGGRG	HMPPVQNQAG	TADFRAFSCE	NGLSVHVRRL	
m731	MNIRFFALT	VLVSLAACAV	PEAYDDGGRG	HMPPVQNQAG	DDFRAFSCE	NGLSVRVRHL	
	10	20	30	40	50	60	

		70	80	90	100	110	120
a731.pep	DGGRIALRLD	GRRAVLSSDV	AASGERYTAE	HGLFGNGTE	WHQKGGEAFFG	FTDAYGNSVE	
	: :						
m731	DSGKVALRLD	GRRAVLSSDV	AASGERYTAE	HGLFGNATE	WHQKGGEAFFG	FTDAYGNSVE	
	70	80	90	100	110	120	

a731.pep	TSCRARX
m731	TSCRARX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

g732.seq
 1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
 51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTTGCC GCCGagaagg
 101 ACGGgcgGGA TAACGAagtc CTGCCGTGTC AATCCATCCG TACGATGGCG

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151 GAGGTTTACG GTCAGATTAA GGCAAACTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
401 TGAAAAGCGG CGATTTCAAT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTCGGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GACTGAAAG
851 CCGTTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCCTGCCG AGTTGAAAAC GATTCCGATG ACGgtattGG TcaaTTCCGG
951 TTCggttCC GCGTCGGAGA TTGtcgCCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCTTT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTACGGC ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GCGGACCTG
1201 GTCGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAC
1251 CCTtgcCGTA CCGCTTGAAG AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGTT TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

g732 . pep

```

1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDGDRNEV LPVQSIRTMA
51  EVYGOIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAEVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGDGDM VLKAVPEDYV YGMGGDPLAG
301 IPAELKTIPT TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFKGKSVQT
351 LIPLNSGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKDK K*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

m732 . seq

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1  ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTCAAT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAAGCGT AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GACTGAAAG
851 CCATTCTCTA AGATTATGTG TACGGGATGG GCGGCGATTC GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTCGCAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCTTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CCGCACTGTA

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1187

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1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GGCGGATTTG
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAGTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732 . pep

```

1  MSKPVFVKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGQIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLAG
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLSNGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKDADKPA VKEKGKKKDK EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKDKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

	10	20	30	40	50	60
m732 . pep	MSKPVFVKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGQIKANY					
g732	MSKPVFVKIALYTLGAISGVAVSLAVQGFAAEKDGRDNEVLPVQSIRTMAEVYGQIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m732 . pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	:					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m732 . pep	VSPIEDTPAERAGVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLRKNADKP					
g732	VSPIEDTPAERAEVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m732 . pep	IVVNLTRAIKVKSVRHHLIEPDYGIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m732 . pep	LDLRDDPGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEDYVYGMGGDSLAG					
g732	LDLRDDPGLLTGAVGVSAFLPSEAVVSTKGRDGKDMVLKAVPEDYVYGMGGDPLAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m732 . pep	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
g732	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
g732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
g732	PLEKDADKPAAKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
m732.pep	PVS NKDKKDKKDKKX					
g732	PVS NKDKKDKKDKKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

```

a732.seq
1  ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTGTCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTTATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACCTGTCTCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGCTGGTGT TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAC CATAACGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTGCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTTCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GGC GGATTG
1201 GTCGGACACA TCGGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
1351 CCGCCAAAAG ACGACCAGTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

```

a732.pep
1  MSKPVFKKIA LYTLGAISGV AVSLAVQGF AAEKDRRDNEV LPVQSIRTMA
51  EVYGOIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAII KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAVPEDYV YGMGDSLAG
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFKGVSQQT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVS NKDKKDK KDKK*

```

1189

a732/m732 99.6% identity in 494 aa overlap

a732.pep	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGGQIKANY					
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGGQIKANY					
	10	20	30	40	50	60
a732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
a732.pep	130	140	150	160	170	180
	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
a732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLEIPDYGIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732	IVVNLTRAIKVKSVRHHLEIPDYGIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
a732.pep	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSA AFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAG					
m732	LDLRDDPGGLLTGAVGVSA AFLPSEAVVVSTKGRDGKDRMVLKAI PEDYVYGMGGDSLAG					
	250	260	270	280	290	300
a732.pep	310	320	330	340	350	360
	IPAELKTIPMTVLVNSGSASASEIVAGALQD HKRAVIVGTQSFGKGSVQT LIPLSNGSAV					
m732	IPAELKTIPMTVLVNSGSASASEIVAGALQD HKRAVIVGTQSFGKGSVQT LIPLSNGSAV					
	310	320	330	340	350	360
a732.pep	370	380	390	400	410	420
	KLTTALYYTPNDRS IQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
m732	KLTTALYYTPNDRS IQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
	370	380	390	400	410	420
a732.pep	430	440	450	460	470	480
	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
a732.pep	490					
	PVS NKDKKDKKDKKX					
m732	PVS NKDKKDKKDKKX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51  GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGGTT TGAAAAACGg cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCC CGGGTGC GCA CGCCATTG G GACTGCTGC

```

1190

```

251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
351 CGGTaaAGGA GGCAAGCGAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

```

1  MMNPCTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDDTS
51  LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

```

1  ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51  GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGACTGCTGC
251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
351 CGGTAAAGGA GGCAAGCGAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

```

1  MMNPKTL SRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
51  LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNPKTL	SRLSLCAAVLALT	ACGGNGQKSL	YYYGGYPDTV	YEGLKNDDT	SLGKQTEKMEK
g733	MMNPKTL	SLCAAVLALT	TACAGGGHKNL	YYYGGYPDTV	YEGLKNDDT	SLGKQTEKMEK
	10	20	30	40	50	60
m733.pep	YFVEAGNKKM	NAAPGAHAHL	GLLLSRSGDK	KEGAFRQFEE	EKRLFPESGVF	MDFLMKTGKG
g733	YFAEAANKKM	NAAPGAHAHL	GLLLSRSGDK	KEGAFRQFEE	EKRLFPESGVF	MDFLMKTGKG
	70	80	90	100	110	120
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

```

1  ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51  GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGACTGCTGC
251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
351 CGGTAAAGGA GGCAAGCGAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

1191

```

1  MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
51 LGKQTEKMEK YFVEAGNKMM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

a733/m733 100.0% identity in 123 aa overlap

```

              10      20      30      40      50      60
a733.pep      MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK
              |||||
m733          MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK
              10      20      30      40      50      60

              70      80      90      100     110     120
a733.pep      YFVEAGNKMMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
              |||||
m733          YFVEAGNKMMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
              70      80      90      100     110     120

a733.pep      GKRX
              |||
m733          GKRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

```

g734.seq
1  ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGGATGCAAA CGATGTTTTG CAGGTTAAAA CCACAAAAGA AGATTCGGCG
151 AAAAGCGAAG CGTTTGCCGA GTTGAAGCC TTTTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCTGT
251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATGCACGT CATCTCTTA TTACGCGGG
451 GCTGTTCGCT CCTTAATCCA ACACCTGAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

```

g734.pep
1  MMKKILAVSA LCLMTAAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
51  KSEAFAELEA FCKGQDTLAG IAEDPTGCR SVVSLNNTCV SLAYPKALGA
101 MRVENAVVIT SPRFTSVHGV ALNQCIKYG AQQQCGLETV YCTSSSYYG
151 AVRSLIQHLK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

```

m734.seq (partial)
1  TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCTGG TCGTGTCTGCT
51  GAACAATACC TGTGTCTGCGC TGGCATACCC GAAAGCCTTG GGCGCGCTGC
101 GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTAC GAGCGTTCAT
151 CAGGTCGCAC TCAACCAAGT CATCAAAAAA TACGGCGTAC AGGGACAATG
201 CGGCTTGGAA ACAGTGTATT GCACATCTTC TTCTTATTAC GGCGGAACTG
251 TCGCTCTTT GATTCAAAAT CTCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

```

m734.pep (partial)
1  SGIAEDEPTG CRSVSVLNNT CVALAYPKAL GALRVDNAVV ITSPRFTSVH
51  QVALNQCIKK YGVQGCGLT TVYCTSSSY GGTVRSLIQN LK*

```

m734/g734 92.4% identity in 92 aa overlap

```

              10      20      30
m734.pep      SGIAEDEPTGCRSVSVLNNTCVALAYPKAL
              :|||
g734          VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVSVLNNTCVSLAYPKAL

```

	40	50	60	70	80	90
m734.pep	GALRVDNAVVTSPRFTSVHQVALNQCIKKYGVQGQCGL	ETVYCTSSSYYG	GGTVRSLIQN			
g734	GAMRVENAVVTSPRFTSVHQVALNQCIKKYGAQGCGL	ETVYCTSSSYYG	GAVRSLIQH			
	100	110	120	130	140	150
m734.pep	LKX					
g734	LKX					
	160					

```
a734.seq
1  ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGACTGCGGC
51  GGCACGGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTTG CAGGTAAAAA CCACAAAAAG AGATTGCAGC
151 AAAAGCGAAG CGTTTGGCGA GTTGGAAGCT TTCTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAACACATG TATTGCACGT CTTCTTCTTA TTACGGGGGA
451 ACTGTGCGCT CATTGTATCA AAATCTCAA TAA
```

```
a734.pep
1  MMKKILAVSA LCLMTAAARA ADTYGYLAVW QNPQNANDVL QVKTTKEDST
51 KSEAFAELEA FCKGQDTLAG IAEDPTGCR SVVSLNNTCV ALAYPKALGA
101 TRVENAVVIT SPRFTSVYQV ALNQCIKKYG AQGCQGLETV YCTSSSYGG
151 TVRSLIONLK *
```

	10	20	30	40	50	60
a734.pep	MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA					
g734	MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVALAYPKALGAMRVENAVVITSPRFTSVYQV					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV					
	70	80	90	100	110	120
	130	140	150	160		
a734.pep	ALNQCIKKYGAQGQCGLETVYCTSSSYGGTVRSLIQNLKX					
g734	ALNQCIKKYGAQGQCGLETVYCTSSSYGGAVRSLIQHLKX					
	130	140	150	160		

m735.seq		S1		S2		S3	
1	ATGAATCTCG	TGAAACTGCT	GGCGAATAAC	TGGCAACCGA	TTGCCATTAT		
51	CGCGCTTGTC	GGCACGGGCT	TGGCTGTGTC	GCACCATCAA	GGCTACAAGT		
101	CGGCATTGTC	GAAGCAGCAG	CGGCTCATCG	ACAAGATGGA	GCGCGACAAG		
151	GCGCAAGCCC	TGCTGTTGTC	GGCTCAAAC	TATGCGCGCG	AACTGGAACT		
201	GGCACGCGCG	GAAGCTAAAA	AATATGAAGT	CAAGGCGCAG	GCTGTCGGGA		
251	TGGCTTTGGC	GAAAAAACAG	CGGGAAGTCA	GCCGCTGTAA	AACGGAAAAA		
301	AAAAAGGAAA	TCGAAAAATG	CCTTAETCAA	GACCGTAAAA	ATGCACGCGG		

351 CGGTTGCATT GACGGCTTTG GCTCTACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pcp

1	MNLVKLLANN	WQPIAIIALV	GTGLAVSHHQ	GYKSAFAKQQ	AVIDKMERDK
51	AQALLLSAQN	YARELELARA	EAKKYEVKAH	AVGMALAKKQ	AEVSRLKTEN
101	KKEIENVLTQ	DRKNASGGCI	DGFGSHGLQL	YNRALGYGN*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1	ATGAATCTCG	TGAAACTGCT	GGCGAATAAC	TGGCAACCGA	TTGCCATCAT
51	CGCGCTTGTC	GGCACGGGTT	TGGCGTGTC	GCACCATCAA	GGCTACAAGT
101	CGGCTTTTGC	GAAGCAGCAG	CGGGTCATTG	AGAAAAATGA	GCGCGACAAG
151	GCGCAAGCCC	TGCTGTTGTC	GGCTCAAAAC	TACGCCCGCG	AACCTGGAAC
201	GGCGCGTGCG	GAAGCTAAAA	AATATGAAGT	C AAGGCGCAC	GCGCTCGGCA
251	TGGCTTTTGGC	GAAAAAACAG	GCGGAAGTCA	GCCGTCTGAA	AACGGAAAAT
301	AAAAAGGAAA	TCGAAAATGT	CCTTACTCAA	GACCGTAAAA	ATGCAGGCGG
351	CGGTTGTATT	CAGGGCTTTG	GCCATCACGG	CTTGCACTC	TACAAGCGCG
401	CCCTCGGCTA	GCGAAATTAA			

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1	MNLVKLLANN	WQPIAIIALV	GTGLAVSHHQ	GYKSAFAKQQ	AVIEKMKRDK
51	AQALLLSAQN	YARELEQARA	EAKKYEVKAH	AVGMALAKKQ	AEVSRLKTEN
101	KKEIENVLTQ	DRKNAGGGCI	DGFGHHGLQL	YKRALGYGN*	

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
a735.pep	70	80	90	100	110	120
	YARELEQARAEAKKYEYVKAHAVGMALAKKQAEVSRDKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARAQAEAKKYEYVKAHAVGMALAKKQAEVSRDKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2503>:

g736.seq

1	ATGAATTTTA	TCCGTTCGT	CGGGGCGAAA	ACCCTCGGCC	TTATTCAATC
51	CTTCGGCAGT	ATCACGCTGT	TTCTGCTGAA	CATTTTGCGC	AAATCCGGCA
101	CGGCTTTTCG	CCGTCCGCGC	CTGAGCGTGC	GCCAAGTGTA	TTTTGCCGGC
151	GTGCTGTCGG	TGCTGATTGT	TGCCGTTTCG	GGGCTGTTCC	TCGGTATGGT
201	TTTGGGTTTG	CAGGCTATA	CGAGTTGTC	GAAAATCAAA	TCGCCCGATA
251	TTTTGGGCTA	TATGGTCGCG	GCTTCTCTGT	TGCGCGAACT	GGGTCCCGTG
301	TTGGCGGCGA	TTCTGTTTGC	CAGCAGCGCG	GGCGGTGCGA	TGACCAGCGA
351	AATCGGTTTG	ATGAAAACGA	CCGGACAGCT	CGAAGCGATG	AACGTGATGG
401	CGGTCAACCC	CGTCGCCCGC	GTGGATTGCC	CGCGTTTTTG	GGCGGGCGTG
451	TTTTCTATGC	CGCTTTTGCC	TTCGATTTTC	AACGTCGCGG	GCATTTTTCG
501	CGCGTATTTG	GTGGCGGTGA	GCTGGCTGGG	TTTGGACAGC	GGATTTTTCG
551	GGCCGCAGAT	GCAGAACAAC	ATTACGATAC	ATTACGATGT	AATCAACGGT

1194

```

601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep

```

1 MNFIRSVGAK TLGLIQSFGS ITLFLNLA KSGTAFARPR LSVRQVYFAG
51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMAVNPVAR VVAPRFWAGV
151 FSMPLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMNN ITIHYDVG
201 LIKSAAFGVA VTLLIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq

```

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTTCGGCAGT ATCACGCTGT TTCTGCTGAA CATTGTGGCG AAATCCGGCA
101 CGGCTTTCGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGCG
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCG TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCGCGAACT GGGTCCCCTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCG CGCGTTTTTG GGCGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT
601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep

```

1 MNFIRSVGAK TLGLIQSLGS ITLFLNLA KSGTAFVRPR LSVRQVYFAG
51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMAVNPVAR VVAPRFWAGV
151 FSMPLLASIF NVAGIFGAYL VGVTLWGLDS GIFWSQMNN ITIHYDVG
201 LIKSAAFGVA VTLLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNLA KSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
m736.pep	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
g736	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
	130	140	150	160	170	180
m736.pep	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
g736	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHYDVIINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVVS					
g736	GIFWPQMNNITIHYDVIINGLIKSAAFGVAVTLIAVHQGFHCIPPTSEGILRASTRVVS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

```

a736.seq
1  ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51  TCTCGGCAGT ATCACGCTGT TTCTGCTGAA TATTCTGGCG AAATCCGGTA
101 CGGCTTTTCGT CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCCG TGTGATTGT TGCCGTTTCA GGGCTGTTTG TCGGCATGGT
201 CTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCGCTGT TGCGCGAACT GGTCCGGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGCTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGAACAGCT CGAAGCGATG AACGTGATGG
401 CGGTAAACCC CGTCGCCCGA GTGGTTGCGC CGCGCTTTTG GCGGGCGTG
451 TTTTCCATGC CGCTTTTGGC TTCGATTTTC AACGTGGCGG GTATTTTCGG
501 CGCGTATTTG GTCGGTGTAA CCTGGCTGGG CTTGGACAGC GGTATTTTCT
551 GGTCGCAAAT GCAGAACAAAC ATCACGATAC ATTACGATGT AATCAACGGT
601 CTGATCAAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCGTCC CGACCTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCCTGCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

```

a736.pep
1  MNFIRSVGAK TLGLIQSLGS ITLFLNILA KSGTAFVRPR LSVRQVYFAG
51  VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMVNPVAR VVAPRFWAGV
151 FSPMLLASIF NVAGIFGAYL VGVTLWGLDS GIFWSQMNN ITIHYDVIING
201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPMLLASIFNVAGIFGAYLVGVTLWGLDS					
m736	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPMLLASIFNVAGIFGAYLVGVTLWGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHYDVIINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVVS					

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```

m736      GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
           190      200      210      220      230      240

           250      259
a736.pep  ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

g737.seq

```

1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51 CATTTCGCGC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCGCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

g737.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51 AQAEKAAWAR VGGKITDIDL EHDGGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

m737.seq..

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51 CATTTCGCGC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCGCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

m737.pep

```

1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

m737/g737

```

           10      20      30      40      50      60
m737.pep  MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRQAQAEKAALAR
           |||||:|||||:|||||:|||||:|||||:|||||
g737       MNIKHLLLTAAATALLGISAPALAHHDGHGDDDHGHAHQHGKQDKIISRQAQAEKAAWAR
           10      20      30      40      50      60

           70      80      90      100      109
m737.pep  VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           |||||:|||||:|||||:|||||:|||||:|||||
g737       VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

1197

a737.seq
 1 ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
 51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
 101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
 151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
 301 GTGATTTCTT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep
 1 MNFKRLLLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
 51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
 101 VISSRRDD*

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLTAAAT	ALMGISAPALAHHDGHG	DDDHGHAHQHSKQDKIISRA	QAEKAALAR		
m737	MNIKHLLLTSAAT	ALLSISAPALAHHDGHG	DDDHGHAHQHNKQDKIISRA	QAEKAALAR		
	10	20	30	40	50	60

	70	80	90	100	109
a737.pep	VGGKITDIDLEHDNGRPHYD	VEIVKNGQEYKVVVDARTGR	VISSRRDDX		
m737	VGGKITDIDLEHDNGRPHYD	VEIVKNGQEYKVVVDARTGR	VISSRRDDX		
	70	80	90	100	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq
 1 ATGTCGCGTG AAACGACCGT ATCCGGCGCG CGCCCCGCCG CCAAACCTGCC
 51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
 101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
 151 GCGGCCGCGC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
 201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
 251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC
 301 GACATCGCCT CTGGGTTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG
 351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCAtcgtt ACCCTGTTTG
 401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
 451 CAGTTTGCCG GCTGGGAAAA CACCCCCCTG CTTCAAAACA TCATCGTTCA
 501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
 551 ACTACCTCAT GTGGGGCATA CTCGCCTCCG CTAACCTCAA CGGACAACGA
 601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
 651 TTTAGGTTTG GTCAATTCTG GCACCATCTT GACCTACATA GCCGCCATCG
 701 CCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
 751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
 801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG
 851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACTTGCC GCGCCAAAGC
 901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
 951 CGGCTGGAAC AGTTTGTCCC AACAAACCTT CCTGATCAAT GCCGAACAGC
 1001 ACACCATACA CGACAACCTT CTCAGCACCT TGTTCAACCA TTCCCAAC
 1051 ATCATCTCTC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
 1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
 1151 CCCCCGCATC ACTTTTCCTG CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
 1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCCTTCGG
 1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
 1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTTCGA
 1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
 1401 CCCC GCCGCT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAAC
 1451 TGCGCTATAT TTCCGCAAAC AGCCCGATGC TGTCTTTTTA TGCCGACTTC
 1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
 1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCTAC TCCGCCACCT

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1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAAACA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

```

1  MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51  AAGLIVLLFL TAGKKLFDVK IPAISELLFA MAAFWWLQAR LMNLIYPGMN
101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KIPAAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFOFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAFO SAPIFGHWGN SFAQQTFLIN AEQHTIHDNF LSTLFTHSHN
351 IILQLLAEMG ISGTLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGI IAFKKAANLG ILTASAAIFA
451 GLLHLDWTYT RLVNSFSPA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEBA TLKALKYRPY SATYRIALYL MRQKVAEAK
551 QWMRATQSY YPYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

```

1  ATGCCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCG
51  GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
151 GCAGCCGGCC TGATTGTCCT GTTGTTCCCTC ACGGCAGGAA AAAAAGTGT
201 TGATGTCAAA ATCCCGCCA TCAGCTTCCT TCTGTTTGCA ATGGCGCGCT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCCTG
351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG CTGGGAAGA CACCCCTCTG TTTCAAAACA TCATCGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCTCATCCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAATC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CGGCTGGAAC AGTTTTGCC AACAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCACAAC
1051 ATCGTCCTCC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTTCGG
1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTCGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCCAGCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TCCGCAAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCgTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

```

1  MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

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1199

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51  AAGLIVLLFL TAGKKLFDVK IPAISFLLFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR
201 KIPAAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TILEFTTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNIYDNL LSNLFTHSHN
351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGI IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQKVAEAK
551 QWMRATQSYV PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/g738

m738.pep	10	20	30	40	50	60
	MPAETTIVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
g738	MSAETTIVSGARPAAKLPIYILPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
m738.pep	70	80	90	100	110	120
	TAGKKLFDVKIPAISFLLFAMAFAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
g738	TAGKKLFDVKIPAISFLLFAMAFAFWYLQARLMNLIYPGMNDIASWVIFILLAVSAWACKSL					
	70	80	90	100	110	120
m738.pep	130	140	150	160	170	180
	VAHFGQERIVTFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
g738	VAHYGQERIVTFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN					
	130	140	150	160	170	180
m738.pep	190	200	210	220	230	240
	NLGHYLMWGI LAAAYLNGQRKIPAAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
g738	NLGHYLMWGI LAAAYLNGQRKIPAAALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
m738.pep	250	260	270	280	290	300
	YFRSDKSNRRTMLGIAAAVFLTALFQFSMN TILEFTTGIRYETAVERVANGGFTDLPRQI					
g738	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNAILTETFTGIRYETAVERVANGGFTDLPRQS					
	250	260	270	280	290	300
m738.pep	310	320	330	340	350	360
	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHNIYDNL LSNLFTHSHNIVLQLLAEMG					
g738	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHTIHDNLFSTLFTSHSHNIIQLLAEMG					
	310	320	330	340	350	360
m738.pep	370	380	390	400	410	420
	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
g738	ISGTLVAATLLTGIAGLLKRSLTPASLFLCALAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
m738.pep	430	440	450	460	470	480
	FLSPAESDGI IAFKKAANLGILTASAAIFAGLLHLDWYTYRLVNAFSPATDDSAKTTLNRK					
g738	FLSPAESDGI IAFKKAANLGILTASAAIFAGLLHLDWYTYRLVNSFSPAADDDSAKTTLNRK					

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEELKSLKYRPHSATYRIALYL					
g738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEELKALKYRPHSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPET					
	550	560	570	580	590	600
m738.pep	KPCCKX					
g738	KPCCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

```

a738.seq
1  ATGCCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
151 GCAGCCGCCG TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACTC GCCGTCAGCG CGTGGGCGCTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATTGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTTCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGTACTTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GCGGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CCGCTGGAAC AGTTTTGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCAACCA TTCCCAACAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGAAGT GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GCGCGCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

```

a738.pep
1  MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALRLQP SPDFYHDAAD
51  AAGLIVLFLF TAGKKLFDVK IPPISFLLFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSQGV VIGHIGQRN NLGHYLMWGI LAAAYLNGQR

```

1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
 251 TILGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
 301 EWRKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNHNDNL LSNLFTSHHN
 351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
 401 SMLEYPLWYV YFLIPFGLML FLSPAESDG IAFKKAANLG ILTASAAIFA
 451 GLLHLDWYTY RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
 501 SLVNFALEPY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAEAK
 551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
 601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALRLQSPDFYHDAAGLIVLLFL					
m738	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
	70	80	90	100	110	120
a738.pep	TAGKKLFDVKIPPIISFLLFMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
m738	TAGKKLFDVKIPAIISFLLFMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a738.pep	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
m738	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a738.pep	NLGHYLMWGILAAAYLNGQRKIPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
m738	NLGHYLMWGILAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
	250	260	270	280	290	300
a738.pep	YFRSDKSNRRTILGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
m738	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a738.pep	EWRKALAAFQSAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTSHHNIVLQLLAEMG					
m738	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHNIDNLLSNLFTSHHNIVLQLLAEMG					
	310	320	330	340	350	360
	370	380	390	400	410	420
a738.pep	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
m738	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
	430	440	450	460	470	480
a738.pep	FLSPAESDGI AFKKAANLGILTASAAIFAGLLHLDWYTRMVNAFSPATDDSAKTLNRK					
m738	FLSPAESDGI AFKKAANLGILTASAAIFAGLLHLDWYTRLVNAFSPATDDSAKTLNRK					
	430	440	450	460	470	480
	490	500	510	520	530	540
a738.pep	INELRYISANSPMLSFYADFSLVNFALEPY PETQTWAEATLKSLKYRPHSATYRIALYL					
m738	INELRYISANSPMLSFYADFSLVNFALEPY PETQTWAEATLKSLKYRPHSATYRIALYL					
	490	500	510	520	530	540

1202

	550	560	570	580	590	600
a738.pep	MRQ GKVAEAKQWMRATQSYYPYLM	PRYADEIRKLPVWAPLLPELLKDCKAFAAA	PGHPEA			
m738	MRQ GKVAEAKQWMRATQSYYPYLM	PRYADEIRKLPVWAPLLPELLKDCKAFAAA	PGHPEA			
	550	560	570	580	590	600
a738.pep	KPCKX					
m738	KPCKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGG CCGAACGGCG ACAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAAC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTc AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGGCCAA ACCCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739.pep

```

1  MAKKPNKPER LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAQPD GTEESGSGLP
101 SPAAPKKNRV KPRPSDAARA ADSLTGTGTQ AENTLKETPV LPTNAPHPEP
151 RKETPEKQAO PKETPKKET PKENHTKPD PKNTPAKPHK EILDNLFF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGG CCGAACGGCG ACAAACCCT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAAC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAGA
501 AAACCATACC AAACCGGACA CCCCAGAAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739.pep

```

1  MAKKPNKPER LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQADTAQT DRQPDDAGTQ AENTLKETPV LPTNVPREPE
151 RKETPEKQAO PKETPKENHT KPDTPKNTTP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

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	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTE PQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSLPSPAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----NHTKPD					
g739	ADSLTGTGTQAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKETPKENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPKHEILDKLF					
g739	PKNTPAKPKHEILDNLFX					
	180	190				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1   ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCTT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTAA CTGCCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGCCTAA ACCCCATAAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1   MAKKPNKPFRLTPKLLIRAVLLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSLP
101 SPAAPKKNRV KPQPADTAQT DRQPDAGAQ AENTLKETPV LPTNVRPEP
151 RKETPEKQAQ PKETPKET PKENHTKPD PKNTPPKPKH EILDNLFX*

```

a739/m739 93.9% identity in 197 aa overlap

	10	20	30	40	50	60
a739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTE PQHTDSPRET					
m739	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a739.pep	EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT					
m739	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a739.pep	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKETPKENHTKPD					
m739	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD					
	130	140	150	160	170	

1204

```

                190
a739.pep      PKNTPPKPHKEILDNLFX
                |||||
m739          PKNTPPKPHKEILDKLF
                180      190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gcCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTGCGCTGCG AAGCGACGTT TTTGTTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATTt
201 GAAACgtcaa ACCATGTTTC TGTATTATCC GATTGTTTTG CTGGTTGTGT
251 ATTTGTTCCA CTATTTTCGGC GCGTTTTTag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPQHLLINGII LACEATFLFK
51 FVLFDTIKHH LKQGFDLKRQ TMLFPIPIVL LVVYLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCGTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCTCCAGC
101 ATCTGATCAA CGGCATCATC CTGCGCTGCG AAGCGACGTT TTTGTTTAAa
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATTt
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KLOHLLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIIL LIVYLFHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

                10      20      30      40      50      60
m740.pep      MSRNLLVRWLA VCLIPLATL AVFAANPPED KLOHLLINGII LACEATFLFK FVLFDTIKHH
                |||||
g740          MSRNLLVRWLA VCLIPLATL AVFAANPPED KPQHLLINGII LACEATFLFK FVLFDTIKHH
                10      20      30      40      50      60

                70      80      90
m740.pep      LKQEFDLKRQ TMLLFIPII LLIVYLFHYFG AFX
                |||
g740          LKQGFDLKRQ TMLFPIPIV LLVYLFHYFG AFX
                70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCCTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTGCGCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATTt
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPQHLLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIIL LIVYLFHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

                10      20      30      40      50      60

```

1205

```

a740.pep      MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPQHLINGIILACEATFLFKFVLFDTIKHH
|||||||:||||||| ||||||||| ||||||||| ||||||||| |||||||||
m740          MSRNLLVRWLVAVCLIPLATLAVFAANPPEDKLQHLINGIILACEATFLFKFVLFDTIKHH
              10      20      30      40      50      60

              70      80      90
a740.pep      LKQEFDLKRQTMLLFIPILLIVYLFHYFGAFX
|||||||:||||||| ||||||||| ||||||||| ||||||||| |||||||||
m740          LKQEFDLKRQTMLLFIPILLIVYLFHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1   GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTAGCCGCCG GCCCTGATTC
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTC GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTTGGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAAACCT ACCTATACCA TAGATTTCGC CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCCCTCCGC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1   VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNGTLTL SAQGAEKTFK AGGKDNSLNT GKLNNDKISR
101 FDFVQKIEVD GQTITLASGE FQYKQDHSA VVALRIEKIN NPKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 HLGKIEHLKT PEQNVELASA ELKADEKSHA VILGDRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGEKV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1   GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAGTTTGG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GCGGCGACAA GGTGCGGAAA AAACCTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTCCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GCGGACATAG CCGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGAAA CGGCAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1   VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHKDKGL
51  QSLTLDQSVR KNEKLKLAAQ GAEKTYGNGD SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSG KMVAKRQFRI

```

1206

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYYTID FAAKQGNNGKI
 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEKGS YSLGIFGGKA
 251 QEVAGSAEVK TVNGIRHIGL AAKQ*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCSLT---	ALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQ			
g741	VNRTTFCCSLTAGPDS	DRLQRRGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEA			
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLAAQGA	EKTY---GNGDSLNTGKLKNDKVS	RFDFIRQIEVDGQLITLES	GE	
g741	SIPQNGTLTLSAQGA	EKTFKAGGKDNSLNTGKLKNDKIS	RFDFVQKIEVDGQTITLAS	GE	
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHSALTAFQ	TEQIQDSEHSGKMKVAKRQFRIGD	IAGEHTSF	DKLPEGGRATYRGT	
g741	FQIYKQDHSAVVALR	IEKINNPKIDSLINQSRFLVSD	LGGEHTAFNQLPDG-KA	EYHKG	
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGGKLTYY	TIDFAAKQGNNGKIEHLKSP	ELNVDLAAADIKPDGKR	HAVISGSVLYN	
g741	AFSSDDADGKLTYY	TIDFAAKQGHGKIEHLKT	PEQNVELASAEKKADEK	SHAVILGDTRYG	
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYSLGIFG	GKAQEVAGSAEVKTVNGIR	HIGLA	AKQX	
g741	GEEKGTYRLALFG	DRAQEIAGSATVKIGEKV	HEIGI	ADKQX	
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq
 1 GTGAACCGAA CTGCCTTCTG CTGCCTTTCT TTGACCGCCG CCCTGATTCT
 51 GACCGCCTGC AGCAGCGGAG GCGGCGGTGT CGCCGCCGAC ATCGGCGCGG
 101 TGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAAGTTTG
 151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAACGAGA AACTGAAGCT
 201 GCGGCGACAA GGTGCGGAAA AAACCTATGG AACGCGGAC AGCCTCAATA
 251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GCTTCGACTT TATCCGTCAA
 301 ATCGAAGTGG ACGGCGAGCT CATTACCTTG GAGAGCGGAG AGTTCCAAGT
 351 GTACAAACAA AGCCATTCCG CCTTAACCGC CCTTCAGACC GAGCAAGTAC
 401 AAGATTCCGA GCATTACGGG AAGATGCTTG CGAAACGCCA GTTCAGAATC
 451 GCGGATATAG CGGGTGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
 501 CAGGGCGACA TATCGCGGGA CGGCATTCCG TTCAGACGAT GCCAGTGGAA
 551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGACA CGGCAAAATC
 601 GAACATTTGA AATCGCCAGA ACTCAATGTT GACCTGGCCG CCTCCGATAT
 651 CAAGCCGGAT AAAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
 701 ACCAAGCCGA GAAAGGCAGT TACTCTCTAG GCATCTTTGG CGGGCAAGCC
 751 CAGGAAGTTG CCGGCAGCGC AGAAGTGGAA ACCGCAAACG GCATACGCCA
 801 TATCGGTCTT GCCGCCAAGC AGTAA

This corresponds to the amino acid sequence <SEQ ID 2538; ORF 741.a>:

a741.pep
 1 VNRTAFCCLS LTAALILTAC SSGGGGVAAD IGAVLADALT APLDHKDKSL
 51 QSLTLDQSVR KNEKLKLAAQ GAEKTYGNGD SLNTGKLKND KVS RFDFIRQ
 101 IEVDGQLITL ESGEFQVYKQ SHSALTALQT EQVQDSEHSG KMKVAKRQFRI
 151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD ASGKLTYYTID FAAKQGHGKI
 201 EHLKSPELNV DLAAADIKPD KKRHAVISGS VLYNQAEKGS YSLGIFGGQA
 251 QEVAGSAEVE TANGIRHIGL AAKQ*

a741/m741 95.6% identity in 274 aa overlap

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	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQAEKTYGNGDSLNTGKLNKDKVSRFDIFIRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLKLAQAQAEKTYGNGDSLNTGKLNKDKVSRFDIFIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSD					
m741	SHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYTIDFAAKQGHGKIEHLKSPELNVDLAASDIKPDKKRHAIVISGSVLYNQAEKGS					
m741	AGGKLTYTIDFAAKQNGKIEHLKSPELNVDLAAADIKPDKKRHAIVISGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAAKQX					
m741	YSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAAKQX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

```

m742.seq
1   ATGGTTTACG GCATTGCCGA AGCCGATGCG GCGCAGACGCA GTGTGCTTAC
51  TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
101 TTATTTTGCC CTGTGAAAAT CAGAAAAC TG CCCCCTTCAG TTCAACGCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTAAGTGCCG ACAAATACAA CCTTTTCTCA GGATTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAATATGC
351 GGC GGGTTT TCGGGTGAGG ATGCGGTAGG CTTTTTGACT GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGATG AAACCGCCAA GGAATACCGG GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTTCA ACAGTATCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACAAGT GTATGAGTGA CCCTTTCGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGCG TTGATGCCGA
651 CAAGGCGGAA TTTGTGCGTA AAGCCCTTGC GAAGGAGGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTTCGGCG GGAGCATGAT TTCTTTGTCT GCTATGCCTA CGGTGATGAA
901 AAGATACGTT CGGAATATCT AGAAATCTAC GAACGCCGCT ACAGAGTACG
951 TCCGAATACG GGGGCAACGC ACGGCGTGTA TGCGGGAAGT TGTGAGGAGG
1001 AGCCGGACGG CGATTTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAC GCCAAGAAAA TAAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACACCGGTA
1201 TATGTCGATG TATATGAGCT GGACGAAAAA GGCAACAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCCTG CCTTTACCGG TTTTTCGGT ACGGTGCCGG
1301 TTTGAAAAAC CGTCAAAGTG GCAGACGACC ATGTTCTTGC GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAACC CATTGCTGTA CTGCCAGCAC
1401 GCGTTTCAAC GTAACGGGCC GACTGCACCT TTTGGGCGGG CTGCACTACA

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1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCCGC ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTGCTCG ATTTCCGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTCCA GTGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCCGTGCA CATATTCGGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

```

m742.pep
  1 MUYGIAEADA GDSSVLTGG MYQKSREVPD FSGIILPCEN QKTAPFSSTP
 51 ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNDGW QLNAEVSYTK
101 NESDAKVGQF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAERKAG FDKCMSDPFA
201 LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAAQRF NSLYDSSFNR
251 KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FFGYAYGDE
301 KIRSEYLEIY ERRYRVRPNT GATHGVYAGS CQEEP DGDLS SPLVRGHKEP
351 DWQAYDEKGN RTVYAEERN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWTKVKV ADDHVPALYN
451 YAKYLNNTKT HSLTASTRFN VTGRHLHLLG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVVS RGAEFELSGE LNEWDKVFAG
651 YTYNKSRYKN AAEVNAERLA KNSSADPYNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

```

a742.seq
  1 ATGGTTTACG GCATTGCCGA AGCCGATGCG GCGACAGCA GTGTGCTTAC
 51 TTTGGGCGCG ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
101 TTATTTTGTC CTGTGAAAAT CAGAAACTG CCCGTTTCTG TCAACGCCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCCGCG TTGAGTGCTG ACAAATACAA CCTTTTCTCA GGTTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAACATGC
351 GCGGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTCGA GCAGTACCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACGAGT GTATGAGTGC CCCTTTTGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGTG TTGATGCCGA
651 CAAGTCGGAA TTTGTGCGATA AAGCCCTTGC GAAGGAAGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTCCGGCG GGAGCATGAT TTCTTTGTCT GCTATGCCTA CGCGCATGAA
901 AAGATACGTT CCGAATATCT GGAAATCTAC GAACGCCGCC ACAGAGTACG
951 TCCGAATACA GGGGCAACGC ACGGCGTGTA TGCGGGAAGT TGTCAGGGGG
1001 AGCCGGACGG TGATTTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAT GCCAAGAAAA TAAAAACCGA GCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACGCCAGTA

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```
a742.pep
1  MVGIAEADA GDSSVLTLGG MYQKSREVPD FSGIILSCEN QKTAPFSSPT
51  ACNRPQLQPR NTLYGEDHWR LSADKYNLFS GFKHVFDNGW QLNAEVSYTK
101 NESDAKVGQF NTKLNEHWAAGL SDEDAVGFELT EKNEVIPFEP KDKALEKLLKA
151 YRDETAKEYR ERKDDFVKNR FDNATAFEQYR SRRAAERKAG FDECM SAPFA
201 LDFICQGSWG DPGVDADKSE FVDKALAKEG IFNNAQREHF NSLYDSSFN
251 KATNRRYSY MPLRHTKD DR QWGIKLDLTG TYGLFGREHD FVVGAYGDE
301 KIRSEYLEY ERRHRVRPNT GATHGVYAGS CQGE PDGDL SFLVRGHKEP
351 DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQTNP D GTPAFTGFSG TVFVWKT VKV ADDHV PALYN
451 YAKYLNNTKT HSLTAGTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYQG
501 PASDFQNTAS IKADQDHYTA KMQGHKLTPQ AGITYDLTPQ QSIYGSYTKI
551 FKQDNDVDVS AKTVLPPLVG TNYEVGWKGA FLQGRLNASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGVVS RGAEFELSGE L NEDWKV FAG
651 YTYNKSRYKN AAEVNAERLA KNTGADPYNF SNFTPVHIFR FGTSFHI PNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYGNNYNN IRTGANNFYG EPRTVSMKLD WOF*
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	10	20	30	40	50	60
a742.pep	MVYGIAEADAGDSSVLT	LGGMYQKSREVP	DFSGIILSCENQKT	APFSSTPACNRPL	QLQPR	
m742	MVYGIAEADAGDSSVLT	LGGMYQKSREVP	DFSGIILPCENQKT	APFSSTPACNRPL	QLQPR	
	10	20	30	40	50	60
	70	80	90	100	110	120
a742.pep	NTYLGEDWSRLSADKYN	LFSGFKHVF	DNGWQLNAEVSYTKNES	DAKVGVQFFLKNEHAAGL		
m742	NTYLGEDWSRLSADKYN	LFSGFKHVF	DNGWQLNAEVSYTKNES	DAKVGVQFFLKNEYAAGL		
	70	80	90	100	110	120
	130	140	150	160	170	180
a742.pep	SDEDAVGFLTEKNEVIP	FEPKDKALEKLKAYRDE	TAKEYRERKDDFVKNR	FDNTAFEQYR		
m742	SGEDAVGFLTEKNEVIP	FEPKDKALEKLKAYRDE	TAKEYRERKDDFVKNR	FDNTAFEQYR		
	130	140	150	160	170	180
	190	200	210	220	230	240
a742.pep	SRRAAERKAGFDECM	SAPFALDFICOGSWG	DPGVADKSEFVDKAL	AKEGIFNNA	AORF	

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|||||:|||||:|||||
m742  SRRAAERKAGFDKCMSDPFALDFICQSSWGDPGVDADKAEFVDKALAKEGIFNNAQRFP
      190      200      210      220      230      240
      250      260      270      280      290      300
a742.ppe NSLYDSSFNRKATANRRYSYMLRHTKDDRWGIKLDLTGTYGLFGREHDFVGYAYGDE
      |||||
m742  NSLYDSSFNRKATANRRYSYMLRHTKDDRWGIKLDLTGTYGLFGREHDFVGYAYGDE
      250      260      270      280      290      300
      310      320      330      340      350      360
a742.ppe KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGEFPGDLSSPLVRGHKEPDWQAYDEKGN
      |||||:|||||
m742  KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGEFPGDLSSPLVRGHKEPDWQAYDEKGN
      310      320      330      340      350      360
      370      380      390      400      410      420
a742.ppe RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQTNP
      |||||
m742  RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQTNP
      370      380      390      400      410      420
      430      440      450      460      470      480
a742.ppe GTPAFTGFSGTVPVWKTVKVADHVPALYNYAKYLNKTHSLTAGTRFNVTGRLHLLGG
      |||||:|||||
m742  GTPAFTGFSGTVPVWKTVKVADHVPALYNYAKYLNKTHSLTAGTRFNVTGRLHLLGG
      430      440      450      460      470      480
      490      500      510      520      530      540
a742.ppe LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQ
      |||||:|||||
m742  LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTPYAGITYDLTPQ
      490      500      510      520      530      540
      550      560      570      580      590      600
a742.ppe QSIYGSYTKIFKQQDNVDVSAKTVLPLVGTNYEVGWKGAFQLQGRNLNASFALFYLEQKNR
      |||||
m742  QSIYGSYTKIFKQQDNVDVSAKTVLPLVGTNYEVGWKGAFQLQGRNLNASFALFYLEQKNR
      550      560      570      580      590      600
      610      620      630      640      650      660
a742.ppe TVVDFGYVPGAGGKQGSFQTVAKPIGVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKN
      |||||
m742  TVVDFGYVPGAGGKQGSFQTVAKPIGVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKN
      610      620      630      640      650      660
      670      680      690      700      710      720
a742.ppe AAEVNAERLAKNTGADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
      |||||:|||||
m742  AAEVNAERLAKNSSADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
      670      680      690      700      710      720
      730      740      750      760      770      780
a742.ppe RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
      |||||
m742  RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
      730      740      750      760      770      780
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a742.ppe WQFX
      |||
m742  WQFX
```

a742/ p25184
sp|P25184|PUPA_PSEPU FERRIC-PSEUDOBACTIN 358 RECEPTOR PRECURSOR
>gi|94923|pir||S15169

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ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi145723 (X56605)
 pseudobactin uptake protein [*Pseudomonas putida*]Length = 819
 Score = 152 bits (381), Expect = 6e-36
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADHDV-PALYNYAKYLNTNKTHSLTAGTRFNVVTGRLHLLGGLHYTRYETSQTKDM 494
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y
 Sbjct: 511 QTPKPGDDEIIPGI----QYNISNRQSGYFVASRFNLTDDLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQFASDFQTASSIKADQDHYTAKMQGHKLTPTYAGITYDLTPQQSIYGSYTKIFKQQ 554
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q
 Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRLNASFALFYLEQKNRTVVDFGYVPGAGGK 614
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG
 Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGEFLEGRNLNANIALYMVKRDNLAESTNEVVPDSGGL 668

Query: 615 QGSFQTVAKPIGKVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674
 S + + +G + ELSGE+ W VF GY++ ++
 Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPGWNVFTGYSHRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFREGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +
 Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGEWKLTLLGGGVNWNKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
 RY + + +L N+ + Y Y G+ YG PR ++ L + F
 Sbjct: 768 TSLMARYRINESLAATLNVNNIFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAAATT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
 151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTTCAG GCTTGCAGAC
 351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
 401 TGACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
 451 TCTCCGAGTA CCGATTGGC GGTATTGAC CATATTGAAG TTGTACGGGG
 501 TGCAACGGGG TTGACCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
 551 TGATCCGTAA GTGA

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep
 1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPQS VSVITRSRLD DKAHVHLEEA
 101 MKNTTGTVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
 151 SPSTD LAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAAATT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTCTG
 151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTTCAG GCTTGCAGAC

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351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTTTATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

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This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
  1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPOS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

	10	20	30	40	50	60
a743.pep	MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT					
m743	MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a743.pep	IDRMSTATGMRIAGKDTPOSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL					
m743	IDRMSTATGMRIAGKDTPOSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a743.pep	SRGFYIDQIGEDGITVNVAGRSYGTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG					
m743	SRGFYIDQIGEDGMTVNVAGRSYGTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG					
	130	140	150	160	170	180
a743.pep	TVNLIRKR					
m743	TVNLIRKX					

g744.seq not found yet
g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```

m744.seq
  1 ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
 51 CAGAAAGAAGA GAAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
101 AATATTTGGA TGAATTATGT GAACCAAATA TTTCTGTTTT AATCGGAGAA
151 AAGGGAACGT GAAAGACAGC ATATGCTGTT TATTAACTA ATAACCTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACGTGTTT AGATTTTACA
301 AGTATTTGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAAGCCTTAG
401 ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTGTATCC GGAATTTGTA
451 CAAGCAATAA CTTTAATAGA AAATCAAAA GAAGTCGCGG AAATGATTTT
501 TGGAAAATTT GTTAACTAG GTGAAGAGGA ATCCCAACAA ATAACTTTTA
551 CAGAAAGTAA ATTCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATTGA
651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTAAATAA TGATATCTTC
751 CTTTCCATTA AAGATAGTAA GGAAGGATG AGAGTTGTGT TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAAT ACCAACTTTC
851 AAGATAATTC AGTATTTTAA GACTGGAGGA CCGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGTAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTTCCAT
1001 GGAATGCTCC TAATTACAT GATGAGTATA AAAATTTAAC TTCATTATT
1051 AGCTTCCTAA GAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTACTT
1201 GGTGAAATCA AAGATCATCT TTTGTTTTAT TATAGTCAAA GTGATTATCA
1251 AAATTCCTCG AAATTTTTTG AATTTTAAA CGGGAAAGAT AGATTAAAT

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1213

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1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTTA AAGATAGAAA TTATGCAAAT
1501 ATTTCTCCTA AAATAAAAC TGAAACTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGAACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

m744.pep

```

1 MKPLKLTLEFG FVDAANYRRR ENKDLFNRIE VKGEYLDELG EPNISFLIGE
51 KGTGKTAYAV YLTNNFYKNI HATTKEVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIFNKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEEESQQ ITFTESKFQA NLGFIERKFK
201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQNQN TKLQDNSVFL DWRTDYKSYR
301 SSKIFGVFDH LLRTQQEKQD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKSKSDED VVAEDFDNTS FQREYSIYLL
401 GEIKDHLLFY YSQSDYQNFH KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKEMS TANEFLQFLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTFFKNK Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

m745.seq

```

1 ATGTTTTGGC AACTGACCGT TGTTCAGTA ACCGCCGTCA TTGCACTGGG
51 GACAATATTC ATCAATAAGA AACTTCAAA GCAAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAA TGTAGTAAGC CGACAATCAT
151 ATTTGCGCCT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TGCCTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTGT TTTAAACGGC TGCATGCGAC
351 CAACTTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGTTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTGTG GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

m745.pep

```

1 MFVQLTVVSV TAVIALGTIF INKKTSKQKA TLDVILNDYQ DAQFVEADNH
51 ISPYIRGTAV DDNNARIDLY EIQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPV MKIREERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

g746.seq

```

1 ATGTCCGAAA ACAAAACAAA CGAAGTCCTG ACCGTTACG AACAGCTGAA
51 ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTGC CGACAGCAAT
151 CCCGACCCGC AGGCCGCGCA AACCGGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCACAA ACCCTGCCT TGAAATCCGC CGCCGAAAC GGGGAAACCG
251 CCGCGACAAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAACACGTA GCGCGCCGC TGGTGCTGAT
351 TAACGACCCG CTCGAAGACA GCAACATCAA AGGTTTGAA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCGAAGCA GGCAAAACAA
451 CGCGCTGCCG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTGAAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAAC TGCTGCCGAA AAAACCAAAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

```

q746.pap

1	MSENKQNEVL	TGYEQLKRRN	RRRLVTASSI	VAASCILLAA	ALSSDPADSN
51	PAPQAGETGA	TESQTANTAQ	TPALKSAAEN	GETAADKPQD	LAGEDKPSAA
101	DSEISEPENV	GAPLVLINDR	LEDLSNIAEK	ESEKLQQAET	AKTEPKQAKQ
151	RAAEKVSATA	DSTDTVAVEK	PKRTAEPKPK	KAERTAEPK	KAKETKTAEK
201	VADKPKTAAE	KTKPDTAKSD	SAVKEAKKD	KAEGKKTAEK	DRSDGKKHET
251	AQKTDKADK	KTAEKEKSGK	AGKKAIIQAG	YAEKARALSI	QRKMKAAGID
301	STITEIMTDN	GKVVYRVKSSN	YKNARDAERD	LNKLRVHGIA	GOVTNE*

m746.seq

1	ATGTCGCAAA	ACAAACAAAA	CGAAGTCCTG	AGCGGTTACG	AACAACCTCAA
51	ACGGCGCAAC	CGCGCGCGCC	TCGTAACGGC	AAGTTGCCTG	GTTGCCGCTT
101	CCTGCTCCTT	GCTGGCAGCC	GCCCTCAGTT	CCGGCCCTGC	CGGAACAGACT
151	CCCGCGCAAA	CAAGCGCGCT	AGAAAAAANA	CGCGCAGGTG	CGGCACAACAC
201	CCCTGCTCTT	AAATCGCGCG	CCGACAAACC	GCAGGACTTG	GCAGGCGAAG
251	ACAAGCCCTT	TGCCGCGCCG	AGCGAAATCA	CGCAGCTTGA	AAACGTAGGC
301	CGCGCGCTGG	TGCTGATTAA	CAGCGCCTC	GAGACAGCA	CAATCAAAGC
351	TTTGGAAGCA	TCCGAGAAAC	TGCAACAGGC	AGAAACCGCC	AAAACCGCAC
401	CGAAGCAGGC	AAACAACCG	TGTCGCCAAA	AAGTGCCCGC	AAC TGCCGAC
451	AGTACGGATA	CGGTAGCGGT	GTA AAAACCG	AAACGCACTG	CCGAAACAAA
501	ACC GCAAAA	GCGGAACGCA	CTGCCAAAGC	CAAGCCCAAG	GCCAAAGAAA
551	CCAAAACCGC	CGAAAAGATT	GCCGCAAAAC	CGAAAAC TGC	CGCCGAAAAA
601	ACCAAACCGC	ATACGGCAAT	ATCCGACAGC	CGGTTAAAG	AGGCGAAAAA
651	AGCCGACAAG	GCTGAAAGCA	AAAAAACAGC	CGAAAAAGAC	TGCTCGGACG
701	GCAAAAAGCA	CGAAACCGCA	CAAAAAACCG	ACAAAGCGGA	CAAGACCCAA
751	ACCGCCGAGA	AGGAAAAATC	CGGTAAAAAA	GCCGCCATTG	AGGCAGGTTA
801	TGCCGAAAAA	GAACCGCGCT	TAAGCTTCCA	CGCCAAAATG	AAGGCCGCGG
851	GTATCGATT	GACCATACC	GAAATTATGA	CCGACAACGG	CAAAGTTTAC
901	CGCGTCAATT	CAAGCAACTA	TAAAAACGCA	AGGGATGCGC	AACCGGATTT
951	GACCAAAATT	CGCGTACAGC	GTATCGCCGG	TCAGGTAACG	AATGATAATG

m746.pgp

1	MSENKQNEVL	SGYEQLKRRN	RRRLVTASCL	VAASCILLAA	ALSSGPAEQT
51	AGETSGVNER	AAGAAQTPAL	KSADAPQODL	AGEDKPSAAD	SEISEPENVG
101	APLVLINERL	EDSNKIGLEA	SEKLQQAETA	KTAPKQAKOR	AAEKVPATAD
151	STDTVAVEKP	KRTAETKPQK	AERTAKAKPK	AKETKTAKEV	ADPKPTAAEK
201	TKPDTAKSDS	AVKEAKKADK	AESKKTAEKD	RSDGKKHETA	QKTDKADKTK
251	TAEEKSGGKK	AAIQAGYAEK	ERALSLOQRM	KAAGIDSTIT	EIMTDNGKVY
301	RVKSSNYKNA	RDAERDLNKL	RVHGIAGOVF	NE*	

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

m746/g746 89.9% identity in 346 aa overlap

```

      10      20      30      40      50
m746.pep  MSENKQNEVLSTGYEQLKRRNRRLVTASCLVAASCILLAAALSSGPAEQT----AGETSG
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g746      MSENKQNEVLSTGYEQLKRRNRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGA
          10      20      30      40      50      60

      60      70      80      90      100      109
m746.pep  VENKAAGAAQTPALKSAA-----DKPQDLAGEDKPSAADSEISEPENVGAPLVLINER
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g746      TESQTANTAQTPALKSAAENGETAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDR
          70      80      90      100      110      120

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1215

[illegible]

a746.seq

1	ATGTCCGAAA	ACAAACAAAA	CGAAGTCCTG	AGCGGTTACG	AACAACTCAA
51	ACGGCGCAAC	CGCGCGCCGC	TCGTAACGGC	AAGTTGCCTG	GTTGCCGCCT
101	CCTGCATCCT	GCTGGCAGCC	CGCCTCAGTT	CGGGCCCTGC	CGAACAGACT
151	CGCGCGGAAA	CAAGCGCGGT	AGAAAACAAA	CGGGCAGGTG	CGGCACAAAC
201	CCCTGCCTTT	AAATTCGCGC	CCGACAAACC	GCAGGACTTG	GCAGGCGAAG
251	ACAAAGCCTT	TGCCCGCCAG	AGCGCAATCA	CGGAGCCTCA	AAACGCTAGG
301	CGCGCGCTGG	TGCTGATTTA	AGCCAGCCCT	GAGACAGCA	ACATCAAAAG
351	TTTGGAAGCA	TCCGAGAAAC	TGCAACAGGC	AGAAACCGCC	AAAACCGCAC
401	CGAAGCAGGC	AAAAACAACG	CTGCGCGAAA	AAGTGCCGGC	AAGTCCGCGC
451	AGTAGCGATA	CGGTAGCGGT	TGAAAAACCG	AAACGCAGTC	CGGAAACAAA
501	ACCGCAAAAA	GCGGAACGCA	CTGCCAAAGC	CAAGCCCAA	GCCAAAGAAA
551	CCAAAACCGC	CGAAAAAGTT	GCCGACAAAC	CGAAATCTGC	CGCGGAAAAA
601	ACCAAAACCG	ATACGGGAAA	ATCCGACAGC	CGGGTAAAG	AGGCAAAAAA
651	AGCGGACAAG	GCTGAAAGCA	AAAAAACAGC	CGAAAAAGAC	CGTTCGGACG
701	GCAAAAAACA	CGAAACGGCA	CAAAAAACCG	ACAAAGCGGA	CAAGACCAA
751	ACCGCCGAGA	AGGAAAAATC	CGGTAAAAA	GCCGCATTC	AGGCAGTTA
801	TGCCGAAAAA	GAACGCGCCT	TAGGCTTCCA	GGCAGAAATG	AAAGCGGCGG
851	GTATCGAATT	CAGCATCACC	GAAATTATGA	CCGACACGCG	CAAAGTTTAC
901	CGCGTCAATC	GAACCAACTA	TAAAAACGCA	AGGGATGCCG	AACCGCTATT
951	GACAAAAATT	CGCGTACACG	TATTCGCGCG	TCAGGTAACG	AATGAATTA

a746.pap

1	MSENKQNEVL	SGYEQLKRRN	RRRLVTASCL	VAASCILLAA	ALSSGPAEQT
51	AGETSGVENC	AAGAAQTPAL	KSAADKPDQL	AGEDKPSAAD	SEISEPENVG
101	APLVLINDRL	EDSNIKGLEA	SEKLQQAETA	KTAPKQAKOR	AAEKVPATAD
151	STDTVAVEKP	KRTAETKPKQ	AERTAAKAPK	AKETKTAEVK	ADPKPTAAEK
201	TKPDTAKSDS	AVKEAKKADK	AESKLTAKEM	RSDGKKHETA	QKTDKADTKK
251	TAEKEKSGKA	AAIQAGYAEK	ERALSQRMKD	KAAGIDSTIT	EIMTDNGKVV
301	RVKSSNYGNN	RDAERDLNKL	RVHGATQGVN	NE*	

Homology with a predicted ORF from *N. meningitidis*

a746/m746: 99.7% identity in 332 aa overlap

	10	20	30	40	50	60
a746.pep	MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK					
m746	MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK					
	10	20	30	40	50	60

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	70	80	90	100	110	120
a746.pep	AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA					
m746	AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a746.pep	SEKLOQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQKAERTAKAKPK					
m746	SEKLOQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQKAERTAKAKPK					
	130	140	150	160	170	180
	190	200	210	220	230	240
a746.pep	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
m746	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
	190	200	210	220	230	240
	250	260	270	280	290	300
a746.pep	OKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY					
m746	OKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY					
	250	260	270	280	290	300
	310	320	330			
a746.pep	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
m746	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
	310	320	330			

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

m747.seq

1	CTGACCCCTT	GGGCGGATGC	ATATGCAGAT	TTGCGCGGCA	AAACCAAAGT
51	GATGACGACC	CAGATGGGTG	CTTCCCGCGA	TGTCAGCAAA	AGCGCCAAAG
101	GTTGGAGTGT	CGGTATCGGT	CTGAATGTAG	GCAAACAGTT	GACCGACAGC
151	GTCGGTCTCG	AGTTTGATCC	ATACTACCGT	CACAAAACAA	TCTACAAACC
201	CCGTGAGATT	GTCTTGGACG	GTGACAAAAC	CAAAATGGGC	CGCTCCAAAT
251	CCAACGAGTA	CGGCTTCCGC	GTAGCCGCAA	CGTTCTATAG	TCAATTAAAA
301	TCAAAATAG				

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>:

m747.pep

1	LTPWADAYAD	LRGKTKVMTT	QMGASRDVSK	SAKGWSVGIG	LNVGKQLTDS
51	VGLEFDPYYR	HKTIYKPREI	VLDGDKTKMG	RSKSNEYGFR	VAATFYSQLK
101	SK*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

a747.seq

1	CTAACCCCTT	GGGCGGATGC	ATATGCAGAT	TTGCGCGGCA	AAACCAAAGT
51	GATGACGACC	CAGATGTGTG	CTTCCCGCGA	TGTCAGCAAA	AGCGCCAAAG
101	GTTGGAGTGT	CGGTATCGGT	CTGAATGTAG	GCAAACAGTT	GACCGACAGC
151	GTCGGTCTCG	AGTTTGATCC	ATACTACCGT	CACAAAACAA	TCTGCAAACC
201	CCGTGAGATT	GTTTGGACG	GCGACAAAAC	CAAAATGGGC	CGCTCCAAAT
251	CCAACGAGTA	CGGCTTCCGC	GTAACCGCAA	CGTTCTATAG	TCAATTAAAA
301	TCAAAGTAG				

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>:

a747.pep

1	LTPWADAYAD	LRGKTKVMTT	QMCASRDVSK	SAKGWSVGIG	LNVGKQLTDS
51	VGLEFDPYYR	HKTICKPREI	VLDGDKTKMG	RSKSNEYGFR	VTATFYSQLK
101	SK*				

Computer analysis of this amino acid sequence gave the following results:

1217

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

	10	20	30	40	50	60
a747.pep	LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGSVIGLNVGKQLTDSVGLFDPYYR					
m747	LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKGSVIGLNVGKQLTDSVGLFDPYYR					
	10	20	30	40	50	60

	70	80	90	100
a747.pep	HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX			
m747	HKTIYKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX			
	70	80	90	100

a747/m80195

gi|150271 (M80195) outer membrane protein [*Neisseria meningitidis*] Length = 272
 Score = 59.3 bits (141), Expect = 6e-09
 Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGSVIGLNVGKQLTDSVGLFDPYYR 60
 + PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+
 Sbjct: 174 INPWSEVKFDLNSRYKLNTGVTNLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95
 +T + E + GD + ++ EYG RV F
 Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

1	ATGAGTCAAA	ACCAACCCGC	ACAACCGACC	AAACGCAATC	TGTTCAAAAC
51	CGCCCTTGCC	GTCGGCGCAA	TCGGCGCAAT	CGGAGGTAT	TTCGGCGGCA
101	AAAAACAGGG	CGAAACCGCC	GAACGCACCG	CCGAAAGCCA	ACACTCGCCC
151	CAAGCCTATC	CCTGCTACGG	CGAACATCAG	GCAGGTATCG	TTACGCCGCG
201	GCAGGCGTTT	TCCATTATGT	GCGCCTTCGA	CGTAACCGCG	CAAAGTGCCA
251	AGCAGCTGGA	AAACCTGTTC	CGCACACTGA	CCGCCCGCAT	CGAGTTTCTC
301	ACCCAAGGCG	GAGAATACCA	AGACGGCGAC	GACAAACTCC	CGTCAGCCGG
351	CAGCGGCATT	TTGGGTAAAG	CCTTCAACCC	CGACGGATTG	ACCGTTACCG
401	TGGGGGTGGG	CAGCAGCCTG	TTTGACGGCC	GGTTCGGACT	CAAAGACAAA
451	AAAACGGTTC	ATTTGCAGGA	AATGCGCGAC	TTCCCAACG	ATAAGCTGCA
501	AAAAGCTGG	TGCGACGGCG	ATTTGAGCCT	GCAAATCTGC	GCCTTCACCC
551	CCGAACCTG	CCAAACCGCC	CTGCGCGACA	TCATCAAACA	CACCGCCCAA
601	ACCGCCGTCA	TCCGCTGGAG	TATCGACGGG	TGGCAGCCTA	AATCCGAACC
651	CGGCGCGATG	GCGGCGCGCA	ACCTGTTGGG	CTTCCGAGAC	GGCACGGGCA
701	ACCCAAGGT	TTCCGATCCC	AAAACCGCCG	ACGAGGTTTT	ATGGACGGGC
751	GTGGCCGCCA	ACAGCCTCGA	CGAACCGGAG	TGGGCGAAAA	ACGGCAGCTA
801	TCAGGCAGTC	CGCCTTATCC	GCCGCTTTGT	CGAGTTTGG	GACAGGACGC
851	CGCTTCAAGA	GCAAACCGAC	ATTTTCGGGC	GGCGAAAATA	CAGCGGGGCG
901	CCGATGGACG	GCAAAAAAGA	AGCCGACCAA	CCGGATTTCG	CCAAAGACCC
951	CGAGGGTGAT	ATCACGCCCA	AAGACAGCCA	TATGCGCCTG	GCGAATCCGC
1001	GCGATCCCGA	ATTCCTCAAA	AAACACTGCC	TCTTCCGCCG	CGCCTACAGC
1051	TATTCTCGCG	GACCCGCCCTC	AAGCGGACAG	CTTGATGTCG	GGCTGGTGTT
1101	CGTCTGCTAT	CAGGCAAATC	TTGCCGACGG	TTTCATCTTC	GTGCAAAACC
1151	TCCTCAACGG	CGAACCCTG	GAAGAATACA	TCAGCCCTT	CGGCGGCGGC
1201	TATTCTTCG	TCTTGCCCGG	CGTGGGAAAA	GGCGGATTCT	TGGGACAAGG
1251	GCTGCCGGGC	GTATAA			

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

1	MSQNQPAQPT	KRNLFKTLA	VGAIGAIGGY	FGGKKQGETA	ERTAESQHSP
51	QAYPCYGEHQ	AGIVTPRQAF	SIMCAFQVTA	QSAKQLENLF	RTLTAIEFL
101	TQGGEYQDGD	DKLPSAGSGI	LGKAFNPDGL	TVTVGVGSSL	FDGRFGLKDK
151	KTVHLQEMRD	FPNDKLQKSW	CDGDLSLQIC	AFTPETCQTA	LRDIIKHTAQ
201	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSDP	KTADEVLTWG
251	VAANSILDEPE	WAKNGSYQAV	RLIRRFVEFW	DRTPLOEQTD	IFGRRKYSGA
301	PMDGKKEADQ	PDFAKDPEGD	ITPKDSHMRL	ANPRDPEFLK	KHCLFRAYS
351	YSRGPASSGQ	LDVGLVFVCY	QANLADGFIF	VQNLLNGEPL	EYISPFGGG

1218

401 YFFVLPGVGK GGFLGQGLPG V*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2563>:

m748.seq
 1 ATGAGCAAAA AACAAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
 51 CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
 101 AAAACACGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA AACTCGCCC
 151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
 201 GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
 251 AGCAGCTGGA AAACCTGTTC CGCACGCTGA CCGCCCGCAT CGAGTTTCTC
 301 ACCCAAGGCG GCGAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG
 351 CAGCGGCATT TTGGGCAAAG CCTTCAACCC CGACGGGTTG ACCGTTACCG
 401 TGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
 451 AAACCGATT ATTTGAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
 501 AAAAAAGCTGG TGCAGCGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
 551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
 601 ACCGCCGTTA TCCGTTGGAG TATCGACGGG TGGCAGCCCA AATCCGAACC
 651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTACGGGAC GGCACGGGCA
 701 ACCCAAAGT TTCCGATCCC AAAACTGCCG ACGAGGTTT GTGGACGGGG
 751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
 801 TCAGGCAGTC CGCCTTATCC GCCACTTTGT CGAGTTTGG GACAGGACGC
 851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GGCGCAAATA CAGCGGTGCG
 901 CGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTTG CCAAAGACCC
 951 CGAGGGTGAT ATCAGCCCA AAGACAGCCA TATACGCCTG GCGAATCCGC
 1001 GCGATCCCGA ATTCTCAAA AAACACCGCC TCTTCGCGCG CGCCTACAGC
 1051 TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTCG GGCTGCTGTT
 1101 CGTCTGCTAT CAGGCAAACC TTGCCGACGG ATTCATCTTC GTGCAAAACC
 1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCCTT CGGCGCGCGC
 1201 TATTTCTTCG TCTTGCCCGG CGTGGAAAAA GGCGGCTTTT TGGGGCAAGG
 1251 GCTGCTGGGC GTATAA

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>:

m748.pep
 1 MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP
 51 QAYPCYGEHQ AGIVTPQQAF SIMCAFDVTA QSAKQLENLF RLTARIEFL
 101 TQGGYQDGD DKLPPAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
 151 KPIHLQEMRD FSNKLOKSW CDGDLQLQIC AFTPETCQAA LRDIKHTVQ
 201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWTG
 251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLQEQT D IFGRRKYSGA
 301 PMDGKKEADQ PDFAKDPEGD ITPKDSHRL ANPRDPEFLK KHRLFRAYS
 351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLNNGEPL EEYISPFGGG
 401 YFFVLPGVEK GGFLGQGLLG V*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/g748 95.0% identity in 421 aa overlap

	10	20	30	40	50	60
m748.pep	MSKKQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGGKKQGETA	ERTAESQHSP	QAYPCYGEHQ
g748	MSQNQPAQPT	KRNLFKTAIA	AGAVGAIGGY	FGGKKQGETA	ERTAESQHSP	QAYPCYGEHQ
	10	20	30	40	50	60
m748.pep	AGIVTPQQA	SIMCAFDVTA	QSAKQLENLF	RRTLTARIEFL	TQGGYQDGD	DKLPPAGSGI
g748	AGIVTPQQA	SIMCAFDVTA	QSAKQLENLF	RRTLTARIEFL	TQGGYQDGD	DKLPSAGSGI
	70	80	90	100	110	120
m748.pep	LGKAFNPDGL	TVTVGVGSSL	FDGRFGLKDK	KPIHLQEMRD	FSNKLOKSW	CDGDLQLQIC
g748	LGKAFNPDGL	TVTVGVGSSL	FDGRFGLKDK	TVHLQEMRD	FPNDKLOKSW	CDGDLQLQIC
	130	140	150	160	170	180
m748.pep	AFTPETCQA	ALRDIKHTVQ	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSDP
g748	AFTPETCQA	ALRDIKHTVQ	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSDP
	190	200	210	220	230	240
m748.pep	AFTPETCQA	ALRDIKHTVQ	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSDP
g748	AFTPETCQA	ALRDIKHTVQ	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSDP

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2565>:

1	ATGAGCAAAA	ACCAACCCGC	ACAACCGACC	AGGCGCACTC	TTTTTAAAC
51	CGCGATCGCA	GCTGGAGCAG	TCGGCGCAAT	CGGAGGTTAT	CTCGGGCGCA
101	AAAAACGGGG	CGAAACCCGC	GAACGCACCG	CCGAAAGCCA	ACTACGCGCC
151	CAAGCCTATC	CTGTCTACGG	CGAACATCAG	GCAGGCATCG	TATCGCGCGA
201	GCAGGCGTTT	TCGATTATGT	GCGCCTTCGA	CGTAACCCGG	CBAAGTGCCA
251	AGCAGCTGGA	AAACCTGTTC	CGCAGCGCTA	CGCCCCGCAT	CGAGTTTCTC
301	ACCAAGGGCG	CGGAATACCA	AGACGGCGAC	CGCAAACTTC	CGCGACCGGG
351	CAGCGGCATT	TTGGGCAAG	CCTTCAACCC	CGACGGGTGT	ACCGTTACCG
401	TGGGGGTTGG	CATTCAGCTG	TTTGACGGCC	GGTTCGGACT	CAAAGACAAA
451	AAACCGATTTC	ATTTCGAGGA	AATGCGCGAC	TTTCTCCAAG	ATAAGCTGCA
501	AAAAAGCTGG	TGCGACGGCG	ATTTAGCCTT	GCAAACTCTG	GCCTTACCCC
551	CCGAAACCTG	CCAAGCCGCC	CTGCGCGACA	TCATCAAAAC	CAACCGTCCAA
601	ACCGCCGTTA	TCGCGTTGAG	TATCGACGGA	TGGCAGCCTA	AATCCGAACC
651	CGGCGCGATG	GCGGCGCGCA	ACCTGTTGGG	CTTCCGCGAC	GGCACGGGCA
701	ACCCCAAAAT	TTCCGCAACC	AAAACCTGCC	AGCAGGTTTT	GTGGACGGGG
751	GTGGCCGCCA	ACAGCCTCCA	CGAACCGGAG	TGGCGGAAAA	ACGGCAGTGA
801	TCAGGCAGTC	CGCCTTATCC	GCCACTTTGT	TGAGTTTTGG	GACAGGACGC
851	CGCTTCAAGA	GCAAAACGAC	ATTTTCGGCG	GGCGCAAAAT	CACGCGGCCG
901	CCGATGGACG	GCAAAAAGA	AGCCAGACAA	CCGGATTTTG	CCAAAGACCC
951	CGAGGGGAAT	ACCAAGCCCA	AAGACAGCCA	TATACGCCTG	GCGAATCCGC
1001	CGCATCCCGA	GTTCTTTAAA	AAACACCGCC	TCTTCCGCGC	CGCCTACAGC
1051	TATTCGCGCG	GACTCGCCTC	AAGCGGACAG	CTTGATGTCG	GGCTGGTGTT
1101	CGTCTGCTAT	CAGGCAAAAC	TGCGCGACGG	ATTACTTCTC	GTGCAAAACG
1151	TCCTCAACGG	CGAAGCCGTG	GAAGAAATACA	TCAGCCCCCT	CGGCGGCGGC
1201	TATTTCTTCG	CTTTCGCCGG	CGTGAAAAAA	GGCGGCTTTT	TGGGGCAAGG
1251	GCTGCTGGGC	GATATAA			

a748.pgp

1	MSKNQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGKKRGETA	ERTAESQHS
51	QAYPCYGEH	AGLVTPOQAF	SIMCAFVDTA	QSAQLENLF	RTDITRIEFL
101	TQGGBYQDGD	DKLPAPAGSI	LKGAFNPDLG	TVTYVGGSSL	FDGGRFGLKDR
151	KPIHLQEMRD	FSNDKLQKSW	CDGDLSLQIC	AFTPETCOAA	LRDIIKHTVQ
201	TAIVRWSIDG	WQKSPSEGAM	AARNLLGFPRD	GTGNPKVSDP	KTDAEVLVTW
251	VAVNSLDEPE	WAKNGSYQAV	RLIRHFVEFW	DRTLQEQSTD	IFGRKKYSGA
301	PMDGKKEADQ	PDFAKDPEGN	TFPKDSHRL	ANPRDPEFLK	KHRLFRRAYS
351	YSRGLASSGG	LDVLGVFCVY	QANLADGFIF	VQNLLNGEPL	E EYISPFGGG
401	YFFVLPGVEK	GGFLGQGLLG	V		

Computer analysis of this amino acid sequence gave the following results:

1220

Homology with a predicted ORF from *N meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

a748.pep	MSKNQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKRGETAERTAESQHSPQAYPCYGEHQ
m748	MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSPQAYPCYGEHQ
a748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRITLTARIEFLTQGGEYQDGDGDKLPPAGSGI
m748	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRITLTARIEFLTQGGEYQDGDGDKLPPAGSGI
a748.pep	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSLQIC
m748	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSLQIC
a748.pep	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
m748	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
a748.pep	KTADDEVLTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQETDIFGRRKYSQA
m748	KTADDEVLTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQETDIFGRRKYSQA
a748.pep	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRAYSYSRGLASSGQ
m748	PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRAYSYSRGLASSGQ
a748.pep	LDVGLVFVCYQANLADGFIQVQNLNNGELEEYISPFGGGYFFVLPVGEKGGFLGQGLLG
m748	LDVGLVFVCYQANLADGFIQVQNLNNGELEEYISPFGGGYFFVLPVGEKGGFLGQGLLG
a748.pep	VX
m748	VX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

g749.seq

1	ATGAGAAAAT	TCAATTGAC	CGCATGTGCC	GTGATGCTTG	CCTTGGGTTT
51	GACCGCGTGC	CAGCCGCCGG	AGGCGGAGAA	AGCCGCGCCG	GCCGCGTCCG
101	GTGAGACCCA	ATCCGCCAAC	GAAGCGGTT	CGGTCGGTAT	CGCCGTCAAC
151	GACAAATGCT	GCGAACCGAT	GAATCTGACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCATATAT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AGGGCGTGAT	GGTGGTGGAC	GAACGCGAAA	ATATCGCCCC	GGGGCTTTCC
301	GACAAAATGA	CCGTAAccct	GCTGCCGGGC	GAATACGAAA	TGACCTGCGG
351	CCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAGCCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAA	AACTGCCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTACGTTCA	AGGCGAGGTT	AAAGAGCTGG	CGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGCCACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGTGTG	AAGACGACTT
651	CAAAGACGGT	GCGAAAGATG	CCGGGTTTAC	CGGCTTCCAC	CGTATCGAAC
701	ACGCCCTTTG	GGTGGAAAAA	GACGTATCCG	GCGTGAAGGA	AACCGCGGCC
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAG	AAAGAAATCG	ACGCATTGGC

1221

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801 Gttccctccg GGCAAAGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 CGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TGCGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCTGTCG TTGATTGAGG CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGCACCATA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

g749.pep

```

1 MRKFNLTAALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIQAVN
51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPLGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
151 DYKAYVQGEV KELAATKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPIV DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

m749.seq

```

1 ATGAGAAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCACTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAACGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCTT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
501 CAAACTTTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGCGGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTTTAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCGG GCGTGAAGGA AATTGCAGCG
751 AAACCTGATG CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTTGC
801 GTTCTCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCCG CTGATCGAGG CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCTT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

m749.pep

```

1 MRKFNLTAALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIQAVN
51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPLGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPIV DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

m749.pep      10      20      30      40      50      60
MRKFNLTAALSVMALALGLTACQPPEAEKAAPASGEAQTANEGGSVSIQAVNDNACEPMELT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g749          10      20      30      40      50      60
MRKFNLTAALSVMALALGLTACQPPEAEKAAPASGETQSANEGGSVGIQAVNDNACEPMNLT

```

	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
g749	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
m749.pep	130	140	150	160	170	180
	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVADSGFKDTANEADLEKLPOPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
m749.pep	190	200	210	220	230	240
	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
g749	KAKSLFAATRIVHYERIEPIAELFSELDPVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
m749.pep	250	260	270	280	290	300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
m749.pep	310	320	330	340	350	360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDTNFKQVNEILAKYRTKDGFEYDKLG					
g749	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDTNFKQVNEILAKYRTKDGFEYDKLS					
	310	320	330	340	350	360
m749.pep	370	380	389			
	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

a749.seq

```
1 ATGAGAAAAAT TCAATTGTAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCGCGTGC CAGCCGCCGG AGCGCGAGAA AGCTGCGCCG CGCAGCTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTC AAC
151 GACAAATGCTT GCGAAACCGAT GGAATCTACC GTGCGGAGCG GACAGGTTGTT
201 GTTCAATATT AAAAAACAAC GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGCGGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACCTTCC
301 GATAAAATGA CCGTCACCCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTTGGT GGTAAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CTTATGTTCA AGCGGAAGTC AAAGAGCTGG TGGCGAAAAA
501 CAAACCTTTT ACCGAAGCCG TCAAAGCAGG CGACATTTGAA AAGCGGAAAT
551 CCCTGTTTGC CGACACCCCG GTCCCATTAC AAGCATTCGA ACCGATTTGCC
601 GAGCTTTTTCA CGGAATCTGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAAGGA AATTGCAAGC
751 AAATCTATGA CCGATGTCCA AGCCCTGCAA AAAGAAATCG ACGCATTTGG
801 GTTTPCTCGG GCGAAGGTGG TCCGCGCGCG GTCCGAAGTG ATTGAAGAA
851 TGGCGGGCAG TAAATTCAGC GGGCAAGAAG ACCGGTACAG CCACACCGAT
901 TTAGAGCTACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCCTGCGATTT
951 GTTCCGTCGG TTGATCGAGA CCAAAAAACA AGCCTTGGTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCCTT
1101 ACAGGGCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCCA CTTCCGGGCA
1151 TACTCGGCTT GAAATAA
```

a749.pep

1	MRKFNLTLALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSI	AVN
51	DNACEPMLT	VPSGQVVFNI	KNNSGRKLWE	EILKGVMMVD	ERENIAPGLS	
101	DKMTVTLLPG	EYEMTCGLLT	NPRGKLVTVD	SGFKDPTANE	DLEKLSQPLA	
151	DYKAYVQGEV	KELVAKTKTF	TEAVKAGDIE	KAKSLFADTR	VHYSERVEPIA	
201	ELFSELDPMI	DAREDDTKDG	AKDAGFTGFH	RIEYALWVEK	DVSGVKEIAA	
251	KLMTDVEALQ	KEIDALAFPP	GKVVGGASEL	IEEVAGSKIS	GEDDYSHTSD	

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301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGIILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
a749.pep	MRKFNL	TALSVMLALGLTACQP	PEAEKAAPAASGEAQTANEGGSV	SI	AVNDNACEPMELT	
m749	MRKFNL	TALSVMLALGLTACQP	PEAEKAAPAASGEAQTANEGGSV	SI	AVNDNACEPMELT	
	10	20	30	40	50	60
	70	80	90	100	110	120
a749.pep	VPSGQV	VFNKNNSGR	KLEWEILKGV	MVVDRENIAPGL	SDKMTVTLLPGEYEMTCGLLT	
m749	VPSGQV	VFNKNNSGR	KLEWEILKGV	MVVDRENIAPGL	SDKMTVTLLPGEYEMTCGLLT	
	70	80	90	100	110	120
	130	140	150	160	170	180
a749.pep	NPRGKL	VVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE				
m749	NPRGKL	VVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE				
	130	140	150	160	170	180
	190	200	210	220	230	240
a749.pep	KAKSLFADTRVHYERIEPIAELFSELD	VIDAREDDFKDGAKDAGFTGFHRIEYALWVEK				
m749	KAKSLFADTRVHYERIEPIAELFSELD	VIDAREDDFKDGAKDAGFTGFHRIEYALWVEK				
	190	200	210	220	230	240
	250	260	270	280	290	300
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKV	VVGASELIEEVAGSKISGEEDRYSHTD				
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKV	VVGASELIEEVAGSKISGEEDRYSHTD				
	250	260	270	280	290	300
	310	320	330	340	350	360
a749.pep	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTD	TNFKQVNEILAKYRTK	DGFETYDKLG			
m749	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTD	TNFKQVNEILAKYRTK	DGFETYDKLG			
	310	320	330	340	350	360
	370	380	389			
a749.pep	EADRKALQASINALAEDLAQLRGIILGLKX					
m749	EADRKALQASINALAEDLAQLRGIILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq

1	GTGAAACCGC	GTTTTATTG	GGCAGcctGC	GCCGTCCTGC	CGGCCGCCCTG
51	TTCCGCCGAA	CCTGCCGCCG	AAAAAACTGT	ATccgCCGCA	TCCCAAGCCG
101	CATCCACACC	TGTCGCCACG	CTGACCGTGC	CGACCGCGCG	GGGCGATGCC
151	GTTGTGCCGA	AGAATCCCGA	ACgcgtcgcc	gtgtAcgaCt	ggCGGCCGTt
201	ggaTACGCTG	ACCGAGCCGG	GCGTGAATGT	GGGCGCAACC	ACCGCGCCGG
251	TGCGCGTGGA	CTATTGCGAG	CCTGCATTG	ACAAGCGCGG	AACGGTGGGG
301	ACGCTGTTTG	AGCCCCGATTG	CGAATCCCTG	CACCGCCACA	ATCCCGAGTT
351	TGTCATTACC	GGCGGGCCGG	GTGCGGAAGC	GTATGAACAG	TTGGCGAAAA
401	ACGCGACCAC	CATAGATTG	ACGGTGGACA	ACGGCAATAT	CCGCACCAGC
451	GGCGAGAAGC	AGATGGAGAC	CCTGTCGCGG	ATTTTCGGTA	AGGAAGCGCG
501	CGTGGCGGAA	TGAATGCGC	AGATTGACGC	GCTGTTCGCC	CAAAAGCGCG
551	AAGCCGCCAA	AGGCAAAGGA	CGCGGGCTGG	TGCTGTCGGT	TACAGGCAAC
601	AAGGTGTCCG	CCTTCGGCAC	GCAATCGCGG	TTGGCAAGTT	GGATACACGG
651	CGACATCGGC	CTGCCGCCCG	TGGACGAATC	TTTACGCAAC	GAAGGGCACG
701	GGCAGCCCGT	TTCTTCGAA	TACATCAAAG	AGAAAACCC	CGGCTGGATT
751	TTTCATCATCG	ACCGCACCGC	CGCCATCGGG	CAGGAAGGGC	CGGCTGCCGT

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```

801 GGAAGTGTG GATAACGCGC TGGTATGCGG CACGAACGCT TGGAAGCGCA
851 AGCAAATCAT CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCGCG
901 CGGCAGTTGA TACAGGCGGC GGAACAGTTG AAGGCGGCGT TTGAAAAGGC
951 AGAACCCGTT GCGGCGCAGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2574; ORF 750.ng>:

```

g750.pep
1  VKPRFYWAAC AVLPAACSPE PAAEKTVSAA SQAASTPVAT LTVPTARGDA
51  VVPKNPERVA VYDWAALDTL TEPGVNVGAT TAPVRVDYLQ PAFDKAATVG
101 TLFEPPCESL HRHNPQFVIT GPGAEAYEQ LAKNATTIDL TVDNGNIRTS
151 GEKQMETLSR IFGKEARVAE LNAQIDALFA QKREAAKGKG RGLVLSVTGN
201 KVSAFGTQSR LASWIHGDIG LPPVDESRLN EGHGQPVSEF YIKEKNPGWI
251 FIDRTAAIG QEGPAAVEVL DNALVCGTNA WKRKQIIVMP AANYIVAGGA
301 RQLIQAAEQL KAAFEKAEPV AAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2575>:

```

m750.seq
1  GTGAAACCGC GTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG
51  TTCGCCCGAA CCTGCCGCCG AAAAAACTGT ATCCGCCGCA TCCGCATCTG
101 CCGCCACGCT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
151 AATCCCCGAA GCGTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
201 CGAATTGGGC GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT
251 ATTTGCAGCC TGCATTGAC AAGCGGCGAA CGGTGGGGAC GCTGTTCCGAG
301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351 CGGGCCGGGC GCGGAAGCGT ATGAACAGTT AGCGAAAAAC GCGACCACCA
401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
451 ATGGAGACCT TGGCGCGGAT TTTCCGGCAAG GAAGCGCGCG CGGCGGAATT
501 GAAGGCGCAG ATTGACGCGC GTTTCGCCCA AACGCGCGAA GCCGCCAAAG
551 GCAAAGGACG CGGGCTGGTG CTGTCGGTTA CGGGCAACAA GGTGTCCGCC
601 TTCGGCAGCG AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
651 ACCGCCTGTA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
701 CCTTCGAATA CATCAAAGAG AAAAACCCTG ATTGGATTTT CATCATCGAC
751 CGTACCGCCG CCATCGGGCA GGAAGGGCCG GCGGCTGTCG AAGTATTGGA
801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG
851 TCATGCCTGC CGCGAACTAC ATTGTCGCGG GCGGCGCGCG GCAGTTGATT
901 CAGGCGGCGG AGCAGTTGAA GCGGCGGTTT AAAAAGGCAG AACCCGTTGC
951 GCGGGGGAAA AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2576; ORF 750>:

```

m750.pep
1  VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
51  NPERVAVIDW AALDTLTELG VNVGATTAPV RVDYLQPAFD KAATVGTLFE
101 PDYEALHRYN PQLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
151 METLARIFGK EARAELKAO IDALFAQTRE AAKGKGRGLV LSVTGNKVSA
201 FGTQSRLASW IHGDIGLPPV DESLRNEGHE QPVSEFYIKE KNPDWIFIID
251 RTAAIGQEGP AAVEVDNAL VRGTNAWKRK QIIVMPAANY IVAGGARQLI
301 QAAEQLKAAF KKAEPVAAGK K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 93.8% identity in 322 aa overlap

```

m750.pep      10      20      30      40      50
VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASA----ATLTVPARGDAVVPKNPERVA
|||||
g750          10      20      30      40      50      60
VKPRFYWAACAVLPAACSPEPAAEKTVSAAASQAASTPVATLTVPARGDAVVPKNPERVA
|||||

m750.pep      60      70      80      90     100     110
VYDWAALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVIT
|||||
g750          70      80      90     100     110     120
VYDWAALDTLTEPGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDCESLHRHNPQFVIT
|||||

m750.pep     120     130     140     150     160     170
GGPGAAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFA
|||||

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g750      GGFGEAEYEQAKNATTIDLTVDNGNIRTSGEKQMETLSRIFGKEARVAELNAQIDALFA
           130      140      150      160      170      180

           180      190      200      210      220      230
m750.pep  QTREAAKGRGLVLSVTGNKVSFAFGTQSRSLASWIHGDIGLPPVDESLRNEGHGQPVSF
           |||||
g750      QKREAAKGRGLVLSVTGNKVSFAFGTQSRSLASWIHGDIGLPPVDESLRNEGHGQPVSF
           190      200      210      220      230      240

           240      250      260      270      280      290
m750.pep  YIKEKNPDWIFIIDRTAAIGQEGPAAVEVDNALVRGTNAWKRKQIIVMPAANYIVAGGA
           |||||
g750      YIKEKNPDWIFIIDRTAAIGQEGPAAVEVDNALVCGTNAWKRKQIIVMPAANYIVAGGA
           250      260      270      280      290      300

           300      310      320
m750.pep  RQLIQAAEQKAAFEKAPVAAGKKX
           |||||
g750      RQLIQAAEQKAAFEKAPVAAQX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2577>:

```

a750.seq
1   GTGAAACCGC  GTTTTATTG  GGCAGCCTGC  GCCGTCCTGC  TGACCGCCTG
51  TTCGCCCGAA  CCTGCCGCCG  AAAAAACTGT  ATCCGCCGCA  TCCGCATCTG
101 CCGCCACACT  GACCGTGCCG  ACCGCGCGGG  GCGATGCCGT  TGTGCCGAAG
151 AATCCCGAAC  GCGTCGCCGT  GTACGACTGG  GCGGCGTTGG  ATACGCTGAC
201 CGAATTGGGT  GTGAATGTGG  GCGCAACCAC  CGCGCCGGTG  CGCGTGGATT
251 ATTTGCAGCC  TGCATTGAC  AAGGCGGCAA  CGGTGGGGAC  GCTGTTTCGAG
301 CCCGATTACG  AAGCCCTGCA  CCGCTACAAT  CCTCAGCTTG  TCATTACCGG
351 CGGGCCGGGC  GCGGAAGCGT  ATGAACAGTT  GCGGAAAAAC  GCGACCACCA
401 TAGATCTGAC  GGTGGACAAC  GGCAATATCC  GCACCAGCGG  CGAAAAGCAG
451 ATGGAGACCT  TGGCGCGGAT  TTTGCGCAAG  GAAGCGCGCG  CGGCGGAATT
501 GAAGGCGCAG  ATTGACGCGC  TGTTCGCCCA  AACGCGCGAA  GCCGCCAAAG
551 GCAAAGGACG  CGGGCTGGTG  CTGTCGGTTA  CGGGCAACAA  GGTGTCCGCC
601 TTCGGCACGC  AGTCGCGGTT  GGCAAGTTGG  ATACACGGCG  ACATCGGCCT
651 ACCGCTCTGA  GACGAATCTT  TACGCAACGA  GGGGCACGGG  CAGCCTGTTT
701 CCTTCGAATA  CATCAAAGAG  AAAAACCCTG  ATTGGATTTC  CATCATCGAC
751 CGTACCGCCG  CCATCGGGCA  GGAAGGGCCG  GCGGCTGTCG  AAGTATTGGA
801 TAACGCGCTG  GTACGCGGCA  CGAACGCTTG  GAAGCGCAAG  CAAATCATCG
851 TCATGCCTGC  CGCGAACTAC  ATTGTCGCGG  GCGGCTCGCG  GCAGTTGATT
901 CAGGCGGCGG  AGCAGTTGAA  GGAGGCGTTT  GAAAAGGCAG  AACCCGTTGC
951 GGCGGGGAAA  GAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2578; ORF 750.a>:

```

a750.pep
1   VKPRFYWAAC  AVLLTACSPE  PAAEKTVSAA  SASAATLTVP  TARGDAVVPK
51  NPERVAVYDW  AALDTLTELG  VNVGATTAPV  RVDYLQPAFD  KAATVGTLFE
101 PDYEALHRYN  POLVITGGPG  AEAYEQAKN  ATTIDLTVDN  GNIRTSGEKQ
151 METLARIFGK  EARAELKAQ  IDALFAQTR  AAKGKGRGLV  LSVTGNKVSA
201 FGTSRLASW  IHGDIGLPPV  DESLRNEGHG  QPVSFYEIKE  KNPDWIFIID
251 RTAAIGQEGP  AAVEVDNAL  VRGTNAWKRK  QIIVMPAANY  IVAGGSRQLI
301 QAAEQKKEAF  EKAEPVAGK  E*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

```

a750/m750  98.8% identity in 321 aa overlap

           10      20      30      40      50      60
a750.pep  VKPRFYWAACAVLLTACSPEPAAEKTVSASASAAATLTVPARGDAVVPKNPERVAVYDW
           |||||
m750      VKPRFYWAACAVLLTACSPEPAAEKTVSASASAAATLTVPARGDAVVPKNPERVAVYDW
           10      20      30      40      50      60

           70      80      90      100     110     120
a750.pep  AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYALHRYNPQLVITGGPG
           |||||
m750      AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYALHRYNPQLVITGGPG

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	70	80	90	100	110	120
	130	140	150	160	170	180
a750.pep	AEAYEQLAKNATTIDLTVDNGNIRTSGEKOMETLARIFGKEARAAELKAQIDALFAQTRE					
m750	AEAYEQLAKNATTIDLTVDNGNIRTSGEKOMETLARIFGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a750.pep	AAKGKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSFYEYIKE					
m750	AAKGKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSFYEYIKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a750.pep	KNPDWIFIIDRTAAIGQEGPAAVEVLNVLNRGTNAWKRKQIIVMPAANYIVAGGSRQLI					
m750	KNPDWIFIIDRTAAIGQEGPAAVEVLNVLNRGTNAWKRKQIIVMPAANYIVAGGARQLI					
	250	260	270	280	290	300
	310	320				
a750.pep	QAAEQLKEAFKAEPVAAAGKEX					
m750	QAAEQLKAAFKKAEPVAAAGKKX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

m751.seq..

```

1  ATGGCTTGGA GTATGTTTGC CACAACCCAA GCCGATAGAG CCGTAAGGTC
51  TGCAACTGCA CCTAAAGAAA TGTGGTTCCA TAAGAAGATA ATAGATGAAA
101 AAACAGGTAA AGTATCCTTT GATACCAGAC AAATTTGGTC ATTGAATGAT
151 TTAAGCAAGG AAGAACTGGC AAGCATTCAA GACACAAATG GCAAAGTTAT
201 TACTGTGTCT AATCCTGGTA TTTTCAATAA TCGAGAAGAT TCATTAAGCA
251 ACGCAGCAAA ACAAAATCGT AATAGTACAA ACGGTAGTGG TGTATTGCA
301 GTCATGAATC CTCCAACAGG GAAATATAAA TCTGATTCTA ATAACAAAAT
351 AAAAGATTTT TTATGGCTCG GTTCAAGTCT TGTCTCTGAA CTGATGTATG
401 TCGGTTACGA CCAATTAAAT AATAAAGTGT TCCAAGGCTA TTTACCCAAA
451 ACCAATTCAG AAAAACTGAA TCAAGATATT TATCGAGAGG TTCAAAAAAT
501 GGGTAACGGC TGGTCGGTTG ATACCAGTAA TCACAGTCGT GGGGGAATTA
551 CAGCAAGCGT TTCCTTAAAA GATTGGGTAA ACAATCAAAA ACAAAATGGC
601 ATTGCCCCAA TCAGAAAAGC ACGTTTCTAT GGTACAGCCA CAAATGTGCA
651 GAATGATTAC GCCGATGTTT TACAGAAAAA CGGCTATACC TATACGGGTG
701 CAGACGGCAA AACTTATAAC AGCGGATCCT ACTCAATCGT GCATGATAAA
751 GATTTTGTGG GGAACAAATG GATACCTTTC TTGCTAGGAA CCAATGACAC
801 CACACAAGGT ACATGTAAGG GGTGTGCTA TTCGCATAGC AGTTATTTTG
851 CGGAGGTGCC AAAAGCAGGT ACAAAGAAT TTGATGACTA TGTAATAATA
901 TGGGGTGAAG TTGAATATGA CGCTCAAGGT AAGCCAATTA ACAATCTAA
951 ACCCATACTG GTAGAACCAA ACAAACAAA AGATAATGAA AAATATGAAA
1001 AAGAAGCTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

m751.pep..

```

1  MAWSMFATTQ ADRAVRSATA PKEMWFHKKI IDEKTGKVSF DTRQIWSLND
51  LSKEELASIQ DTNGKVITVS NPGIFNNRED SLSNAAKQNR NSTNGSGVIA
101 VMNPPPTGKYK SDSNNKIKDF LWLGSSLVSE LMYVGYDQLN NKVFQGYLPK
151 TNSEKLNQDI YREVQKMNG WSVDTSNHSR GGITASVSLK DWVNNQKQNG
201 IAPIRKARFY GTATNVQNDY ADVLQKNGYT YTGADGKTYN SGSYSIVHDK
251 DFIGNWKWIPF LLGTNDTTQG TCKGLCYSHS SYFAEVPKAG TKEFDDYVKI
301 WGEVEYDAQG KPINKSKPIL VEPNKTCDNE KYEKEAF*

```

a751.seq not found yet

a751.pep not found yet

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

```
m752.seq..
1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCCGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCAT CCGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAGC GGTAAGATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
651 TACCAATAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGCGG TGGAAAATCC GTTTATCCAT CCGTTGTCC
851 AAGCTATTAT CTTGCATTTT CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAACACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAACCG GAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

```
m752.pep
1  MKISRPPEFT LLQQEYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51  DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAILHF LIGYIHFFGD
301 GNGRTARALF YWFMLNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
351 DLTIFYIYQC DIIKRAVDL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALAYVAP QDLLERLEKK *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

```
m752-1.seq
1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCCGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCAT CCGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAGC GGTAAGATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
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651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTT CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTT TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCCT ATTTTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA AAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRELLKSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTFFIYYQC DIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIETAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALFYVAP QDLLERLEKK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTTAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTGC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TGCGCCAGTT ATTTCTTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAI WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLES D RHLRDNSDWN
101 CGDNIWLIQW FAPLGHSQHM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```
m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTTG GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTGTC TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CTTTGCTTGG CTGCCAATGA ATTTTATGTC ATGCAGACCA TCAAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCGGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTTAAT CCATTCTTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTCGT CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATTA
1051 AACCTGACTA ACCACGGTAA GAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCCTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```
m754.pep
1  MMKSILTVSG NMRKPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVROND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HHGRFVSVSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANFLC MQTIKQAGIA VAQTSLSLSDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIHQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDL SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKPTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*
```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```
m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTAATCCGAT ATTAAACCA
101 TCTTGGCTAG ACATGGATTT GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CAGTGAAGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAATGAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTTACC
251 GCCTTGAAAG TGATTTGAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA
```

1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

```
m755.pep.
  1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
 51 REGISEAHGT IAIQELTARF DWFYSCISNI KFYRLES DLN AQFIADGVYQ
101 AKQAF LQRVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

```
m756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGCA GATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

```
m756.pep
  1 MTANFAQTLV EIQDSLRYRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYGA E LVSDGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

```
a756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGCA GATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

```
a756.pep
  1 MTANFAQTLV EIQDSLRYRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYGA E LVSDGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLRYRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLRYRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVVPYGAELVSDGNFTAV					
a756	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVVPYGAELVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

m757.seq

```

1  ATGAAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAAAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGCGC ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCAC TGACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

m757.pep (lipoprotein)

```

1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSGLTI LTVDTKADK
101 ITAVRVVWNT DAMPQKAEKL SKAAAALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPSV VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

m758.seq

```

1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAC TGTGGAATTT CCCGTCTGCT ACGGCGGCGA ATACGGCCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGCGGCG TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGACAGAA GGATTGAGCC
501 ATGA

```

1232

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1  ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101  AGGGCAAACCT GGTGGAATTT CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
151  GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201  CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251  CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301  CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351  CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401  TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTGAA TCCGCGGACC
451  CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
501  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

	10	20	30	40	50	60
m758.pep	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
a758	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m758.pep	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAAGSVGIGGSQT					
a758	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAAGSVGIGGSQT					
	70	80	90	100	110	120
	130	140	150	160		
m758.pep	GVYPFASPGGWQIIGRTELP LFRADLNPPTLLAAGDQVRFVAERIEPX					
a758	GVYPFASPGGWQIIGRTELP LFRADLNPPTLLAAGDQVRFVAERIEPX					
	130	140	150	160		

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1  ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51  TCTTTTGGCC GTTCCCTG CTTACTCATC CATTGTCCGC AACGATGTCG
101  ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTACCGTA
151  GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201  GGTTCTCAAC GGCATCCCA TGCCCGACTT CCGCGTCAGC AACCGCCAAA
251  CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAG
301  AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351  AGAACAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGGACT
401  ACGACTACCA CCTTCCCGC CTCAACAAAC TGGTTACCGA AATCTCACCT
```

```

451 ACCGCACTCA GCAGCGTACC CTTGCTTGGA AACGGCCAGC CAAAGGCCAA
501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTGTACGA CTCGGCTCAG
551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACACG AACCGCCCCG
601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAGTAT TGGGGTTCCA
651 AAACCACGGC TTACTCGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCC CCCTGTTTGC CTTCGACAAG
751 CATGAAAACC GCTGGGTGCT TGCGGGCGTA CTCAGCACCT ACGCCGCTT
801 CGATAATTTC TTCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCGGGCT GACCACCAAC
901 GAACTCATAT GGC CGCAGCAA CGGTAATGGC AACAGCACCC TGCAAGGGCT
951 CAACGAACGC ATCACCTGTC CCATTGCAAA CCCTTCGCTT GCCCCACAAA
1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA
1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
1101 AGGCGCAGGC GCATTGCAGT TCGACAGCAA CTTACCGTC GTCGGTAAAA
1151 ACCACACATG GCAAGGTGCA GCGGTTATCG TAGCCGACGG CAAACGCGTC
1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC
1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCAGGGC GACATCGCA
1301 TCGGGGAAGG CACTGTCGTA CTCGCCAAA AAGCTGCTTC AGACGGCAGC
1351 AAACAAGCAT TCAACCAAGT CGGCATCACC AGCGGCAGGG GCACGGCCGT
1401 CCTCGCCGAC AGCCAGCAAA TCAAACCCGA AAACCTCTAT TTCGGCTTCA
1451 GGGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTT TACCCATATC
1501 CGCCATGCGG ACGGCGGCGC GCAAATCGTC AATCACAACC CTGACCAAGC
1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTCT
1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTTACGAA
1651 TACATCAACC CGCACCGCAA CCGTCGGACC GACTACTTCA TACTCAAACC
1701 CGGCGGCAAC CCGCGCAAT TTTTCCCGTT AAATATGAAA AACTCAACAA
1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCCGA ACAAGTCGCC
1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG
1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG
1901 AAGCAGCCAT AGAAAAAACC CGCCATATCG CAAATGCCGC CGTATACGGC
1951 AGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
2001 ACGCACCGAC AGCACGCTGT TGCTCAACGG CGGCATGAAC CTTAACGGGG
2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTCAGGCAG GCCCGTACCC
2101 CATGCTACG ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG
2151 GACCACGGC AGCTTCAAGG CTGCACGGT CACCCTGCGA AACCATGCCC
2201 GACTGACGGC AGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCCCA
2251 TACGATCTGT CCGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
2301 ATGCTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCAACGCCG
2351 TTTTAAAGC CGAAACTAT CGTGCACTAC CTGCAACGCA AGTACGCGGC
2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT
2451 GTACGGCAGC ATCCGTGCCG GCAAAGACAC CGCATCCGC ATGGAAGCAG
2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGGCGC ACTGACGCTT
2551 GACGGCGCAC AAATTACCCT GAACCCCGAT TTCGCCAATA ATACACACAA
2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTCCGGC
2651 CATTCCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
2701 AAAC TGGAAG GGGACAGCCG CGGCGCATTC CAAATCCACG TCAAACACAC
2751 CGGACAAGAA CCTCAAACAA CCGAATCGCT TGCATTGTG AGCCTCAATC
2801 CGAAACACAG CCACCAAGCC CGATTACCC TCCAAAACGG CTATGCCGAT
2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAAA AACAACAACG GATACAGCCT
2901 GTACAACCCG CTCAAAGAGG CCGAACTTCA AATTGAAGCC ACGCGTGCGG
2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC
3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC
3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG
3151 GTGCCCCAAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG
3201 TCAGGTTGCC AAAGCCGCCG ACACGAACGA CCTGACACTC TTCGAAACCG
3251 AACTGGATAC GTATATAGAA CGTG TAGAAA TGGCCGAATC CGAACTTGAC
3301 AAAGCACGGC AAGGCGGCGA TCGCAAGCC GTCGAAACAG CCCGGCACGC
3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA
3401 CCGGCGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAAC GATCAGCCGG
3451 TCGGCCAACA CCGCGTTTC CGAACAGGCC GCCTACAATA CCGGCCGGCA
3501 ACAGGCGGGA CGCGCATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA
3551 ACATCTGGCT GGAACCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
3601 CACCGTCCCT ACCAACAAC TACCAACTAT GCACATATCG GCATCCAAAC
3651 CGGCATCACC GACCGTCTCA GTGTCGTAC GATTTTAACC GATGAGCGCA
3701 CAAACAACCG TTTTGATGAA GGCGTATCCG CCCGAAACCG CAGCAACGGC

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3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCCG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CGGTACGTAC TCACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCC GCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCCG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCCGCCAC AAACAGGCAG GAATCAAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

m759.pep

```

1 MRFTHTTFFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGFTV
51 GASNISIQDK QGKILGRVLN GIMPEDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQ A YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLL G NGQPKANAYL DTDREFPYFVR LSGTQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWVLAV LSTYAGFDNF FNKYIVTQPE FIRSTIRQYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQNSRHRMP SEDAGKTLIL
351 SSRFDNKTLM LADNINQAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKLGAGTL IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGGRDL NGNNLAFTHI
501 RHADGGAQIV NHNPDAQATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
551 YINPHRNRRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAVYG
651 RPEYRYNGAL NLHYRPKRTD STLLNGGMN LNGEVLIEGG NMIVSGRPVP
701 HAYDHQAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHLDDGITA
751 YDLSGIDLGF TQGKTPECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNDRSEL RLKKAHLYGS IRAGKDTAVR MEADSNWTL SSSHTGALT L
851 DGAQITLNP D FANNTNNRNF NTLTVNGTLD GFGTFRFLT G IVRKQNAAPL
901 KLEGDSRGAF QIHVKNTGQE PQTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNNGYSLYNP LKEAELQIEA TRAEHERNQQ AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCAAQG YSADICRQVA KAADTNDLTL FETELDYIE RVEMAESLD
1101 KARQGGDAQ VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAEILSR
1151 SANTAVSEQA AYNTGRQQAG RRIDRHLTD P QQQNIWLETG TQQT DYHSGT
1201 HRPYQQTNY AHIGIQTGIT DRLSVGTILT DERTNNRFD E GVSARNRSNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTHW AGIRLDKTVE
1351 LGQAKLTAF SSDYYHTRQN SGSALSVNDR TLLQQAAGHT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

g760.seq (partial)

```

1 AACAAACGCA ACACCCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
51 CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCG GGCTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGGATGC ATGCAGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCAAGCTGA AGCTGCAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATTCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

g760.pep (partial)

```

1 NNRNTRYAAL GKRVMGVET EISGAITPKW QIHAGYSYLH SQIKTAANPR
51 DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1  ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCACG CTGCCAACCC TGTTGCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTT GACAGCAGCG GCGAGATGGG
501 CCGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGTCTC CGCGTCCGCG CGAGAAAAAC AACCGGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GCGCGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTAAAATGC ACAGCCACGA CGTGTTCGCC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCGAT CGGAAAGCCG ATTCCAATTA TACGTTTGCG GGCAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAGCGT CGCTTTAGAT
1201 GGTTCGCGC CTTGCGCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTGTATGC CAAGACGGTG TTCCGTCCTC TGAAGGTTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCTC CCAACTTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCAG TTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTCGTTT TACCGCATGA AGGATAAAAA CGCCGCCGCA
1651 CCGCTGGACT CAAACAACAA AAAAACCCGT TACGCCGAT TGGGCAACG
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTCGC GCGACGAAGG CATCTTCCTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGAT ACATGAGGCG
1951 GGTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAAT
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCC
2051 GCGTCGGCAG CGAGAGCACC TTTAACATTC CCGGTTCGGA GCGCAGCCTG
2101 ACGGCAAACC TGC GTTACAG TTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1  MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKQ QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQOVKDRNV DTFDQLARKT
101 PGLRVLSNDD GRSSVYARGY EYSEYNIDGL PAQMQSINGT LPNLFADFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THQYKAEAD
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQORR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHS HDVFA
301 DLKHYFGNGG YGKVGMYSD RKADSNYTFA GSKLNNTGQA DVAGLGTDIK
351 QKAFAYDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLSKSVALD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRETPKLKLQ INADNIFNRH YYARVGSEST FNIPGSERSL
701 TANLRYSF*
```

1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRVSFYRMKDKNAAPLDSNNKKTRYAALGKRVMEGVETEISGAMTPKW					
g760				NNRNTRYAALGKRVMEGVETEISGAITPKW		
				10	20	30

	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIKTASNSRDEGI FLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
g760	QIHAGYSYLHSQIKTAAANPRDDGI FLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90

	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMAAAYRFTPKLKLQINADNIFNRHYYARVGSESTFNIPGSESLTANL					
g760	AGMHAGGYATFDAMAAAYRFTPKLKLQINADNIFNRHYYARVGSTNTFNIPGSESLTANL					
	100	110	120	130	140	150

	709
m760.pep	RYSEFX
g760	RYSEFX

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

m761.seq

1	ATGAAAATAT	CATTTCATTT	AGCTTTATTA	CCCACGCTGA	TTATTGCTTC
51	CTTCCCTGTT	GCTGCCGCCG	ATACGCAGGA	CAATGGTGAA	CATTACACCG
101	CCACTCTGCC	CACCGTTTCC	GTGGTCGGAC	AGTCCGACAC	CAGCGTACTC
151	AAAGGCTACA	TCAACTACGA	CGAAGCCGCC	GTTACCCGCA	ACGGACAGCT
201	CATCAAAGAA	ACGCCGCAAA	CCATCGATAC	GCTCAATATC	CAGAAAAACA
251	AAAATTACGG	TACGAACGAT	TTGAGTTCCA	TCCTCGAAGG	CAATGCCGGC
301	ATCGACGCTG	CCTACGATAT	GCGCGGTGAA	AGCATTTTCC	TGCGCGGTTT
351	TCAAGCCGAC	GCATCCGATA	TTTACCGCGA	CGGCGTGCGC	GAAAGCGGAC
401	AAGTGCGCGG	CAGTACTGCC	AACATCGAGC	GCGTGGAAT	CCTGAAAGGC
451	CCGTCTTCCG	TGCTTTACGG	CCGCACCAAC	GGCGCGGCG	TCATCAACAT
501	GGTCAGCAAA	TACGCCAACT	TCAAACAAAG	CCGCAACATC	GGAGCGGTTT
551	ACGGCTCATG	GGCAAACCGC	AGCCTGAATA	TGGACATTAA	CGAAGTGCTG
601	AACAAAAACG	TCGCCATCCG	TCTCACCAGC	GAAGTCGGGC	GCGCCAATTTC
651	GTTCCGCAGC	GGCATAGACA	GCAAAAATGT	CATGGTTTCG	CCCAGCATTG
701	CCGTCAAAC	CGACAACGGC	TTGAAGTGGA	CGGGGCAATA	CACCTACGAC
751	AATGTGGAGC	GCACGCCCGA	CCGCAGTCCG	ACCAAGTCCG	TGTACGACCG
801	CTTCGGACTG	CCTTACCGCA	TGGGGTTCGC	CCACCGGAAC	GATTTTGTCA
851	AAGACAAGCT	GCAAGTTTGG	CGTTCGGACC	TTGAATACGC	CTTCAACGAC
901	AAATGGCGTG	CCCAATGGCA	GCTCGCCAC	CGCACGGCGG	CGCAGGATTT
951	TGATCATTTT	TATGCAGGCA	GCGAAAATGG	CAACTTAATC	AAACGTAAC
1001	ACGCCTGGCA	GCAGACCGAC	AACAAAACCC	TGTCGTCCAA	CTTAACGCTC
1051	AACGCGGACT	ACACCATCGG	CCGTTTGGAA	AACCACCTGA	CCGTAGGCAT
1101	GGATTACAGC	CGCGAACACC	GCAACCCGAC	ATTGGGTTC	AGCAGCGCCT
1151	TTTCCGCCTC	CATCAACCCC	TACGACCGCG	CAAGCTGGCC	GGCTTCGGGC
1201	AGATTGCAGC	CTATTCTGAC	CCAAAACCGC	CACAAAGCCG	ACTCCTACGG
1251	CATCTTTGTG	CAAAACATCT	TCTCCGCCAC	GCCCCGATTG	AAATTCGTCC
1301	TCGGCGGCCG	TTACGACAAA	TACACCTTTA	ATTCCGAAAA	CAAACTCACC
1351	GGCAGCAGCC	GCCAAATACAG	CGGACACTCG	TTCAGCCCCA	ACATCGGCGC
1401	AGTGTGGAAC	ATCAATCCCG	TCCACACACT	TTACGCCTCG	TATAACAAAG
1451	GCTTCGCGCC	TTATGGCGGA	CGCGGCGGCT	ATTGAGCAT	CGATACGTTG
1501	TCTTCCGCCG	TGTTCAACGC	CGACCCCGAG	TACACCCGCC	AATACGAAAC
1551	CGCGGTGAAA	AGCAGTTGGC	TGGACGACCG	CCTCAGCACT	ACGTTGTCTG
1601	CCTACCAAAT	CGAACGCTTC	AATATCCGCT	ACCGCCCCGA	TCCAAAAAAC
1651	AACCCTTATA	TTTATGCGGT	TAGCGGCAAA	CACCGTTCGC	GCGGCGTGGA

1237

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1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGTAATAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

m761.pep

```

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQITDNLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQT D NKTLSNLT L
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQII PKKLY LRGS LGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAAANLLNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

a761.seq

```

1 ATGAAAATAT CATTTTCATT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCCTGTT GCTGCCGCGG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCCG CCTACGATAT GCGCGCGGAA AGCATTTTCC TGC GCGGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT
451 CCGTCCTCCG TGCTTTATGG GCGTACCAAC GCGGCGGGTG TCATCAACAT
501 GGTCAAGCAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTTCGTG GGCAAACCGC AGCCTGAATA TGACATCAA CGAAGTGCTG
601 AACA AAAACG TCGCCATCCG TCTACCGGC GAAGTCGGGC GCGCCAATTC
651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA
701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG GTACGACCG
801 CTTCCGACTG CTTTACCGCA TGGGGTTTCG CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTTCGGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC
1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGTAA AACACCTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCCCT CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTCTGTC
1301 TCGGCGGCGG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG
1501 TCTTCCGCGG TGTTCAACGC CGACCCGAG TACACCGGCC AATACGAAAC
1551 CGGCGTGAAG AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CCTACCAAAT CGAACGTTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC
1651 AACCTTATA TTTATCGGGT TAGCGGCAAA CACCGTTTCG GCGGCGTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1238

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCAGC
1801 CGAGTGGGCA TCCATTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGSTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYRFLG PYRMGFAHRN DFKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTND NKTLSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSASFASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGLGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

m761.pep	10	20	30	40	50	60
	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVVGQSDTSVLKGYINYDEAA					
a761	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVVGQSDTSVLKGYINYDEAA					
	10	20	30	40	50	60
m761.pep	70	80	90	100	110	120
	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
a761	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
	70	80	90	100	110	120
m761.pep	130	140	150	160	170	180
	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVSKYANFKQSRNI					
a761	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVSKYANFKQSRNI					
	130	140	150	160	170	180
m761.pep	190	200	210	220	230	240
	GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG					
a761	GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG					
	190	200	210	220	230	240
m761.pep	250	260	270	280	290	300
	LKWTGQYTYDNVERTPDRSPTKSVDYRFLGPYRMGFAHRNDFVKDKLQVWVRSLEYAFND					
a761	LKWTGQYTYDNVERTPDRSPTKSVDYRFLGPYRMGFAHRNDFVKDKLQVWVRSLEYAFND					
	250	260	270	280	290	300
m761.pep	310	320	330	340	350	360
	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNAYAQQTNDNKTLSNLTNGDYTIGRFE					
a761	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNAYAQQTNDNKTLSNLTNGDYTIGRFE					
	310	320	330	340	350	360
	370	380	390	400	410	420

1239

m761.pep	NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
a761	NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
	370 380 390 400 410 420
m761.pep	QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
a761	QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
	430 440 450 460 470 480
m761.pep	YNKGFAPYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTLSAYQIERF
a761	YNKGFAPYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTLSAYQIERF
	490 500 510 520 530 540
m761.pep	NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
a761	NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
	550 560 570 580 590 600
m761.pep	RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYNSRNKEVTTLPGFARVDAM
a761	RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
	610 620 630 640 650 660
m761.pep	LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761	LGWNHKNVNVTFAAANLFNQKYWRSDSMPGNPRGYTARVNYRFX
	670 680 690 700

g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

m762.seq

1	ATGAAGTGGT	TATTAAATAT	GATAATGAGA	CCTATTAAAT	TTAGTATGGT
51	AAATACGTTA	TTATTTATTG	TTATATGTAG	TTCATTTTTT	GATCTGCTCG
101	TTCAATTATG	TACAATTTTA	TTTCATAGCC	AAAAAATATA	CTTTATTACA
151	TTATTTTTAT	TATTTATTTT	TAATTTTGTT	ACAAAATCTA	TCTATATGGC
201	AATTATTTAT	CCTATTTTAT	ATTTTTTTAC	GATAAAAAAA	TATTATCCTT
251	ACTCTAGGAA	AGTGATAATT	CTATTATCAT	TAGCATTATC	TATATATTTT
301	AGTTTTATGG	ACTTTTACTT	TTTTTCCATA	TATTCAGATA	ACCTTAGCTA
351	TGAAACGGAG	CCTTTACATT	TATACATCCC	TATTATTATT	AATTTTTTCT
401	CACTTTTAGT	TTCTAATTTT	ATTTTATCTT	TTATCAACAA	GTAA

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

m762.pep

1	MKWLLNMIMR	PIKFSMVNTL	LFIVICSSFF	DLLVQLCTIL	FHSQKIYFIT
51	LFLLFIFNFV	TKSIYMAIIY	PILYFFTIKK	YYPYSRKVII	LLSLALSIYF
101	SFMDFYFFSI	YSDNLSYETE	PLHLIPIII	NFFSLVSNF	ILSFINK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

a762.seq

1	ATGAAGTGGT	TATTAAATAT	GATAATGAGA	CCTATTAAAT	TTAGTATGGT
51	AAATACGTTA	TTATTTATTG	TTATATGTAG	TTCATTTTTT	GATCTGCTCG
101	TTCAATTATG	TACAATTTTA	TTTCATAGCC	AAAAAATATA	CTTTATTACA
151	TTATTTTTAT	TATTTATTTT	TAATTTTGTT	ACAAAATCTA	TCTATATGGC
201	AATTATTTAT	CCTATTTTAT	ATTTTTTTAC	GATAAAAAAA	TATTATCCTT
251	ACTCTAGGAA	AGTGATAATT	CTATTATCAT	TAGCATTATC	TATATATTTT

1240

301 AGTTTATGG ACTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
 351 TGAACCGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCT
 401 CACTTTAGT TTCTAATTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pep

1 MKWLLNMIMR PIKFSMVNTL LFIVICSSEF DLLVQLCTIL FHSQKIYFIT
 51 LFLLFIFNFV TKSIYMAIIY PILYFFTIKK YYPYSRKVII LLSLALSIYF
 101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNE ILSFINK*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSEFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSEFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSMDFYFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSMDFYFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIIINFFSLLVSNEILSFINKX					
a762	PLHLYIPIIIINFFSLLVSNEILSFINKX					
	130	140				

g763.seq not yet found

g763.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
 101 CCTATTTTTC CAAATATATC CTACCGGTTT CACTTTTAC CTTGCCACTA
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
 201 GGGCGAGCAA CATTGCGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG
 251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
 501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
 551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
 601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
 701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
 901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
 1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
 1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGCGGCA AGAACGGGTT
 1201 TTGGAAGACA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACATA
 1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC
 1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
 1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACCGG TATTTGCGGA
 1401 ATAA

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

m763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVTAA HAAEKEAYA QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDISKQIEA
251 IDTANLLARY LPKLERYS LD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQYQYR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

a763.seq

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGCTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTTC CAAATATATC CTACCCGTTT CACTTTTTTAC CTTGCCACTA
151 TCCCTTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTCCGCTG ATTTTCAAGC GTCCATTAC CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGTGGG ACAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACAGTT GAACGACTAC ACCGCGCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTGCGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CCGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCACAATA
1251 CGGCATCCGC AACCAGCTGG AAGTAATACG GGCGCGCAG GAAGTCGCCC
1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGGTAGGG TTGGAACCG TATTTGCGGA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

a763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVTAA HAAEKEAYA QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYS LD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQYQYR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

m763 / a763 99.8% identity in 467 aa overlap

```

          10      20      30      40      50      60
m763.pep  MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          |||||||
a763      MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          10      20      30      40      50      60

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m763.pep	70	80	90	100	110	120
	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAAFLPHVSNANASYQRQPPSISSTRETQ					
a763	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAAFLPHVSNANASYQRQPPSISSTRETQ					
	70	80	90	100	110	120
m763.pep	130	140	150	160	170	180
	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
a763	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
	130	140	150	160	170	180
m763.pep	190	200	210	220	230	240
	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAEI AVLAEKQTYENQLNDY					
a763	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAEI AVLAEKQTYENQLNDY					
	190	200	210	220	230	240
m763.pep	250	260	270	280	290	300
	TDLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
a763	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
	250	260	270	280	290	300
m763.pep	310	320	330	340	350	360
	QNSRYPTVSAHVGYNLYTSSAQNNNDYHYRGKGM SVGVQLNLPLYTGGELSGKIHEAEA					
a763	QNSRYPTVSAHVGYNLYTSSAQNNNDYHYRGKGM SVGVQLNLPLYTGGELSGKIHEAEA					
	310	320	330	340	350	360
m763.pep	370	380	390	400	410	420
	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
a763	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
	370	380	390	400	410	420
m763.pep	430	440	450	460		
	NRLEVIRARQEVAQAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
a763	NRLEVIRARQEVAQAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
	430	440	450	460		

1243

g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```

m764.seq
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAAGTAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CCGGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGAAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GGCGCAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GGCGCAGGAG CAGAAGCTGG TTTCCGTGGG GCGCATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGG GGCATTGCA CAGGATGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGCGA
1001 CCGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GCGGGTGCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

```

m764.pep
1  MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEQAFI PAHLELTDTF
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDGQHVQGE TLAELEAVGT DSDVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRQOTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEK
451 TGKRRVLDYL LSPLQTKLDE SFRER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```

a764.seq (partial)
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAAGTAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CCGGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGAAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GGCGCAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GGCGCAGGAG CAGAAGCTGG TTTCCGTGGG GCGCATCGAG CAGCAGAAAA

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701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACGCGGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 AGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

```

a764.pep (partial)
  1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAFLE PAHLELTDTP
 51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVQKQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

```

m764.pep      10      20      30      40      50      60
MFFSALKSFLSRYITVWRNVWAVRDQLKPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR
|||||
a764          10      20      30      40      50      60
MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR

m764.pep      70      80      90      100     110     120
FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVVKAVHVRDQHVQKQE
|||||
a764          70      80      90      100     110     120
FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETVVVKAVHVRDQHVQKQE

m764.pep     130     140     150     160     170     180
TLAELEAVGTDSDVVQSEQALQAAQLSKRLRYEAVLAALESRTVPHIDMAQARSLGLSDAD
|||||
a764         130     140     150     160     170     180
TLAELEAVGTDSDVVQSEQALQAAQLSKRLRYEAVLAALESRTVPHIDMAQARSLGLSDAD

m764.pep     190     200     210     220     230     240
VQSAQVLAQHQQYQAWAAQDAQLQSALRGHQAEQKLVSVAIEQQKTADYRRL
|||||
a764         190     200     210     220     230     240
VQSAQVLAQHQQYQAWAAQDAQLQSALRGHQAEQKLVSVAIEQQKTADYRRL

m764.pep     250     260     270     280     290     300
RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA
|||||
a764         250     260     270     280     290     300
RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA

m764.pep     310     320     330     340     350     360
LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVIAPDD
|||||
a764         310     320     330     340     350     360
LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD

m764.pep     370     380     390     400     410     420
DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVDHDAVSHEQLGLVYT

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1245

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|||||
a764      DKMDVEVLVLNKDIGFVEQQDAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
              370      380      390      400      410      420

              430      440      450      460      470
m764.pep  AVVSLDKHTLNIDGKAVNLTAGMNVTAETIKTGKRRVLDYLLSPLQTKLDESFREXR
|||||
a764      AVVSLDKHTLNIDGK
              430

```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```

m765.seq
1  ATGTTAAGAT  GCCGTCGGAA  ATCCGTTTGT  GATTCAGACG  GCATTTTTTT
51  GAAATTTAAT  TTTTAAAGGA  GTAAACCTAA  ATATGAAATT  TCCTTCCTTC
101 CTTCTTTTAA  ACGGATACTC  TGCCTGTCGG  CAGTAATCTC  GGTATTGGGG
151 GCTTGTGCGG  TCGTTGCTGA  TGTTTACGGT  CATGATTCCG  CCACAATGAA
201 CGCTGCGGCT  GCCAAAGATT  ATATGAAAAC  GGTGAGTTA  AACAAAGCTG
251 CCGGCAATGT  CGATACCACA  TCCAGAACAG  CCCGCAGGGT  GCAGGCAGTA
301 TTTTCGACGTA  TGCTGCCTTA  TGCCGATGCG  GCAAATAATA  CCAGCCATAA
351 GTTTGACTGG  AAAATGACGG  TTTTCAAAAA  CGATGAGCTG  AACGCGTGGG
401 CAATGCCCGG  TGGAAAAATG  GCGTTTTATA  CGGGGATAGT  CGACAAACTC
451 AAGCTGACCG  ATGACGAAAT  TGCCGCCATT  ATGGGGCATG  AATGACGCA
501 CGCCCTGCAT  GAACACGGTA  AAAATAAGGT  CGGGCAGCAA  ATCTTGACCA
551 ATACGGCGGC  GCAGATAGGC  ACGCAGATTA  TATTAGACAA  AAAACCGGAT
601 ACTAATCCGG  AATTGGTCCG  ATTGGGTATG  GATATTTTGG  GGACGTACGG
651 TCTTACCTTG  CCTTATAGCC  GCAGCTTGGA  AGAAGAAGCC  GATGAGGGGG
701 GAATGATGTT  GATGGCGCAG  GCAGGCTATC  ATCCGGCGGC  CGCTGTCAGG
751 GTTTGGGAAA  AAATGAATCA  GGAAAACGAC  CAAAACGGCT  TTATTTATGC
801 TATTACCTCT  ACTCATCCGA  CAAACAATGC  CCGTATAGAA  AATCTAAAC
851 GGTGTGTGCC  GACCGTTATG  CCGGTTTATG  AGCAAAGTGT  CAGAAATAAG
901 GGGCGCGTTA  ATAAAAACG  TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```

m765.pep
1  MLRCRPKSVL  DSDGIFLKFN  FLRSKPKEI  SFLPSFKRIL  CLSAVISVLG
51  ACVVVADVYG  HDSATMNAAA  AKDYMKTVEL  NKSAGNVDTT  SRTARRVQAV
101 FRRLPYADA  ANNTSHKFDW  KMTVFKNDEL  NAWAMPGGKM  AFYTGIVDKL
151 KLTDEIAAI  MGHEMTHALH  EHGKKNVQOQ  ILTNTAAQIG  TQIILDKKPD
201 TNPELVGLGM  DILGTYGLTL  PYSRSLEEEA  DEGGMMLMAQ  AGYHPAAAVR
251 VWEKMNQEND  QNGFIYAIT  THPTNNARIE  NLKRLLEPTVM  PVYEQSVRNK
301 GRVНКKRRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```

a765.seq
1  ATGTTAAGAT  GCCGTCGGAA  ATCCGTTTGT  GATTCAGACG  GCATTTTTTT
51  GAAATTTAAT  TTTTAAAGGA  GTAAACCTAA  ATATGAAATT  TCCTTCCTTC
101 CTTCTTTTAA  ACGGATACTC  TGCCTGTCGG  CAGTAATCTC  GGTATTGGGG
151 GCTTGTACGG  TCGTTGCTGA  TGTTTACGGT  CAGGATTCCG  CCACAATGAA
201 TGCTGCGGCT  GCCGAAGATT  ATATGAAAAC  GGTGAGTTG  AACAAAGCTG
251 CCGGCAATGT  CGATACTACA  TCCAAAACAG  CCCGTAGGGT  GCAGGCAGTA
301 TTTTCGACGTA  TGTTGCCTTA  TGCCGATGCG  GCAAATAATA  CCGGCCATAA
351 GTTTGACTGG  AAAATGACGG  TTTTCAAAAA  CGATGAGCTG  AACGCGTGGG
401 CAATGCCCGG  CGGGAAAATG  GCGTTTTATA  CGGGGATAGT  CGATAAATT
451 AAGCTGACCG  ATGGCGAAAT  TGCCGCCATT  ATGGGGCATG  AATGACGCA
501 TGCCCTGCAT  GAACACGGTA  AAAATAAGGT  CGGGCAGAAA  ATCTTGACTA
551 ATATGGCGGC  GCAGATAGGC  ACGCAGATTA  TATTAGACAA  AAAACCGGAC
601 ACTAATCCGG  AATTGGTCCG  ATTGGGTATG  GATATTTTGG  GGATGTACGG
651 CATTACCTTG  CCTTATAGCC  GCAGCTTGGA  AGAAGAAGCC  GATGAGGGGG
701 GAATGATGTT  GATGGCGCAG  GCAGGCTATC  ATCCGGCAGC  CGCTGTCAGG
751 GTTTGGGAAA  AAATGAATCA  GGAAAACGAC  CAAAACGGCT  TTATTTATGC
801 TATTACCTCT  ACTCATCCGA  CAAACAATGC  CCGTATAGAA  AATCTAAAC
851 GGTGTGTGCC  GACCGTTATG  CCGGTTTATG  AGCACAGTGT  TAGAAATAAG
901 GGGCGCGTTA  ATAAAAACG  TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```

a765.pep
1  MLRCRPKSVL  DSDGIFLKFN  FLRSKPKEI  SFLPSFKRIL  CLSAVISVLG

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1246

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51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDGEIAAI MGHEMTHALH EHGKKNVQOK ILTNMAAQIG TQIILDKKPD
201 TNPVLVGLGM DILGMYGITL PYSRSLLEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT STHPTNNARIE NLKRLLEPTVM PVYEHSVRNK
301 GRVNKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

	10	20	30	40	50	60
m765.pep	MLRCRPKSVLDS	SDGIFLKFNF	LRSKPKYEIS	FLPSFKRILCL	SAVISVLGAC	AVVADVYG
a765	MLRCRPKSVLDS	SDGIFLKFNF	LRSKPKYEIS	FLPSFKRILCL	SAVISVLGAC	TVVADVYG
	10	20	30	40	50	60
	70	80	90	100	110	120
m765.pep	HDSATMNAAA	AKDYMKTVEL	NKSAGNVDTT	SRTARRVQAV	FRRMLPYADA	ANNTSHKFDW
a765	QDSATMNAAA	AEDYMKTVEL	NKSAGNVDTT	SKTARRVQAV	FRRMLPYADA	ANNTGHKFDW
	70	80	90	100	110	120
	130	140	150	160	170	180
m765.pep	KMTVFKNDEL	NAWAMPGGKM	AFYTGIVDKL	KLTDDEIAA	IMGHEMTHAL	HEHGKNKVGQ
a765	KMTVFKNDEL	NAWAMPGGKM	AFYTGIVDKL	KLTDGEIAA	IMGHEMTHAL	HEHGKNKVGQ
	130	140	150	160	170	180
	190	200	210	220	230	240
m765.pep	ILTNMAAQIG	TQIILDKKPD	TNPVLVGLGM	DILGTYGLT	LPYSRSLLEEA	DEGGMMLMAQ
a765	ILTNMAAQIG	TQIILDKKPD	TNPVLVGLGM	DILGMYGIT	LPYSRSLLEEA	DEGGMMLMAQ
	190	200	210	220	230	240
	250	260	270	280	290	300
m765.pep	AGYHPAAAVR	VWEKMNQEND	QNGFIYAIT	STHPTNNARIE	NLKRLLEPTV	MPVYEQSVRNK
a765	AGYHPAAAVR	VWEKMNQEND	QNGFIYAIT	STHPTNNARIE	NLKRLLEPTV	MPVYEHSVRNK
	250	260	270	280	290	300
	310					
m765.pep	GRVNKKRRRX					
a765	GRVNKNRRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTTCGG TACATTGCCA TCATTTCGAT CCTTGTTAT TGAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCTG
301 GGTTCGAAAT ATCAGGCAAA CTCGTCTGTG TTAAAGCAG TTTACGAACA
351 AAAAATCCGT TTGAAAACA GGGCTGTTGC CGGAAATGG GCTTTATCTC
401 AAAAAGGTTT TGACGGCAAA AACTGATGC GCGCCTATGA TTCCCCGAA
451 GCTGCCGCCG TCGATTAAA AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPOEQP GKIEVLEFFG
51  YFCVHCHHFD PLLKLGLKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

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1247

101 GLKYQANSV FKA VYEOKIR LENRAVAGKW ALSQKGF DGK KLMRAYDSPE
 151 AAAVALKMQK LTEQY GIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq

```

1   ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCTCA AGAACAGTCG GGTAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTCTGCGG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATG CCTATTGAG GACGGAGCAC GTGGCTGGC
251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CCGCTGCCGT CAATTGTGCG
301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGAAAACA GGTGCGTTGC CGAAAAATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AAACGTATGC GCGCCTATGA TTCCCCGAA
451 GCTGCCGCCG CCGCATTAAA AATGCAGAAA CTGACGGAAC AATACCGCAT
501 CGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGAATT GGTTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep

```

1   MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG
51  YFCVHCHHFD PLLKLKGKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVNLS
101 GLKYQANPAV FKA VYEOKIR LENRSVAGKW ALSQKGF DGK KLMRAYDSPE
151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767	95.8% identity in 214 aa overlap																												
	<table border="0"> <tr> <td></td> <td>10</td> <td>20</td> <td>30</td> <td>40</td> <td>50</td> <td>60</td> </tr> <tr> <td>g767.pep</td> <td>MKFKHLLPLL</td> <td>LSAVLSAQAY</td> <td>ALTEGEDYLV</td> <td>LDKPIPQEQS</td> <td>GKIEVLEFFG</td> <td>YFCVHCHHFD</td> </tr> <tr> <td>m767</td> <td> </td> <td> </td> <td> </td> <td> </td> <td> </td> <td> </td> </tr> <tr> <td></td> <td>10</td> <td>20</td> <td>30</td> <td>40</td> <td>50</td> <td>60</td> </tr> </table>		10	20	30	40	50	60	g767.pep	MKFKHLLPLL	LSAVLSAQAY	ALTEGEDYLV	LDKPIPQEQS	GKIEVLEFFG	YFCVHCHHFD	m767								10	20	30	40	50	60
	10	20	30	40	50	60																							
g767.pep	MKFKHLLPLL	LSAVLSAQAY	ALTEGEDYLV	LDKPIPQEQS	GKIEVLEFFG	YFCVHCHHFD																							
m767																													
	10	20	30	40	50	60																							
	<table border="0"> <tr> <td></td> <td>70</td> <td>80</td> <td>90</td> <td>100</td> <td>110</td> <td>120</td> </tr> <tr> <td>g767.pep</td> <td>PLLLKLKGKAL</td> <td>PSDYLRTEH</td> <td>VVWRPEMLGL</td> <td>ARMAAAVKLS</td> <td>GGLKYQANSV</td> <td>FKAVYEOKIR</td> </tr> <tr> <td>m767</td> <td> </td> <td> </td> <td> </td> <td> </td> <td> </td> <td> </td> </tr> <tr> <td></td> <td>70</td> <td>80</td> <td>90</td> <td>100</td> <td>110</td> <td>120</td> </tr> </table>		70	80	90	100	110	120	g767.pep	PLLLKLKGKAL	PSDYLRTEH	VVWRPEMLGL	ARMAAAVKLS	GGLKYQANSV	FKAVYEOKIR	m767								70	80	90	100	110	120
	70	80	90	100	110	120																							
g767.pep	PLLLKLKGKAL	PSDYLRTEH	VVWRPEMLGL	ARMAAAVKLS	GGLKYQANSV	FKAVYEOKIR																							
m767																													
	70	80	90	100	110	120																							
	<table border="0"> <tr> <td></td> <td>130</td> <td>140</td> <td>150</td> <td>160</td> <td>170</td> <td>180</td> </tr> <tr> <td>g767.pep</td> <td>LENRAVAGKW</td> <td>ALSQKGF DGK</td> <td>KLMRAYDSPE</td> <td>AAAVALKMQK</td> <td>LTEQY GIDST</td> <td>PPTVIVGGKYR</td> </tr> <tr> <td>m767</td> <td> </td> <td> </td> <td> </td> <td> </td> <td> </td> <td> </td> </tr> <tr> <td></td> <td>130</td> <td>140</td> <td>150</td> <td>160</td> <td>170</td> <td>180</td> </tr> </table>		130	140	150	160	170	180	g767.pep	LENRAVAGKW	ALSQKGF DGK	KLMRAYDSPE	AAAVALKMQK	LTEQY GIDST	PPTVIVGGKYR	m767								130	140	150	160	170	180
	130	140	150	160	170	180																							
g767.pep	LENRAVAGKW	ALSQKGF DGK	KLMRAYDSPE	AAAVALKMQK	LTEQY GIDST	PPTVIVGGKYR																							
m767																													
	130	140	150	160	170	180																							
	<table border="0"> <tr> <td></td> <td>190</td> <td>200</td> <td>210</td> </tr> <tr> <td>g767.pep</td> <td>VIFNNGFDGG</td> <td>VHTIKELVAK</td> <td>VREERKRQTP</td> </tr> <tr> <td>m767</td> <td> </td> <td> </td> <td> </td> </tr> <tr> <td></td> <td>190</td> <td>200</td> <td>210</td> </tr> </table>		190	200	210	g767.pep	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	m767					190	200	210												
	190	200	210																										
g767.pep	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP																										
m767																													
	190	200	210																										

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq

```

1   ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCTCA AAAACAGTCG GGCAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTCTGCGG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAATTGGG
201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGCTGGC
251 AGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCCGT CAAGCTGTCA
301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGAAAACA GGTGCGTTGC CGAAAAATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AAACGTATGC GCGCCTACGA CTCTCCTGCG

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1248

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451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

a767.pep

```

1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPKQS GKIEVLEFFG
51 YFCVHCHHFD PLLKLKGLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
101 GLKYQANPAV FKAIVEQKIR LENRSVAEKW ALSQKGFQDG KLMRAYDSPA
151 AAAAASKMQQ LTEQYRIDST PTVVVGKRYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

m767/a767 96.7% identity in 214 aa overlap

a767.pep	10	20	30	40	50	60
	MKLKHLLPLL LSAVLSAQAYALTEGEDYLV LDKPIPKQS GKIEVLEFFGYFCVHCHHFD					
m767	MKLKHLLPLL LSAVLSAQAYALTEGEDYLV LDKPIPKQEQSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
a767.pep	70	80	90	100	110	120
	PLLLKLGKALPSDAYLRTEHV VVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVEQKIR					
m767	PLLLKLGKALPSDAYLRTEHV VVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVEQKIR					
	70	80	90	100	110	120
a767.pep	130	140	150	160	170	180
	LENRSVAEKWALSQKGFQDGK KLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKRYR					
m767	LENRSVAGKWALSQKGFQDGK KLMRAYDSPEAAAAALKMQKLTEQYRIDSTPTVIVVGKRYR					
	130	140	150	160	170	180
a767.pep	190	200	210			
	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

g768.seq

```

1 ATGAATATCA AACAAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51 TGCCACGCAG GCAGCCCGCG AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

g768.pep

```

1 MNIKOLITAA LIASAAFATQ AAPQKPVSA QTAOHSAVWI DVRSEQEFSE
51 GHLHNAVNI PVDQIVRIYE AAPDKDTPVN LYCRSGRRAE AALQELKKA
101 YTNVANHG GYEDLLKKGMK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

m768.seq

```

1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51 TGCCCGCGCAG GCAGCCCGCG AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATCCGCG CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGGCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC

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1249

251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep

1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHLHNAVNI PVDQIVRRIE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGMMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAALIASAAFATQAAPQKPVSAQAQHS	AVWIDVRSEQEFSE	GHLHNAVNI			
m768	MNIKHLITAAALIASAAFAAQAPQKPVSAQAQHP	AVWIDVRSEQEFSE	GHLHNAVNI			
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	VDQIVRRIEAAAPDKDTPVNL	YCRSGRRAEAAALQELKKAG	YTNVANHGGYEDLLKKGMMKX			
m768	VDQIVRRIEAAAPDKDTPVNL	YCRSGRRAEAAALQELKKAG	YTNVANHGGYEDLLKKGMMKX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq

1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCGGCC CAAACCGCGC
 101 AACATTCAGC CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
 201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC
 301 TATACGAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep

1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSVWI DVRSEQEFSE
 51 GHLHNAVNI PVDQIVRRIE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGMMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAAALIASAAFAAQAPQKPVSAQAQHS	AVWIDVRSEQEFSE	GHLHNAVNI			
m768	MNIKHLITAAALIASAAFAAQAPQKPVSAQAQHP	AVWIDVRSEQEFSE	GHLHNAVNI			
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	VDQIVRRIEAAAPDKDTPVNL	YCRSGRRAEAAALQELKKAG	YTNVANHGGYEDLLKKGMMKX			
m768	VDQIVRRIEAAAPDKDTPVNL	YCRSGRRAEAAALQELKKAG	YTNVANHGGYEDLLKKGMMKX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq

```

1   TTGATAATGG TTATTTTTTA TTTTATTTT TGTGGGAAGA CATTTATGCC
51  TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAAGaAAC ACCgtgCGAA CCGGATTTGA GAAGCCGTCC CGAGTTCAGG
151 CTTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGGAGAAGG TACCGGGGCA
201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCCGA ATTGTTGTCG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 AGGGCAGGGT GAAGGAGGCG GTTTCCTATT ACCGGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGGTAAAC GGCGGTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCAGAAAC GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
751 GAGAAAAAAT GGTTCGTGAA AAACGGCTGG TACACGACGG CGGGCGGCGA
801 CGTGTCGGCG AGGGTTTATC CGGGGAATAA GAAATTCAAC GATATGACGG
851 CAGGTGTTTT CGGCGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 CGCCAACGGC GCACGCCTTT ATTTCAACCG TTGGCAAACC CCGAGATGGC
1001 AAACGCTGTC TTCGGCGGAG TGGGGGCGTT TGAAGAATAC GCGCCGGGCG
1051 CGTTCGACA ATACCCATTT GCAAATTTCC AATTCGCTGG TGTTTTACCG
1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTAC CGCGAGCGCA
1151 ACCCGCCGCA CCGTGGCGAC AATTCAACC GTTACGGCCT GCGCTTTGCC
1201 TGGGGGCGAG AATGGGGCGG CAGCGGCCTG TCTTCGCTGT TCCGCCTCGG
1251 CGTGGCGAAA CGGCATTATG AAAAAACCGG CTTCTTCAGC AGTTTTAAAG
1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCCTTGAG CCTTTGGCAC
1351 CGGGCATTGC ATTTCAAAGG CATCACGCCG CGCCTGACGC TGTCGCACCG
1401 CGAAACGTGG AGCAACGATG TGTTTAACGA ATACGAGAAA AACAGGCGCT
1451 TTGTCGAGTT TAACAAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep

```

1   LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAEETPCE PDLRSRPEFR
51  LHEAEVKPID REKVPQVRE KGVQLQVDGE TLLKNPELLS RAMYSAVVSN
101 NIAGIRVILP IYLQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRQ NEAADQFDR LKTEDLPPQL MEQVELYRKA
201 LERERDAWVN GGFSVTREHN INQAPKQQQY GNWTFPKQVD GTAVNYRFGA
251 EKKWSLKNGW YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRTY GNDAYSANG ARLYFNRWQT PRWQTLSSAE WGRCLKNTRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
401 WQEWGSSGL SSLFRLGVAK RHYEKPFFS SFGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq

```

1   TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGCAGGT
201 GCGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCTCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGAT TGCCGCCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCAGCAT TGTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAAAC GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGCTGGTAC ACGACGGCGG GCGGCGACGT
801 GTCCGCGAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CCGCATCGGT TTGCGCGACC GGCAGAAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGCGAGTGG GGGCGTTTGA AGAATACGGC CCGGCGCGCT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TCGCGGCCAA TATTGGATGG GCGGTTTGA TTTTACCAG GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTTGC GCCTCGGCGC

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1251

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1251  GCGGAAACGG  CATTATGAAA  AACCCGGCTT  TTTACGCGGT  TTTAAAGGGG
1301  AAAGGCGCAG  GGATAAGAA  TTGAACACAT  CCTTGAGCCT  TTGGCACCGG
1351  GCATTGCATT  TCAAAGGCAT  CACGCCGCGC  CTGACGTTGT  CGCACCGCGA
1401  AACGCGGAGT  AACGATGTGT  TCAACGAATA  CGAGAAAAAT  CGGGCGTTTG
1451  TCGAGTTTAA  TAAACGTTC  TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

```

m769.pep
  1  LIMVIFYFCG KTFMPARNRW MLLPLLLASA AYAETPREP DLRSRPEFRL
 51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101  IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151  PDAPAVRMRL AALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201  RERDAWKVNG GFSVTREHNI NQAPKRQQYG KWTFFPKQVDG TAVNYRLGAE
251  KKWSLKNQWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301  AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWOTLSSAEW GRLKNTRRAR
351  SDNTHLQISN SLVFYRNARQ YWMGGGLDFYR ERNPADRGDN FNRYGLRFAW
401  GQEWGSGSLG SLLRLGAAKR HYEKPGFFSG FKGERRRDKL LNTSLSLWHR
451  ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

```

m769/g769    95.1% identity in 492 aa overlap

          10      20      30      40      50      59
g769.pep    LIMVIFYFYFCGKTFMPARNRWMLL-PLLASAAYAETPCEPDLSRPEFRLHEAEVKPI
          |||||  |||||  |||||  |||||  |||||  |||||
m769        LIMVIFY--FCGKTFMPARNRWMLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPI
          10      20      30      40      50

          60      70      80      90     100     110     119
g769.pep    DREKVPQGVREKKGKVLQVDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQD
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        DREKVPQGVREKKGKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQD
          60      70      80      90     100     110

          120     130     140     150     160     170     179
g769.pep    KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAAADQFD
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFD
          120     130     140     150     160     170

          180     190     200     210     220     230     239
g769.pep    RLKTEDLPQQLMEQVELYRKALRERDAWKVNGGFSVTREHNNINQAPKQQQYGNWTFPKQV
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        RLKAENLPPQQLMEQVELYRKALRERDAWKVNGGFSVTREHNNINQAPKQQYQKWTFFPKQV
          180     190     200     210     220     230

          240     250     260     270     280     290     299
g769.pep    DGTAVNYRFGAEKKWSLKNQWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        DGTAVNYRLGAEEKWSLKNQWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA
          240     250     260     270     280     290

          300     310     320     330     340     350     359
g769.pep    GLAVFHERRTYGNDAYSANGARLYFNRWQTPRWQTLSSAEWGRLKNTRRARSNDNTHLQI
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        GLAVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQI
          300     310     320     330     340     350

          360     370     380     390     400     410     419
g769.pep    SNSLVFYRNARQYWTGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLRLGVA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769        SNSLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLRLGAA
          360     370     380     390     400     410

          420     430     440     450     460     470     479
g769.pep    KRHYEKPFFSSFKGERRRDKESDTSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE
          |||||  |||||  |||||  |||||  |||||  |||||  |||||

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1252

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m769      KRHYEKPFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

          480      490
g769.pep  KNRAFVEFNKTFX
          |||||
m769      KNRAFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51 AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGAT TGTGCGCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG CCGCGGCGAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGCGAGG GTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCCG CGGCATCGGT TTTGCCGACC GGCAGCAAAG TCGCGGCGTG
901 GCAGTGTTCC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGCGCGA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGCGAGTGG GGGCGTTTGA AGAATACGCG CCGGCGCGCT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTGTC GCCTCGGCGC
1251 GCGGAAACGG CATTATGAAA AACC CGGCTT TTTACGCGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLLPLLASA AYAETPREP DLRSRPEFRL
51 HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQDDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVMRML AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NOAPKROQYG KWTFPKQVDG TAVNYRLGAE
251 KKWSLKNWGY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGGSGLS SLLRLGAAGR HYEKPFFSG FKGERRRDKL LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

```

m769/a769  99.8% identity in 490 aa overlap

          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90      100     110     120
a769.pep  EKVPQVREK GKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQDDKM

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1253

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|||||
m769      EKVPQGVREKGVQLIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQDQDKM
              70          80          90          100         110         120

              130         140         150         160         170         180
a769.pep   LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
|||||
m769      LALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
              130         140         150         160         170         180

              190         200         210         220         230         240
a769.pep   KAENLPPQLMQVELYRKALRERDAWKVNGGFSVTREHNINQAPKROQYGKWTFFPKQVDG
|||||
m769      KAENLPPQLMQVELYRKALRERDAWKVNGGFSVTREHNINQAPKROQYGKWTFFPKQVDG
              190         200         210         220         230         240

              250         260         270         280         290         300
a769.pep   TAVNYRLGAEEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
|||||
m769      TAVNYRLGAEEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
              250         260         270         280         290         300

              310         320         330         340         350         360
a769.pep   AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRKLNTRRARSNDNTHLQISN
|||||
m769      AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRKLNTRRARSNDNTHLQISN
              310         320         330         340         350         360

              370         380         390         400         410         420
a769.pep   SLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLLRLGAAGR
|||||
m769      SLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLLRLGAAGR
              370         380         390         400         410         420

              430         440         450         460         470         480
a769.pep   HYEKPGFFSGFGKERRRKELNTSLSLWHRALHFKGITPRLTSLSHRETRSDNVFNEYEKN
|||||
m769      HYEKPGFFSGFGKERRRKELNTSLSLWHRALHFKGITPRLTSLSHRETRSDNVFNEYEKN
              430         440         450         460         470         480

              490
a769.pep   RAFVEFNKTFX
|||||
m769      RAFVEFNKTFX
              490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCGG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCGC GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC ACGCGCGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTTACAGCG
401 ATAAAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCACGGG GTGCAAGCGG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTC CAACCCGATA AAAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1  MNRLLLLSAA VLPTACGSGE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKRGTGFA FKSQRIVRY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FGSIGIPQTDG VQADTSGKLL AGACIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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101	TGGGCAAAAA	CGACCGTATC	GAAGTGAAG	GATTCGACGA	TCCCGACGTT
151	CAAGGGGTTC	GCTGTATAT	TCGCTATCGA	AAAAAAGCGC	GCTGTGAAGTA
201	ATATGGTCAAT	TTGGAAGAAG	ACGCGTCCGA	CGCATCGGTT	TCGTGGCGTTC
251	AGACGGCATC	TTCGATTTCT	TTTGACGAAA	CCGCCGTGCG	CAAACCGAAA
301	GAAGTTTTC	AACACGGTGC	GAGCTTCGCG	TTCAAGAGCC	GGCAGATTGT
351	CGGTTATTAC	GACCCCAAAC	CAAAACCTT	CGCCTATTTG	GTGTACAGCG
401	ATAAAATCAT	CCAAGGCTCG	CCGAAAAATT	CCTTAAGCGC	GGTTTCTGT
451	TTCGGCGGCG	GCATACCGCA	AACCGATGGG	GTGCAAGCCG	ATACTTCCGG
501	CAACCTGCCT	GCCGGCGCCT	GCATGATTTC	CAACCCGATA	GAAATCTCG
551	ACAAACGCTG	A			

m770.pcp

a770.seq

a770.pep

```

1  MNRLLLLSAA  VLLTACGSGE  TDKIGRASTV  FNILGKNDR1  EVEGFDDPDV
51  QGVACYISYA  KKGGLKEMVN  LEEDASDASV  SCVQTASSIS  FDETAVRKPK
101 EVFKHGASFA  FKSROIYRYY  DPKRKTFAYL  VYSPDKIIQS  PKNSLSAVSC

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1255

151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPDKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

a770.pep	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFD	DPDVQGVACYISYA
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFD	DPDVQGVACYISYA
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA	VRKPKVEVFKHGASFAFKSRQIVRYY
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA	VRKPKVEVFKHGASFAFKSRQIVRYY
a770.pep	DPKRKTFAYLVYSDKIIQGSFKNLSAVSCF	GGGIPQTDGVQADTSGNLLAGACMISNPI
m770	DPKRKTFAYLVYSDKIIQGSFKNLSAVSCF	GGGIPQTDGVQADTSGNLLAGACMISNPI
a770.pep	ENPDKRXX	
m770	ENLDKRXX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

1	ATGGATTAT	TATCGGTTTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTGGC
51	GGTGTGACG	ATGCTGCTTT	TGGCGGCAGT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCACCTT	CACGCCCGAA	AACATCCGCA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACCC	ACCGGAAAT	CTCGTTTGAT	GCGGATATAC	GGCGCAGGCT
201	TCTGCCCCGC	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	ACGGCGGCCG	GGTCGCCGTT	TCCGTCAAAG	AAACCAAAAT	CGGATTGAGC
301	TGGAATAACC	TGTGGTCGGA	TCGGATACAG	GTTGAAAAAT	GGGTGGTTTC
351	GGGTGCGGAT	CTTGCCCTGA	CGCGCGACAG	AAACGGCGCT	TGGAACATCC
401	AAGACCTGTT	CGACGGCGCG	AAACACTCCG	CCTCAGTCAA	CCGCATTATC
451	GTCGAAAACA	GCACCGTCCG	CCTCAATTTC	CTGCAGCAAC	AGCTTATCCT
501	GAAGGAAATC	AGCCTCAACC	TGCAATCCCC	CGATTTCGTC	GGGCAGCAGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGGAGAA	AGCTGTCCGT	CCCGTGGAAA
601	AGCAGGGGGC	TGTTCCCTTC	AGACGGCATC	GGCAGGCCCG	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATCACCATTT
701	CCACCACCGG	CAGCCCTTCT	GTCCGCTTCA	ACGCCGGCGG	AGCGGATGCC
751	GCCGGCCTCG	GCCTGCGTGC	AGACACTTCC	TTCCGCAACC	TCCACCTGAC
801	CGCGCAATC	CCCGCACTGG	CACTCAAAAA	CAACAGCATC	AAAACCGGCA
851	CGGTCAACGG	CACGTTTACC	GCCGGCGGCG	AATATGCCCG	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAAC	ACCGCGCCTT	CAAACCAATT
1001	TCTCCCTCGG	CTCGCCGTTG	GTTTGGAGTC	GGGACAACGG	GCTGGACGCC
1051	CCGCGCCTGC	ACATATCGAC	CCTTCAGGAT	ACCGTCGACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCATA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	ACCCGTTGCC
1201	GCAAAATTC	AATATACGCG	GGAAGGCGCA	CCGCACCTGG	AAGCCGCCGC
1251	CGCGCTGCAA	AAATTAAACC	TCGCCCCCTA	TCTTGACGAA	TTTCGGCAAC
1301	AAAACGGCAA	AATATTCCCC	GACATCCTCG	GCAGGCTGTC	CGGCAACGTC
1351	GAGGCACACC	TCAAAATCGG	CAGCATCCAA	CTCCCCGGCT	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGACCATATC	GCGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACACCC	GTCCCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	TGCGGTCATC	GACCTGACCG	CAAGCGGCGA	AAACCGCAAA
1651	CAGCTTATCC	GCTCGCTGCA	AGGCAGCCTG	TCGCTGAATA	TTTCCAACGG
1701	CGCGTGGCAC	GGCATCGATA	TGGACAGCAT	TTTAAAAAAC	GGCCTTTCCG

1256

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1751  GGAAATCTC  GGGCAGCACA  CCCTTCTACC  GATTCACGCT  CAACAGCGAA
1801  ATTTAGACG  GCATCAGCCG  CCACATCGAT  ACCGAATCT  TCTCCGACAG
1851  CCTCTATGT  ACCAGCAACG  GCTATACCAA  TCTGGATACG  CAGGAATTGT
1901  CTGAAGATGT  CCTATCCGC  AACGCCGTCC  ATCCGAAAAA  CAAACCGATT
1951  CCCTGAAAA  TCACCGGTAC  GGTGGACAAG  CCGTCCATTA  CCGTCGATTA
2001  CGGCAGGCTG  ACCGGCGGCA  TCAATTCGCG  CAAAGAGAAA  CAGAAAATCC
2051  TCGAAGACAC  CCTGCTGGAA  CAATGGCAGT  GGCTCAAACC  TAAAGAACCG
3051  TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

g771.pep

```

1  MDLLSVFHKY  RLKYAVAVLT  MLLLAAVGLH  ASVYRTFTPE  NIRSRLQQSI
51  AHTRKISFD  ADIRRRLLPR  PTVILKNLTI  TEPDGGRRVAV  SVKETKIGLS
101 WKNLWSDRIQ  VEKWVVSAD  LALTRDRNGA  WNIQDLFDGA  KHSASVNRII
151 VENSTVRLNF  LQQQLILKEI  SLNLQSPDSS  GQQFESSGIL  VWRKLSVPWK
201 SRGLFLSDGI  GTPEISPFHF  EASTSLDGHG  ITISTTGSPS  VRFNAGGADA
251 AGLGLRADTS  FRNLHLTAQI  PALALKNNSI  KTGTVNGTFT  AGGEYARWDG
301 SFKLDKANLH  SGIANIGNAE  ISGSFKTPRL  QTNFSLGSPL  VWSRDNLDA
351 PRLHISTLQD  TVDRLPQPRF  ISRLDGSLSI  PNLQNWNAEL  NGTFDRQPVA
401 AKFKYTREGA  PHLEAAAAAQ  KLNLPAPLYD  FRQONGKIFP  DILGRLSGNV
451 EAHKIGSIQ  LPGLQLDDME  TYLHADKDHI  ALSRFKSGLY  GGHTEGGISI
501 ANTRPATYRL  QQNASNIQIQ  PLLQDLFGFH  SFSNGDAVI  DLTASGENRK
551 QLIRSLQSL  SLNISNGAWH  GIDMDSILKN  GLSGKISGST  PFYRFTLNSE
601 ISDGISRHD  TELFSDSLYV  TSNGYTNLDT  QELSEDVLIR  NAVHPKNKPI
651 PLKITGTVDK  PSITVDYGR  TGGINSRKEK  QKILEDTLLE  OWQWLKPKPE
701  *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

m771.seq

```

1  ATGGATTTAT  TATCGGTTTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTGGC
51  CGTGCTGACG  ATACTGCTTT  TGGCGGCAGT  CGGGCTGCAC  GCTTCCGTAT
101 ATCGCACCTT  CACGCCTGAA  AACATCCGCA  GCCGCCTACA  ACAAGCATT
151 GCACACACAC  ACCGGAATAT  CTCGTTTGAT  GCGGACATTC  AGCGCAGGCT
201 CCTGCCCCGG  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251 CGCGCGACCA  GACTGCCGTT  TCCGTCCAAG  AAACCAAAT  CGGATTGAGC
301 TGGAAAAACC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351 GAGTGCAGGA  CTTGCCCTGA  CGCGCGACGG  GAAAGGTGTT  TGGAACATCC
401 AAGACTGTAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATATC
451 GTCGAAAAAC  GCACCGTCCG  CCTCAATTTT  CTGCAGGAAC  AGCTTATCCT
501 GAAGGAAATC  AACCTCAACC  TGCAATCCCC  CGATTCTGTC  GGGCAGCCGT
551 TTGAAAGTTC  GGGCATACTG  GTTTGGGGAA  AGCTGTCCGT  CCCGTGAAA
601 AGCAGGGGGC  TGTTCCTTTC  AAACGGCATC  GGCCCGCCCG  AAATCTCACC
651 GTTCCATTTT  GAAGCTTCCA  CTTCGCTGGA  CGGACACGGC  ATTACCATTT
701 CCACCACCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751 CCGGGCCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801 CGCCCAATC  CCCGCGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851 CCGTCAACGG  CGCATTATAC  GCCGGCGCGC  AATATGCCCG  ATGGGACGGT
901 TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951 CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001 TCTCCCTCAA  TTCGCCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGCG
1051 CCGCGCCTGT  ATGTATCGAC  CCTTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101 ACCCGGTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151 AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCGCCA  AACCGTTGCC
1201 GCGAAATTC  GATACACACA  TGAAGACGCA  CCGCATCTGG  AAGCCGCCGT
1251 CGCACTGCAA  AAATTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301 AAAACGGCAA  AATATTTCCC  GACACCCTCG  CCAAGCTGTC  CGGCGACATC
1351 GAGGCGCACC  TGAATAATCG  AAAAGTCCAA  CTTCCCGGCC  TGCAACTGGA
1401 CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGGCCATATC  GCGCTCAGCC
1451 GTTTCAAGTC  AGGGCTTTAC  GGCGGCCATA  CCGAAGCGCG  CATCAGCATC
1501 GCCAACACCC  GTCCCGCCAC  TTACCGCCTG  CAACAGAAATG  CAAGCAACAT
1551 CCAAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601 GCAACGGGCA  CGCGGTATC  GACCTGACCG  CGGGCGGCGA  AACCCGAAAA
1651 GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGCTAAATA  TTTCCACGG
1701 TGCAATGGCA  GGTATCGACA  TGGACAATAT  CCTGAAAAAC  GGCATTTCGG
1751 GCAAACTGCG  CGACAATGCC  GCACCCAGCA  CACCCTTCCA  CCGATTCAAC
1801 CTCAACAGCG  AAATTTGAGA  CGGCATCAGC  CGCCACATCG  ATACCGAACT
1851 CTTCTCCGAC  AGCCTCTATG  TTACCAGCAA  CGGCTATACC  AATCTGGATA
1901 CGCAGGAATT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CCATCCGAAA
1951 AACAAACCGA  TTCCCTGAA  AATCACCAGC  ACGGTGGACA  AACCGTCCAT
2001 TACCGTCGAT  TACGGCAGGC  TGACCGGCGG  CATCAATTTC  CGCAAAGAGA
2051 AACAGAAAA  CCTCGAAGAC  ACCCTGCTGG  AACAAATGGCA  GTGGCTCAAA
2101 CCTAAAGAAC  CGTA

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1257

This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

```
m771.pep
1  MDLLSVFHKY RLKYAVAVLT ILLLAAGVLH ASVYRTFTPE NIRSRLQQSI
51  AHTHRKISFD ADIQRLLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFSLNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
401 AKFRYTHEDA PHLEAAVALQ KNLNTPYLDD VRQONGKIFP DTLAKLSGDI
451 EAHLKIGKVQ LPGLQLDDME TYLHADKGGH ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGSL SLNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRET
601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTQELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
701  PKEP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

```
m771/g771 90.3% identity in 704 aa overlap
              10      20      30      40      50      60
g771.pep  MDLLSVFHKYRLKYAVAVLTMLLLAAGVLHASVYRTFTPENIRSRLQQSI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771      MDLLSVFHKYRLKYAVAVLTILLAAAGVLHASVYRTFTPENIRSRLQQSI
          10      20      30      40      50      60

              70      80      90      100     110     120
g771.pep  ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771      ADIQRRLPRPTVILKNLTITEPGGDQTAVSVQETKIGLSWKNLWSDQIQIEK
          70      80      90      100     110     120

              130     140     150     160     170     180
g771.pep  LALTRDRNGAWNIQDLFDGAKHSASVNRIIVENSTVRLNFLQQLILKEIS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771      LALTRDRNGAWNIQDLFDGAKHSASVNRIIVENSTVRLNFLQEQILKEINL
          130     140     150     160     170     180

              190     200     210     220     230     240
g771.pep  GQQFESSGILVWRKLSVPWKSRLGLFSLDGIGTPEISPFHFEASTSLDGHG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771      GQQFESSGILVWGLSVWKSRLGLFSLNGIGPPEISPFHFEASTSLDGHG
          190     200     210     220     230     240

              250     260     270     280     290     300
g771.pep  VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771      VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAG
          250     260     270     280     290     300

              310     320     330     340     350     360
g771.pep  SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPVWSRDNGLDAPRL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771      SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAP
          310     320     330     340     350     360

              370     380     390     400     410     420
g771.pep  TVDRLPQPRFISRLDGSLSIPNLQNWNAELNGTFDRQPVAAKFKYTREGAP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771      TVNRLPQPRFISRLDGSLSVNLQNWNAELNGTFDRQTVAAKFRYTHEDAP
          370     380     390     400     410     420

              430     440     450     460     470     480
g771.pep  KLNLAAPYLDEFQONGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMET
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771      KLNLTPLYDDVRQONGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQLDDMET
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
          KLNLTPLYDDVRQONGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQLDDMET
```

1258

	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG---STPFYRFT					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

a771.seq

```

1  ATGGATTAT  TATCGGTCTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTAGC
51  CGTGTGACG  ATACTGCTTT  TGGCGGCAAT  CGGGCTGCAC  GCTTCCGTAT
101  ATCGCATCTT  CACACCTGAA  AACATCCGAA  GCCGCCTCCA  ACAAGCATT
151  GCCATACGCG  ACCGGAATAT  CTCGTTTGAT  GCGGATATAC  AGCGCAGGCT
201  TCTGCCCCGG  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251  GCGGCGACCG  GACTGCCGTT  TCCGTCCAAG  AAACCAAAAT  CGGATTGAGC
301  TGGAAAAACC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351  GAGTGCAGAA  CTTGCCCTGA  CGCGCGACGG  GAAAGGTGTT  TGGAACATCC
401  AAGACCTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATTATC
451  GTCGAAAAAC  GCACCGTCCG  CCTCAATTTC  CTGCAGGAAC  AGCTTATCCT
501  GAAGGAAATC  AACCTCAACC  TGCAATCCCC  CGATTGCTCG  GGGCAGCCGT
551  TTGAAAGTTC  GGGCATACTG  GTTTGGGGAA  AGCTGTCCGT  CCCGTGGAAA
601  AGCAGGGGGC  TGTTCCTTTC  AGACGGCATC  GGCACGCCCA  AAATCTCACC
651  GTTCCATTTT  GAAGCTTCCA  CTTGCTGGA  CGGACACGGC  ATTACCATTT
701  CCACCACCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751  GCCGCGCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801  CGCCCAAATC  CCTACGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851  CCGTCAACGG  CGCATTTACC  GCCGCGCGCG  AATATGCCCA  ATGGGACGGT
901  TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951  CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001  TCTCCCTCAA  TTCGCCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGGG
1051  CGCGCCTGT  ATGTATCGAC  CCTTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101  ACCCCGTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151  AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCGCCA  AACCCTTGCC
1201  GCGAAATTCA  GATACACACA  TGAAGACGCA  CCGCATCTGG  AAGCCGCCGT
1251  CGCACTGCAA  AAATTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301  AAAACGGCAA  AATATTTCCT  GACACCTTCG  CCAAGCTGTC  CGGCGACATC
1351  GAGGCGCACC  TGAAAATCGG  AAAAGTCCAA  CTTCCCGGCC  TGCAACTGGA
1401  CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGGCCATATC  GCGCTCAGCC
1451  GTTTCAGTTC  AGGGCTTTAC  GGCGGCCATA  CCGAAGGCGG  CATCAGCATC
1501  GCCAACACCC  GTCCCGCCAC  TTACCGCCTG  CAACAGAATG  CAAGCAACAT
1551  CCAAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601  GCAACGGCGA  CGCGGTATC  GACCTGACCG  CGGGCGGCGA  AACCAGAAAA
1651  GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGCTAAATA  TTTCCAACGG
1701  TGCATGGCAC  GGTATCGACA  TGGACAATAT  CCTGAAAAAC  GGCATTTCGG
1751  GCAAACTGCG  CGACAATGCC  GCACCCAGCA  CACCCCTCCA  CCGATTACAG
1801  CTCAACAGCG  AAATTTCAGA  CGGCATCAGC  CGCCACATCG  ATACCGAACT
1851  CTTCTCCGAC  AGCCTCTATG  TTACAGCAAA  CGGCTATACC  AATCTGGATA
1901  CGCAGGAATT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CCATCCGAAA
1951  AACAAACCGA  TTCCCTTGAA  AATCACCAGT  ACGGTGGACA  AACCCTCCAT
2001  TACCGTCGAT  TACGGCAGGC  TGACCGGCGG  CATCAATTCG  CGCAAAGAGA
2051  AACAGAAAT  CCTCGAAGAC  ACCCTGCTGG  AACAAATGGA  GTGGCTCAAA
2101  CCTAAGAAC  CGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1259

a771.pep

```

1  MDLLSVFHKY RLKYAVAVLT ILLLAIGLH ASVYRIFTPE NIRSRLQQSI
51  ANTHRKISFD ADIQRRLLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KQASVNRRI
151 VENSTVRLNF LQEQILILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTV
401 AKFRYTHEDA PHLEAAVALQ KLNLTPLYDD VRQONGKIFP DTLAKLSGDI
451 EAHKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTGGGSI
501 ANTREATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGS SLNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRT
601 LNSEISDGI RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEQKILED TLLEQWQWLK
701 PKEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

a771.pep	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPENIRSRLQQSI	10	20	30	40	50	60
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQQSI	10	20	30	40	50	60
a771.pep	ADIQRRLLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE	70	80	90	100	110	120
m771	ADIQRRLLPRPTVILKNLTITEPGGDQTAHSVQETKIGLSWKNLWSDQIQIEKWVSSAE	70	80	90	100	110	120
a771.pep	LALTRDGKGVWNIQDLIDSQKQASVNRRIVENSTVRLNFLQEQILILKEINLNQSPDSS	130	140	150	160	170	180
m771	LALTRDGKGVWNIQDLIDSQKQASVNRRIVENSTVRLNFLQEQILILKEINLNQSPDSS	130	140	150	160	170	180
a771.pep	GQPFESSGILVWGKLSVPWKSRLGLFLSDGIGTPKISPFHFEASTSLDGHGITISTTGSPS	190	200	210	220	230	240
m771	GQPFESSGILVWGKLSVPWKSRLGLFLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS	190	200	210	220	230	240
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSIKIETVNGAFTAGGEYAQWDG	250	260	270	280	290	300
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG	250	260	270	280	290	300
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD	310	320	330	340	350	360
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD	310	320	330	340	350	360
a771.pep	TVNRLPQPRFISRLDGSLSV PNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ	370	380	390	400	410	420
m771	TVNRLPQPRFISRLDGSLSV PNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ	370	380	390	400	410	420
a771.pep	KLNLTPLYDDVRQONGKIFPDTLAKLSGDI EAHKIGKVQLPGLQLDDMETYLHADKGHI	430	440	450	460	470	480
m771	KLNLTPLYDDVRQONGKIFPDTLAKLSGDI EAHKIGKVQLPGLQLDDMETYLHADKGHI	430	440	450	460	470	480

1260

	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTNNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTNNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

g772.seq

1	GTGTTCCGCA	CGGTCTTGCG	GACTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGTCGCAAG	TTCTTTCAGG	TTGTTGCGTA	TGGTTTTCGCG	GCGTTGGCGG
101	AAGGCGAGTT	TCACCAAGTTT	GGCGAAATGA	TCGAAATCGT	CCGCCTTGCC
151	GATACGGTGT	TTCACCGGAA	TCATGCGCAC	CACTGCGGAA	TCGATTTTCG
201	GCGCGGGATC	GAACGATTTCG	GGCGGCACGT	CAATCAGCAG	CTCCATATCG
251	AAAAAATATT	GCAGCATCAC	ACCCAAGCGA	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATGCGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCATAT
351	CGCGGACATC	GTCCGCCACC	TCCGCCAGTT	TGAACAAAAG	CGGCGTGGAG
401	ATGTTATACG	GCAGGTTGCC	GACGATTTTC	TTTTTGCTG	AGATGCCGTT
451	GAAATCAAAC	TGCAACACGT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTACAGACG	CATACGATGT	CGCGGTCGAT	TTGACAACG
551	TGCAGGCGGT	TCAGCTTTT	CGCCAAAGGT	TCGGTAATTG	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCC	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC
701	TTGCGGGGCT	TGTGTTCTTT	CATCGTGTTT	CCTCTTCGGT	TGAAACCCCG
751	CCCTTTAGGG	CGGCAGGATC	AGACTCTGTT	TGGGCGGGGC	GTAACCCCTT
801	CCAAATCAGG	ACGACACATA	GGGCGGTGCT	TTATGTGTCG	TCCTGTGTGT
851	TGGAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTCGGC	ATTGTAA

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

g772.pep

1	VFGTVLRD	DA	DCLQII	IVVGK	FFQV	VAYGFA	ALAE	GEFHQF	GEMIEIVRLA
51	DTVFHR	NHAA	HCGIDF	FRRGI	ERFGR	HVNQQ	LHIE	KILQHH	TQATVVVAFR
101	RGNHAL	DHFF	LQHKV	HIGDI	VRHLR	QFEQK	RRGD	VIRQVA	DDFLFA*DAV
151	EIKLQ	HVAFV	NHQFIR	KRQR	FQAYD	VAVD	FDNV	QAVOLF	RORFGNCRQT
201	RADFNH	DIIR	LRAHGV	DNIA	DNPRV	LQKIL	PETL	AGFVFF	HRVSSSVETP
251	PFRAAG	SDSV	WAGRN	PFQIR	TTHRA	VLYVS	SCVLE	HKCVY	SIRLMSAL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

m772.seq

1	ATGTTCCGCG	CGGTCTTGCG	GATTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGCCTGCAAG	CTCTTTCAGA	TTGTTGCGTA	TGGTTTTCGCG	GCGTTGGTGG
101	AAGGCGAGTT	TCACGAGTTT	GGCAAAATGC	TCGAAATCGT	CCGCCTTGCC
151	GATGCGGTGT	TTCACCGGAA	TCATACGGAC	GACGCGGGAA	TCCACTTTCG
201	GCGCAGGGTC	GAACGATTTCG	GGCGGTACGT	CAATCAGCAT	TTCCATATCG
251	AAAAAATATT	GCAGCATCAC	GCCCAAGCGG	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATACGCTCGA	CCACTTCTTT	TTGCAGCATA	AAGTGCATAT
351	GACGACATC	GTCCGCCACC	TCCGCCAGCT	TGAACAAAAG	CGGTGTGGAA
401	ATGTTGTACG	GGAGGTTGCC	GACGATTTTC	TTTTTGCTG	CGATGCCGTT
451	GAAATCAAAC	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTACAGACG	CATACGATGT	CGCGGTCGAT	TTGACAACG
551	TGCAGGCGGT	TCAGCTTTT	CGCCAAAGGT	TCGGTAATCG	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCT	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC

1261

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701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTTTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

m772.pep

```

1 MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GKMLEIVRLA
51 DAVFHRNHTD DGGIHFRRRV ERFGRYVNOH FHIEKILQHH AQAQVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEOK RCGNVVREVA DDFLFACDAV
151 EIKLOQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RADFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLYVS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

m772/g772 85.2% identity in 298 aa overlap

	10	20	30	40	50	60
g772.pep	VFGTVLRTDADCLQIIVVGKFFQVVAYGFAALAEGEFHFQ	GEMIEIVRLADTVFHRNHAAH				
m772	MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
	10	20	30	40	50	60
g772.pep	HCGIDFRRGIERFGRHVNQQLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI					
m772	DGGIHFRRRVVERFGRYVNOHFHIEKILQHHAAQAQVVAFRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
g772.pep	VRHLRQFEQKRGRDVIRQVADDFLFAFXDAVEIKLQHVAFVNHQFIRKRQRQTAYDVAVD					
m772	VRHLRQLEQKRCGNVVREVADDFLFAFACDAVEIKLOQYIAFVNHQFIRKRQRQTAYDVAVD					
	130	140	150	160	170	180
g772.pep	FDNVQAVQLFRQRFNGCRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFNGRRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
g772.pep	HRVSSSVETPPFRAAGSDSVWAGRNPFQIRTTTHRAVLYVSSCVLEHKCVYSIRLMSALX					
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLYVSSCVLKHKCVYSIRLMSALX					
	250	260	270	280	290	299

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

a772.seq

```

1 ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51 CGCCTGCAAG CTCTTTTCTAGA TTGTTGCGTA TGGTTTTGCG GCGTTGGTGG
101 AAGGCGAGTT TCACGAGTTT GGCGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTTCG
201 GCGCGGGGTC GAACGATTTCG GCGGCAACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGAGCAGTA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTTGCC GACGATTTTC TTTTTCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTAGACGCG CATAAGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGCGGTT TCAGCTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGACCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAATTCG CCCGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

1262

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
1  MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GEMLEIVRLA
51  DTVFHRNHAD DGRIHFRRGV ERFGHRVNHQ FHIEEILQHH AQAQVAVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNHDII RLAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

```
m772/a772    95.6% identity in 298 aa overlap

          10      20      30      40      50      60
a772.pep    MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD
              |||||
m772         MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD
              10      20      30      40      50      60

          70      80      90      100     110     120
a772.pep    DGRIHFRRGVFRGRHVNHQFHIEEILQHHAAQAVVAFRRGNHTIDHFFLQHKVHIDDI
              |||||
m772         DGGIHFRRRVERFGRYVNHQFHIEKILQHHAAQAVVAFRRGNHTLDHFFLQHKVHIDDI
              70      80      90      100     110     120

          130     140     150     160     170     180
a772.pep    VRHLRQLEQKRRGNVVGQVADDFLACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD
              |||||
m772         VRHLRQLEQKRCGNVREVADDFLACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD
              130     140     150     160     170     180

          190     200     210     220     230     240
a772.pep    FDNVQAVQLFRQRFGNRRQTRTDFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF
              |||||
m772         FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF
              190     200     210     220     230     240

          250     260     270     280     290     299
a772.pep    HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX
              |||||
m772         HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX
              250     260     270     280     290
```

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
1  ATGGGATTGG GTGCAACGAC TTTTGTGGT TCGGGTGCTA TAGGCGGAGG
51  TCTGTGCACT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG
251 CCGTATGGGG ATTGGAACG CTGATTACGC GCAAATTGGG AAACCTGGCA
301 ACGGGTGTGA AAACCTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGCTT GTCTGCCAAT
451 GCAAGGTTAC CTAAAAATTT TAAACATTT GATTATTTTG ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AAACCTGGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCGCGA CAAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA
```

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
1  MGLGATTFVG SGAIGGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSRQL
51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
101 TGVKTSLSLTPK TADVQRNLS QSEVGIKWGK GIEGQGPWE DYVGKGLSAN
151 ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKPEQL YSTMKGYIDK
201 TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEYGKSQ
251 NITVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAAATGTTA AACGGGAAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251 CTTCCGGCAG GACATACGTC CAAAACTCG ACGACCGCAA ATTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATCAA AACGGCAGGT
401 TTTCTGCCGC AGCCGCCTTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGGAACGTG GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCAACCGCG CCCGAAGTCA TATTCAAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCAGAGCCT
651 GATACAGACC TATCCCGGCA GCCCGCGGCG AAAACGCGCC GCCGAGCCG
701 TACGCAAAAC ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRITYV QKLDDRKLKE
101 HYLNTEGGSA SAHTVETAQN LYNQALKHYQ NGRFSAAAAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVEIGGRY ANRFKDSPTA PEVIFKIGEC
201 QYRLQOKDIA RATWRSLIQT YPGSPAARKA AA AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC
51  CTGTGCTTCC GTTTCACCCG TTCCGGCAGG CAGCCAAACC GAAATGTCGA
101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT
251 CTTCCGGCAG GGCATACGTC CAAAACTCG ACGACCGCAA GTTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTCGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATAAA AGCGGCAAGT
401 TTTCTGCCGC TGCCTCCCTG TTGAAAGGCG CGGACGGAGG CGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCAACCGCG CCTGAAGCCA TGTTCAAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCAGAGCCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGAGCCG
701 TGCACAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDDRKLKE
101 HYLNTEGGSA SAHTVETAQN LYNQALKHYK SGKFSAAAAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVEIGGRY ANRFKDSPTA PEAMFKIGEC
201 QYRLQOKDIA RATWRSLIQT YPGSPAARKA AA AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFIIWLSVSASCASVLPVPEGSRT	EMPTQENASDGIPYPVPTLQDRLDYLEGKI				
m774	MKIKLPLFIIWLSVSASCASVSPVAGSQTEM	STRENASDGIPYPVPTLQDRLDYLEGKI				
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGR	TYVQKLD	DRKLKEHYLNTEGGSASAHTVETAQN			
m774	VRLSNEVETLNGKVKALEHAKTHSSGR	AYVQKLD	DRKLKEHYLNTEGGSASAHTVETAQN			
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHYQNGRFSAAAALLKGADGGD	GGSIAQRSMYLLQLQSRARMGN	CESVIEIGGRY			
m774	LYNQALKHYKSGKFSAAASLLKGADGGD	GGSIAQRSMYLLQLQSRARMGN	CESVIEIGGRY			
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQOK	DIARATWRS	LIQTYPGSPA	AKRAAAV	RRKRX	
m774	ANRFKDSPTAPEAMFKIGECQYRLQOK	DIARATWRS	LIQTYPGSPA	AKRAAAV	RRKRX	
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

```

1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCCG TATCCGCCGC
51  CTGTCTTCC  CCTGTTTCCC GCAATATTCA GGATATGCCG CTCGAACCGC
101 AGGCAGAGGC AGGTAGTTCG GACGCTATTC CCTATCCCGT TCCCACTCTG
151 CAAGACCGTT TGGATTATCT GGAAGGCACA CTCGTCCGCC TGTCGAACGA
201 AGTGGAAACC TTAAACGGCA AAGTCAAAGC ACTGGAGCAT GCGAAAACAC
251 ACCCTTCCAG CAGGGCATACT GTCCAAAAC TCGACGACCG CAAGTTGAAA
301 GAGCATTACC TCAATACCGA AGGCGGCAGC GCATCCGCAC ATACCGTCGA
351 AACC GCACAA AACCTCTACA ATCAGGCACT CAAACACTAT AAAAGCGGCA
401 GGT TTTCTGC CGCTGCCTCC CTGTTGAAAG GCGCGGACGG AGGCGACGGC
451 GGCAGCATCG CGCAACGCAG TATGTACCTG TTGCTGCAAA GCAGGGCGCG
501 TATGGGCAAC TGCGAATCCG TCATCGAAAT CGGAGGGCGT TACGCCAAC
551 GTTTCAAAGA CAGCCCAACC GCGCCTGAAG CCATGTTCAA AATCGGCGAA
601 TGCCAAATACA GGCTTCAGCA AAAAGACATT GCAAGGGCGA CTTGGCGCAG
651 CCTGATACAG ACCTATCCCG GCAGCCCGGC GGCAAAACGC GCCGCCGCAG
701 CCGTGCGCAA ACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

```

1  MKTKLPLFII WLSVSAACSS PVSRIQDMR LEFQAEAGSS DAIPYPVPTL
51  QDRLDYLEGT LVRLSNEVET LNGKVKALEH AKTHPSSRAY VQKLD
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFIIWLSVSAACSSPVSRIQDMR	LEFQAEAGSSDAIPYPVPTLQDRLDYLEGT				
m774	MKIKLPLFIIWLSVSASCAS-VSPVAGSQTEM	STRENASDGIPYPVPTLQDRLDYLEGK				
	10	20	30	40	50	

1265

```
          70      80      90      100     110     120
a774.pep  LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLLDRKLKEHYLNTEGGSSAHTVETAQ
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      IVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLLDRKLKEHYLNTEGGSSAHTVETAQ
          60      70      80      90      100     110

          130     140     150     160     170     180
a774.pep  NLYNQALKHYKSGRFSAAASLLKGADGGDGGGSIQRSMYLLQLSRARMGNCSVIEIGGR
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      NLYNQALKHYKSGKFSAAASLLKGADGGDGGGSIQRSMYLLQLSRARMGNCSVIEIGGR
          120     130     140     150     160     170

          190     200     210     220     230     239
a774.pep  YANRFKDSPTAPEAMFKIGECQYRLQKQDIARATWRSLIQTYPGSPAAKRAAAAVRKRX
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      YANRFKDSPTAPEAMFKIGECQYRLQKQDIARATWRSLIQTYPGSPAAKRAAAAVRKRX
          180     190     200     210     220     230
```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```
m790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCGA TACGACCATC AACACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTGAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGgTCG
551 CCCCCTCGCA GTACACGTTT GCCGTTGCCA TGCCCCGACAC GTCCATGTCC
601 CCGGTTATCG AAAAGGGAGA CTTGCTGGTG GTCGAGCCGC GTATGTGCCC
651 TGCGGACGAA GACATCGCGC TGATTGAACT GTCCGACAAG CGGCTGGTCC
701 TCGCGCACCT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 GGCAGGCCGT CTGAAGCCTT TGACCTGCCC GAAGGCAGCA CGATTTTAGG
801 TGTGGTGTCT GAGTCAAAAA ACGGTTTATG TCCGCGGCAC AGGCAAGAAG
851 GCGTGTGATG TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCGACCC GGAATCAGC
951 CGTATGCTTT CTTCGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```
m790.pep
1  MARRSKTFEE AAAEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSIV LNDVQGDTTI NNHHTHTNNH SDADGKALSM
151 RLTPRPLLSL RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMCPADE DIALIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGMI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPV NA*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```
a790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCGA TACGACCATC AACACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ACGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTGAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCC
551 CCCCCTCACA ATATACGTTT GCCGTTGCCA TGCCCCGACAC GTCCATGTCC
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TGCGGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTCC
701 TCGCGCACCT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
```

1266

```

751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCG GAAGGCAGCG TGATTTTAGG
801 TGTGGTGCTG GAGTCAAAA ACAGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTAT TCGGATTACC GCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDITI NNHHTHTNNH SDADGKALSM
151 RLTPRPLLSL RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

```

a790/m790    98.2% identity in 342 aa overlap

a790.pep      10      20      30      40      50      60
MARRSKTFEEAAEEVEERFGHRGIKLVFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW
|||||
m790          10      20      30      40      50      60
MARRSKTFEEAAEEVEERFGHRGIKLVFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW

a790.pep      70      80      90      100     110     120
GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII
|||||
m790          70      80      90      100     110     120
GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV

a790.pep     130     140     150     160     170     180
LNDVQGDITINNHHHTHTNNHSDADGKALSMRLTPRLLSDRQAAAFARTGKLTGSFDLFA
|||||
m790         130     140     150     160     170     180
LNDVQGDITINNHHHTHTNNHSDADGKALSMRLTPRLLSDRQAAAFARTGKLTGSFDLFA

a790.pep     190     200     210     220     230     240
SVVAPSQYTF AVAMPDTSMSPVIEKGDLLVVEPRMRPADEDIVLIELSDKRLVVAHLVID
|||||
m790         190     200     210     220     230     240
SVVAPSQYTF AVAMPDTSMSPVIEKGDLLVVEPRMCPAEDIALIELSDKRLVVAHLVID

a790.pep     250     260     270     280     290     300
IAGRMLIYQTGRPSEALDLPESGVILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGTI
|||||
m790         250     260     270     280     290     300
IAGRMLIYQTGRPSEAFDLPEGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGMI

a790.pep     310     320     330     340
SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
|||||
m790         310     320     330     340
SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

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g791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTAATTGTTT
51  TGGTTTGTGT TTTGGTTTTT GTGTATTGG AGTGGGCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AACTGCCGT CTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AAATGCCGT GACTATTAT TCGGCGGATG GAGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GGCGATTTCC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGATGT TTGGGTGTT GCCCGGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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1267

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401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTTGAG TTGTATTTC AATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC AATAAGATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCCAAG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAACT GCATTATGAG CGGTTTGTTC GGAAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TGCGGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTGCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTATAC AGCTGCCCGG CGGCAGGCGG GTTGCGCTTG
1151 ACAGGCGCGC CTTGGGTTT GCGGCCGAG CGGTGATAA TGAGAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGTTT AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACACAGA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CGCGCTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACCGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCCGTC CGAGCTGCGG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGGAGGCA TATAGTGAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGCG ACGTGATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTTGG TGGCAGGGCA
1851 AAATGCCGCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAACG ACAATAAAGA
2001 TCGGTGTTT GTCGGTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAAATGC CTGAAGGTGT GGTACGACG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTGTAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

```

g791.pep
1  MVNYYSAMIK KILTTCEGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAEDKRFY
101 RHWGVDVWVG ARAAVGNVVS GSVQSGASTI TQOVAKNFYL SSEKTFTRFK
151 NEVLLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNMMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFVYTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMVPA VVLDTKKKN VVIQLPGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRVAV QAMRQPGSTF KPFVYSAAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTFKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPELSE ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAF QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVFTA VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKQGGK MKMPEGVVSS NGEYMKERM VTDPLMLDN
751 SGIAPQPSRR AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAT AAGATTTTAA CCACTTGTTT
51  TGGTTTGGTT TTTGGGTTTT GTGTATTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACCTGCCG CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTAT TCGGCGGATG GGGAAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GGCGATTTCC
251 CAGAGGTGTT CGGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

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1268

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451 AATGAGGTGT TGCTTGCCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAACT GCATTACGAG CGGTTTGTTC GGAAATCGA
801 TCAGAGTGCG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTGATC CGCGGCAGCA GCTACCGCGG TCGGAAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAATAAATG
1201 GGGGAGGACC GTATCCGCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAT TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGCG GCATTATCT AAGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGAC ACCTAAAAAT TCAGACGGCA GATATCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGCGAGGCA TATAGCGTAT
1751 TTGCGAACCG CGGATATAGG GTTCTTCGCG ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTGG TGGCTGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCATATAT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGTTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGCGGTG TCGGCTACGG CGGTACGATT
2101 CGGGTGCCGG TTTGGGTGGA CTATATGCGT TTGCGTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGCG CTGAAGGTGT GGTGAGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

m791.pep

```

1 MVNYYSAMIK KILTTCTFGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEORREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSEDV EETVSQYLSG
351 LYTVDKMMPA VVLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDRLRAQM QPLVAGQNAQ QAIIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPVVTA VYIGFDKPKS MGRVGYGGTI
701 ACPVWVDYMR FALKGKQKKG MKMPEGVVS NGEYYMKERM VTDPLGLTDN
751 SGIAPOPSRR AKEDDGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

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g791/m791 97.3% identity in 805 aa overlap

```

g791.pep      10      20      30      40      50      60
MVNYYSAMIKKILTTCTFGLFFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
|||||
m791          10      20      30      40      50      60
MVNYYSAMIKKILTTCTFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY

g791.pep      70      80      90      100     110     120
SADGEVIGMYGEORREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
|||||
m791          70      80      90      100     110     120
SADGEVIGMYGEORREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS

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1269

	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
m791	RADHQKVATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDTTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIRRGAVIRVKNNGGRW					
m791	VVLDTTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQEPLLOGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPLLOGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPKGPNPNSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI					
m791	KGMTASTVVNDAPISLPKGPNPNSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQQYIRRFGRFPSELPAASLMAAGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRFSSELPAASLMAAGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGLRLAQMQPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGLRLAQMQPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWFGFNPDPVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKQKKG					
m791	TTNDNKDAWFGFNPDPVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKKG					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVSSNGEYMKERMVTDPLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVSSNGEYMKERMVTDPLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```

1   ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51  TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCGT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GGCGATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGCGCATGGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
351 TGTGCTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTATT AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGATTTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGCTGTC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAACG GCATTACGAG CGGTTTGTTC GGAAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGGGAAGAA TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGCGGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGGTGGATGC AAAAACCAGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTTCGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCCG GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCGG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GGCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGCG ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTTGG TGGCCGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TCGGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGCGGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGCAAGGGG ATGAAATGCT CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 ACGCGTATTG CGCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGACAGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```

1   MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVKYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMPPA VVLDVTKKKN VVIQLPGRR VTLDRRALGF AARAVNNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVQEPLQGG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPKVAEAE YSVFANGGYR VSSHVIDKIY
601 DRDGRLLRAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNNDKDAWF VGFNPDVVTA VYIGFDPKPS MGRVGYGGTI
701 AVPVWVDYMR FALGKQKQKG MKMPEGVVSS NGEYMKERM VTDPLGLDLN
751 SGIAPQPSRR AKEDDGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

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a791/m791 99.9% identity in 805 aa overlap

10 20 30 40 50 60

1271

a791.pep	MVNYYSAMIKKILTTTCFLVFGFCVFGVGLVAIAILVTYPKLPSSLDSLQHYQPKMPLTIY
m791	MVNYYSAMIKKILTTTCFLVFGFCVFGVGLVAIAILVTYPKLPSSLDSLQHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE
	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKGEDAYTQGFKVYTTV
	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
m791	RADHQKVATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA
	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
m791	VVLDTVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
m791	AVVQEPLLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI
	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
m791	GVGYAQQYIRRFGFRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
m791	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
m791	TTNDNKDAWVFGFNPDDVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKGQKG
	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
m791	MKMPEGVSSNGEYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGQAADDEV
	MKMPEGVSSNGEYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGQAADDEV

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	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLP	SNTGSKQQQLD	SLFX			
m791	RQDMQETPVLP	SNTGSKQQQLD	SLFX			
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```

1   ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCCGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGGAAAGAGG CGCCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAC
451 AGGATTTTCG AACTGTATTT AAACCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAACCG GCcgcaGACC
551 TGACcAAACA GcAggcggcG aaactgacgg tactcgtccc cgccccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcatgggtt cggcaaatTA ccccaaaagc aaacggactg
701 attgttccag atatggaat gccgcctgaa ctggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```

1   MFRIVKWLIA LPVGIFIFFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKKP AADLTQQAA KLTVLVPAPF
201 YYSDHPSKR LRNKTNIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```

1   ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCCGAACA GCGGCGAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTTAC CGACAAAGAC
451 AGGATTTTTG AACTGTATTT AAACCAATC GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA GCCGCGTCCC GGTATTTTTA TCAAAATACC GCCGCCAAGC
551 TGACCAAACA GCAGGCGGCA AAACGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAAA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```

1   MFRIVKWLIA LPVGIFIFFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQAA KLTARVPAPL
201 YYADHPKSKR LRNKTNIVLK RMGSAELPES DTD*

```

g792 / m792 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIAL	LPVGIFIFFN	AYVYGNIIY	RAVAPHRTAF	MSMRMKQFEQ	EGRDVALDYR
m792	MFRIVKWLIAL	LPVGIFIFFN	AYVYGNIIY	RAVAPHRTAF	MSMRMKQFEQ	EGRDVALDYR
	10	20	30	40	50	60
	70	80	90	100	110	120
g792.pep	WVPYNRISTN	LKKALIASD	VRFAGHGGF	GDGIQNAIRR	NRNSGEVKAG	GSTISQQLAK

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m792	WMPYKRISTNLKKALIASEDARFAGHGGFDWGGIQNAIRNRNRNSGKVKAGGSTISQQLAK	70	80	90	100	110	120
g792.pep	NLFLNESRNYLRKGEEAAITAMMEAVTDKNRIFELYLNSIEWHYGVFGAEAAASRYFYKKP	130	140	150	160	170	180
m792	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEAAASRYFYQIP	130	140	150	160	170	180
g792.pep	AADLTQQAAKLTVLPAPFYSDHPKSKRLRNKTNIVLRRMGSAANYPKAKRTDCSRYGN	190	200	210	220	230	240
m792	AAKLTQQAAKLTARVPAPLYADHPKSKRLRNKTNIVLKRMGSAELPESDIDX	190	200	210	220	230	
g792.pep	AAXTGVRTAYVFVWDLX	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2685>:

```
a792.seq
1 ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51 CTTTTTCAAT GACCTATGTTG ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CCCCCCATCG GACTGCGCTTT ATGTGCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTGCGCG ATGTGCGCAT GGATTACCGC TGGATGCCCT ACAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGCGACGG CCGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCGGAACA CGCGCAAAGT GAAGGCGGGC GGCCTGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAAG
401 CGCAAGAAGC AGCGATTACC GCGATGATGG AAGCCGTTAC GCACAAAGAC
451 AGGATTTTTTG AACTGTATTT AAACCAATC GAATGGCACT ACGGCGTTTT
501 CGCGCGGGAA CGCGCGTCCC GGATTTTCTT TCAAAATACC CGCCGCAAGC
551 TGACCAAAAC GCAGCGCGCA AACTGACGGA CGCGCGTCCG CGCCGCCGCT
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGGCT
701 GA
```

This corresponds to the amino acid sequence <SEQ ID 2686; ORF 792.a>:

```
a792.pep
1  MFRIIKWLIA  LPVGIFIFFN  AYYVNGNIITY  RAVAPHRTAF  MSMRMKQFEQ
51  EGRDVALDYR  WMPYKRISTN  LKKALIASED  ARFAGHGGFD  WGGIQNAIRR
101 NRNSGKVKAG  GSTISQQLAK  NLFNLNRSY  IRKGEEAAIT  AMMEAVTDKD
151 RIFELYLSNI  EWHYGVFGAE  AASRYFYQIP  AAKLTQKQAA  KLTARVPAPL
201 YYADHPKSKR  LRNKTNIIVL  RMSGAELEPS  DTD*
```

m792/a792 99.6% identity in 233 aa overlap

		10	20	30	40	50	60
a792.pep		MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
m792		MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
		10	20	30	40	50	60
		70	80	90	100	110	120
a792.pep		WMPYKRISTNLKKALIASEDARFAGHG GFDWGGIQNAIRNRNRNSGKVKAGGSTISQQLAK					
m792		WMPYKRISTNLKKALIASEDARFAGHG GFDWGGIQNAIRNRNRNSGKVKAGGSTISQQLAK					
		70	80	90	100	110	120
		130	140	150	160	170	180
a792.pep		NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEAAASRYFYQIP					
m792		NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEAAASRYFYQIP					
		130	140	150	160	170	180
		190	200	210	220	230	
a792.pep		AAKLTQQA AKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSAELPESD TD X					
m792		AAKLTQQA AKLTARVPAPLYYADHPKSKRLRNKTNIVLKRMGSAELPESD TD X					
		190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2687>:

g793.seq

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```

1  ATGTTGATTA  AAAGCGAATA  TAAGCCCCGG  ATGCTGCCCA  AAGAAGAGCA
51  GGTCAAAAAG  CCGATGACCA  GTAACGGACG  GATTAGCTTC  GTCCTGATGG
101 CAATGGCGGT  CTTGTTTGCC  TGTCTGATTG  CCCGCGGGCT  GTATCTGCAG
151 ACGGTAACGT  ATAACTTTTT  GAAAGAACAG  GGCAGCAACC  GGATTGTGCG
201 GACTCAAGCA  TTGCCGGCTA  CACGCGGTAC  GGTTCGGAC  CGGAACGGTG
251 CGGTTTTGGC  GTTGAGCGCG  CCGACGGAGT  CCCTGTTTGC  CGTGCCATAA
301 GATATGAAGG  AAATGCCGTC  TGCCGCCCAA  TTGGAACGCC  TGTCCGAGCT
351 TGTGCGATGT  CCGGTCGATG  TTTTGAGGAA  CAAACTCGAA  CAGAAAGGCA
401 AGTCGTTTAT  TTGGATCAAG  CGGCAGCTCG  ATCCCAAGGT  TGCCGAAGAG
451 GTCAAAGCCT  TGGGTTTGGA  AAACCTTGTA  TTTGAAAAAG  AATTAAAACG
501 CCATTACCCG  ATGGGCAACC  TGTTTGACA  CGTCATCGGA  TTTACCGATA
551 TTGACGGCAA  AGGTCAGGAA  GGTTCGAAC  TTTGCTTGA  AGACAGCCTG
601 TATGGCGAAG  ACGGCGCGGA  AGTTGTTTTG  CGGGACCGGC  AGGGCAATAT
651 TGTGGACAGC  TTGGACTCCC  CGCGCAATAA  AGCACCGCAA  AACGGCAAAG
701 ACATCATCCT  TTCCCTCGAT  CAGAGGATTC  AGACCTTGGC  CTATGAAGAG
751 TTGAACAAGG  CGGTGGAATA  CCATCAGGCA  AAAGCCGGAA  CGGTGGTGGT
801 TTTGGATGCC  CGCACGGGGG  AAATCCTCGC  CTTGGCCAAT  ACGCCCGCCT
851 ACGATCCCAA  CAGACCCGGC  CGGGCAGACA  GCGAACAGCG  GCGCAACCGT
901 GCCGTAACCG  ATATGATCGA  ACCTGGTTCG  GCAATCAAAC  CGTTCGTGAT
951 TGCGAAGGCA  TTGGATGCGG  GCAAAACCGA  TTTGAACGAA  CGGCTGAATA
1001 CGCAGCCTTA  TAAATCGGA  CCGTCTCCCG  TGCGCGATGA  TACCCATGTT
1051 TACCCCTCTT  TGGATGTGCG  CGGCATTATG  CAGAAATCGT  CCAACGTCGG
1101 CACAAAGCAA  CTGTCTGCGC  GTTTCGGCGC  CGAAGAAATG  TATGACTTCT
1151 ATCATGAATT  GGGCATCGGT  GTGCGTATGC  ACTCGGGCTT  TCCGGGGGAA
1201 ACTGCAGGTT  TGTTGAGAAA  TTGGCGCAGG  TGCGGGCCCA  TCGAACAGGC
1251 GACGATGTCT  TTCGGTTACG  GTCTGCAATT  GAGCCTGCTG  CAATTGGCGC
1301 GCGCCTATAC  CGCACTGACG  CACGACGGCG  TTTTGCTGCC  GCTCAGCTTT
1351 GAGAAGCAGG  CGGTTGCGCC  GCAAGGCAAA  CGCATATTCA  AAGAATCGAC
1401 CGCGCGCGAG  GTACGCAATC  TGATGGTTTC  CGTAACCGAG  CCGGGCGGCA
1451 CCGGTACGGC  GGGTGCGGTG  GACGGTTTCG  ATGTCGGCGC  TAAAACCGGC
1501 ACGGCGCGCA  AGTTCGTCAA  CGGGCGTTAT  GCCGACAACA  AACACGTCGC
1551 TACCTTTATC  GGTTTTGCCC  CCGCCAAAAA  CCCCCGTGTG  ATTGTGGCGG
1601 TAACCATCGA  CGAACCAGCT  GCCACGGCT  ATTACGGCGG  CGTAGTGCCA
1651 GGGCCGCCCT  TCAAAAAAAT  TATGGGCGGC  AGCCTGAACA  TCTTGGGCAT
1701 TTCCCGGACC  AAGCCACTGA  CCGCCGCGAG  CGTCAAAACA  CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

g793.pep

```

1  MLIKSEYKPR  MLPKEEQVKK  PMTSNGRISF  VLMAMAVLFA  CLIARGLYLQ
51  TVTYNFLKEQ  GDNRIVRTQA  LPATRGTVSD  RNGAVLALSA  PTESLFAVPK
101 DMKEMPSAAQ  LERLSELVDV  PVDVLRNKLE  QKGKFSFIWK  RQLDPKVAEE
151 VKALGLENFV  FEKELKRHYP  MGNLFAHVIG  FTDIDKGQOE  GLELSLEDSL
201 YGEDGAEVVL  RDRQGNIVDS  LDSPRNKAPO  NGKDIIILSLD  QRIQTLAYEE
251 LNKAVEYHQA  KAGTVVVLDA  RTGEILALAN  TPAYDPNRP  RADSEQRNR
301 AVTDMIEPGS  AIKPFVIAKA  LDAGKTDLNE  RLNTQPYKIG  PSPVRDDTHV
351 YPSLDVRGIM  QKSSNVGTSK  LSARFGAEEM  YDFYHELIG  VRMHSGFPGE
401 TAGLLRNWRR  WRPIEQATMS  FGYGLQLSL  QLARAYTALT  HDGVLLPLSF
451 EKQAVAPQK  RIFKESTARE  VRNLMVSVTE  PGGTGTAGAV  DGFVVGAKTG
501 TARKFVNTRY  ADNKHVATFI  GFAPAKNPRV  IVAVTIDEPT  AHGYVGGVVA
551 GPFFKKIMGG  SLNILGISPT  KPLTAAAVKT  PS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

m793.seq

```

1  ATGTTGATTA  AGAGCGAATA  TAAGCCTCGG  ATGCTGCCCA  AAGAAGAGCA
51  GGTCAAAAAG  CCGATGACCA  GTAACGGACG  GATCAGCTTC  GTCCTGATGG
101 CAATAGCGGT  CTTGTTTGCC  GGTCTGATTG  CTCGCGGACT  GTATCTGCAG
151 ACGGTAACGT  ATAACTTTTT  GAAAGAACAG  GGCAGCAACC  GGATTGTGCG
201 GACTCAAAAC  TTGCCGGCTA  CACGCGGTAC  GGTTCGGAC  CGGAACGGTG
251 CGGTTTTGGC  GTTGAGTGGC  CCGACGGAGT  CCCTGTTTGC  CGTGCCATAA
301 GAGATGAAGG  AAATGCCGTC  TGCCGCACAA  TTGGAACGCC  TGTCCGAGCT
351 TGTGCGATGT  CCGGTTGATG  TTTTGAGGAA  CAAGCTCGAA  CAGAAAGGCA
401 AGTCGTTTAT  CTGGATTAAG  CGGCAGCTCG  ATCCCAAGGT  TGCCGAAGAG
451 GTCAAAGCCT  TGGGTTTGGA  AAACCTTGTA  TTTGAAAAAG  AATTAAAACG
501 CCATTACCCG  ATGGGCAACC  TGTTTGACA  CGTCATCGGA  TTTACCGATA
551 TTGACGGCAA  AGGTCAGGAA  GGTTCGAAC  TTTGCTTGA  AGACAGCCTG
601 CATGGCGAAG  ACGGCGCGGA  AGTCGTTTTG  CGGGACCGGC  AGGGCAATAT
651 TGTGGACAGC  TTGGACTCCC  CGCGCAATAA  AGCCCCGAAA  AACGGCAAAG
701 ACATCATCCT  TTCCCTCGAT  CAGAGGATTC  AGACCTTGGC  CTATGAAGAG
751 TTGAACAAGG  CGGTGGAATA  CCATCAGGCA  AAAGCCGGAA  CGGTGGTGGT
801 TTTGGATGCC  CGCACGGGGG  AAATCCTCGC  CTTGGCCAAT  ACGCCCGCCT
851 ACGATCCCAA  CAGGCCCGGC  CGGGCAGACA  GCGAACAGCG  GCGCAACCGT
901 GCCGTAACCG  ATATGATCGA  ACCCGGTTTC  GCAATCAAAC  CGTTGTGAT
951 TGCGAAGGCA  TTGGATGCGG  GCAAAACCGA  TTTGAACGAA  CGGCTGAATA

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```

1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACGT TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATG GCGCAGGTGG CGGCCTATCG AACAGCGCAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCGTCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTCCGT AACCGAGCCG GGCGGCACCG
1451 GTACGGCGGG TCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

m793.pep

```

1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKFSIWIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIIISLD QRIQTAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNRRRW RPIEQATMSF GYGLQLSLLQ LARAYTALH DGVLLPVFSFE
451 KQAVAPQGKR IFKESTAREV RNLMSVTPEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIAFFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PPFFKIMGGS LNILGISPTK PLTAAAVKTP S*

```

g793/m793 98.5% identity in 582 aa overlap

```

g793.pep      10      20      30      40      50      60
                MLIKSEYKPRMLPKKEEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ
                |||||
m793          10      20      30      40      50      60
                MLIKSEYKPRMLPKKEEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ

g793.pep      70      80      90      100     110     120
                GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVPKDMKEMPSAAQLERLSELVDV
                |||||
m793          70      80      90      100     110     120
                GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV

g793.pep      130     140     150     160     170     180
                PVDVLRNKLEQKGKFSIWIKRQLDPKVAEEVKALGLENFVFEKELKRHPYMGNLFAHVIG
                |||||
m793          130     140     150     160     170     180
                PVDVLRNKLEQKGKFSIWIKRQLDPKVAEEVKALGLENFVFEKELKRHPYMGNLFAHVIG

g793.pep      190     200     210     220     230     240
                FTDIDGKGQEGLELSLEDSLYGEDGAEVVLDRQGNIVDSLSPRNKAPQNGKDIIISLD
                |||||
m793          190     200     210     220     230     240
                FTDIDGKGQEGLELSLEDSLHGEDGAEVVLDRQGNIVDSLSPRNKAPKNGKDIIISLD

g793.pep      250     260     270     280     290     300
                QRIQTAYEELNKAVEYHQAAGTAVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR
                |||||
m793          250     260     270     280     290     300
                QRIQTAYEELNKAVEYHQAAGTAVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR

g793.pep      310     320     330     340     350     360
                AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIM
                |||||
m793          310     320     330     340     350
                AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRD-THVYPSLDVRGIM

g793.pep      370     380     390     400     410     420
                QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS
                |||||
m793          360     370     380     390     400     410
                QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS

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	430	440	450	460	470	480
g793.pep	FGYGLQLSLLQLARAYTALTHDGVLLPLSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE					
m793	FGYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE					
	420	430	440	450	460	470
	490	500	510	520	530	540
g793.pep	PGGTGTAGAVDGFVDGAKTGTARKFVNNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT					
m793	PGGTGTAGAVDGFVDGAKTGTARKFVNNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT					
	480	490	500	510	520	530
	550	560	570	580		
g793.pep	AHGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
m793	AHGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
	540	550	560	570	580	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

a793.seq

1	ATGTTGATTA	AGAGCGAATA	TAAGCCTCGG	ATGCTGCCCA	AAGAAGAGCA
51	GGTCAAAAAG	CCGATGACCA	GTAACGGACG	GATCAGCTTC	GTCCTGATGG
101	CAATAGCGGT	CTTGTTCGCC	GGTCTGATTG	CTCGCGGACT	GTATCTGCAG
151	ACGGTAACGT	ATAACTTTTT	GAAAGAACAG	GGCGACAACC	GGATTGTGCG
201	GACTCAAACA	TTGCCGGCTA	CACGCGGTAC	GGTTTCGGAC	CGGAACGGTG
251	CGGTTTTTGG	GTTGAGTGCG	CCGACGGAGT	CCCTGTTTGC	CGTGCCCTAA
301	GAGATGAAGG	AAATGCCGTC	TGCCGCACAA	TTGGAACGCC	TGTCGAGCT
351	TGTCGATGTG	CCGGTTGATG	TTTTGAGGAA	CAAGCTCGAA	CAGAAAGGCA
401	AGTCGTTTAT	CTGGATTAAG	CGGCAGCTCG	ATCCCAAGGT	TGCCGAAGAG
451	GTCAAAGCCT	TGGGTTTGGG	AAACTTTGTA	TTTGAATAAG	AATTAAACG
501	CCATTACCCG	ATGGGCAACC	TGTTTGACACA	CGTCATCGGA	TTTACCGATA
551	TTGACGCGAA	AGGTCAGGAA	GGTTTGGAAC	TTTCGCTTGA	AGACAGCCTG
601	CATGGCGAAG	ACGGCGCGGA	AGTCGTTTTG	CGGGACCGGC	AGGGCAATAT
651	TGTGGACAGC	TTGGACTCCC	CGCGCAATAA	AGCCCCGAAA	AACGGCAAAG
701	ACATCATCCT	TTCCTCGAT	CAGAGGATTC	AGACCTTGGC	CTATGAAGAG
751	TTGAACAAGG	CGGTCAATA	CCATCAGGCA	AAAGCCGGAA	CGGTGGTGGT
801	TTTGGATGCC	CGCACGGGGG	AAATCCTCGC	CTTGCCCAAT	ACGCCCGCCT
851	ACGATCCCAA	CAGGCCCGGC	CGGGCAGACA	GCGAACAGCG	GCGCAACCGT
901	GCCGTAAACG	ATATGATCGA	ACCCGGTTCG	GCAATCAAAC	CGTTGTGAT
951	TGCGAAGGCA	TTGGATGCGG	GCAAAACCGA	TTTGAACGAA	CGGCTGAATA
1001	CGGACGCTTA	TAAATCGGAA	CCGTCTCCCG	TGCGCGATAC	CCATGTTTAC
1051	CCCTCTTTGG	ATGTGCGCGG	CATCATGCAG	AAATCGTCCA	ACGTCGGCAC
1101	AAGCAAACCTG	TCTGCGCGTT	TCGGTGCCGA	AGAAATGTAT	GACTTCTATC
1151	ATGAGTTGGG	CATCGGTGTG	CGTATGCACT	CGGGCTTTCC	GGGCGAAACT
1201	GCAGGTTTGT	TGAGAAATTG	GCGCAGGTGG	CGGCCTATCG	AACAGGCGAC
1251	GATGTCCTTC	GGTTACGGCC	TGCAATTGAG	CCTGTGCAAA	TTGGCGCGCG
1301	CCTATACCCG	ACTGACGCAC	GACGCGGTTT	TACTGCCCGT	CAGCTTTGAA
1351	AAACAGGCGG	TTGCGCCGCA	AGGCAAAACG	ATATTCAAAG	AATCGACCGC
1401	GCGCGAGGTA	CGCAATCTGA	TGGTTCCCGT	AACCGAGCCG	GGCGGCACCG
1451	GTACGGCGGG	TGCGGTGGAC	GGTTTCGATG	TCGGCGCGAA	AACCGGCACG
1501	GCGCGCAAGT	TCGTCAACGG	GCGTTATGCC	GACAACAAAC	ACATCGCTAC
1551	CTTTATCGGT	TTTGCCCCCG	CCAAAATCC	CCGTGTGATT	GTGGCGGTAA
1601	CCATTGACGA	ACCGACTGCC	CACGGTTATT	ACGGCGGCGT	AGTGGCAGGG
1651	CCGCCCTTCA	AAAAAATTAT	GGGCGGCAGC	CTGAACATCT	TGGGCATTTC
1701	CCCGACCAAG	CCACTGACCG	CCGCAGCCGT	CAAAACACCG	TCTTAA

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

a793.pep

1	MLIKSEYKPR	MLPKKEQVKK	PMTSNGRISF	VLMAIAVLFA	GLIARGLYLQ
51	TVTYNFKLEQ	GDNRIVRTQT	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
101	EMKEMPAAQ	LERLSELVDV	PVDVLRNKLE	QKGKFSFIWK	RQLDPKVAEE
151	VKALGLENFV	FEKELKRHYF	MGNLFAHVIG	FTDIDGKGQE	GLESLSDSL
201	HGEDGAENVL	RDRQGNIVDS	LDSPRNKAPK	NGKDIILSLD	QRIQTLAYEE
251	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRP	RADSEQRNR
301	AVTDMIEPGS	AIKPFVIAKA	LDAGKTDLNE	RLNTQPYKIG	PSPVRDTHVY
351	PSLDVRGIMQ	KSSNVGTSLK	SARFGAEEMY	DFYHELIGIV	RMHSGFPGET
401	AGLLRNWRRW	RPIEQATMSF	GYGLQLSLLQ	LARAYTALTH	DGVLLPVSE
451	KQAVAPQGKR	IFKESTAREV	RNLMVSVTEP	GGTGTAGAVD	GFDVGAKTGT
501	ARKFVNNGRY	DNKHVATFIG	FAPAKNPRVI	VAVTIDEPTA	HGYGGVVAG
551	PPFKKIMGGS	LNILGISPTK	PLTAAAVKTP	S*	

a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
m793	10	20	30	40	50	60
a793.pep	70	80	90	100	110	120
m793	70	80	90	100	110	120
a793.pep	130	140	150	160	170	180
m793	130	140	150	160	170	180
a793.pep	190	200	210	220	230	240
m793	190	200	210	220	230	240
a793.pep	250	260	270	280	290	300
m793	250	260	270	280	290	300
a793.pep	310	320	330	340	350	360
m793	310	320	330	340	350	360
a793.pep	370	380	390	400	410	420
m793	370	380	390	400	410	420
a793.pep	430	440	450	460	470	480
m793	430	440	450	460	470	480
a793.pep	490	500	510	520	530	540
m793	490	500	510	520	530	540
a793.pep	550	560	570	580		
m793	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcggtttca ATCATTTTCAT AATGGTAACG ATTATTATAT ATGTGATTTC
51  CCTGCAAAC AAGCCGCTCC GCCGCCCGG CGTCCCCTT TATCCGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTCACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCCG CATAACCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTGCCG CCTTCAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCGTTTTTCA ATCAGGAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 CAAAGGCATC CGCAATATCA CGGGGCGCCT GATGCTCGAC CACAGCCTGT

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1278

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551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTCGCCG
601 TTTATGACGC CCCAAATCC GACTATGCTG TCTGCCGGTA TGGTTATGGT
651 CGCGCCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTCGGTCAA AAAACTGATG CGCGCATCTT TTTCCGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAGCCTG
851 TCGGTGTCCG GATGTTCCGC CTTGACGAAC TGATCCGCCA AAGTTTTACC
901 AACCGCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGGCGAC GGCAAACTGC CCGCCGTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCACAAATG TTGGAACGG CTTATTTTACG
1251 CCGGTTTGCA CAAGATTTCA TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCGCGCGGC
1501 GACGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

g794.pep

```

1 VRFNHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCFE YVTDSPMNF
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRMLMD HSLWGEVGSF DHFEADSGSF
201 MTFPPNPTML SAGVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILTD MNKRSDNLIA
351 RSVFLKLGDD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMQAM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVAKNIISGG
501 DGWLDKLMC KERRA*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

m794.seq

```

1 GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTCCCAC TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC
301 AACCCGCGCT CCACAATGAA ACTCGTTACC GCGTTGCGG CCTTCAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTAT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGAT GCTCAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTG AAGCCGACAG CGGTCGCCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAGCCTG
851 TCGGTGTCCG GATGTTCCGC CTTGACGAAC TGATCCGGCA AAGTTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCCG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGGCGAC GGCAAACTGC CCGCCGTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGT CGGGCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCACAAATG TTGGAACGG CTTATTTTACG
1251 CCGGTTTGCA CAAGATTTCA TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGCGCGGC
1501 GATGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

m794.pep

```

1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFE YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV

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1279

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101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLD AOKQLREQGI LNITGHLMLD HSLWGEVGGSP DDFEADSGSP
201 FMTPPNPMTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSDNLIA
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPFA GTDGTLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*

```

g794/m794 95.5% identity in 515 aa overlap

	10	20	30	40	50	60
g794.pep	VRFNHFIMVTIIIIYVISPANKPVRRPGVPTYPALPYNCFYVTDSPMNFPKTAASLLLL					
m794	VRLNHFIMIAIIIIYVISPANKPARRHSVPTYPALPYNCFYVTDLPMNFPKTAASLLLL					
	10	20	30	40	50	60
g794.pep	ASLAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS					
m794	ASLAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS					
	70	80	90	100	110	120
g794.pep	NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLRDKGIRNITGRMLMD					
m794	NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQKQLREQGILNITGHLMLD					
	130	140	150	160	170	180
g794.pep	HSLWGEVGS PDHFEADSGSPFMTPPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
m794	HSLWGEVGS PDDFEADSGSPFMTPPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
	190	200	210	220	230	240
g794.pep	QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
m794	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
	250	260	270	280	290	300
g794.pep	NRWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTD MNKRSDNLIA RSVFLKLGGD					
m794	NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTD MNKRSDNLIA RSVFLKLGGD					
	310	320	330	340	350	360
g794.pep	GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVTARMAQMLETAYFSPFA					
m794	GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVTARMAQMLETAYFSPFA					
	370	380	390	400	410	420
g794.pep	QDFIDTLPFA GTDGTLRNRFKQSGGLRLKTGT LNNVRALAGYWLGDKPM AVVVIINSGR					
m794	QDFIDTLPFA GTDGTLRNRFKQSGGLRLKTGT LNNVRALAGYWLGDKPM AVVVIINSGR					
	430	440	450	460	470	480
g794.pep	AVSLLPDLN FVAKNIISGGDGWLDKLMCKERRAX					
m794	AVSLLPDLN FVANNIISGGDGWLDKLMCKERRAX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

```

a794.seq
1  GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTAT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACACGGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTCGCATTC CGCAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAGTC ATCATGACC ACCGCTCGGA TGTCCCCGTC

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1280

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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTGCGGACG AATTACCGCT GGGCGACCGA GTTAAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCGG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTTCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGGCGCGAC GGCAAAC TGC CCGCGTTTC
1101 CGAACACGGA CGCTCTGCCG TCCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGT GAAAACGGTT CAGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCGAAATG TTGGAACCG CTTATTTACG
1251 CCCGTTTGCA CAAGATTTC ACGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGCGACGC TCACAATGT CCGCGCCCTT GCAGGTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCGGTTTCCC
1451 TTGTTGCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGCGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAAGGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

```

a794.pep
1  VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCF YVTDLPMNFP
51  KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLV TFAAFKTFGS NYRWATEFKS NGTVNDGTL DNLWAGSGD
151 PVFNQENLL VQRQLREQGI RNITGHLMLD HSLWGEVGS DDFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILTD MNKRSNLI A
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLV ENGSGLSRKE
401 RVTARMMQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
451 TGTLNNVRL AGYWLGDKEP AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDALMC KERRA*

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a794/m794 98.6% identity in 515 aa overlap

	10	20	30	40	50	60
a794.pep	VRLNHFIMIA	IIIIYVISPAN	KPARRHSVPT	YPALPYNCF	YVTDLPMNFP	KTAASLLLLL
m794	VRLNHFIMIA	IIIIYVISPAN	KPARRHSVPT	YPALPYNCF	YVTDLPMNFP	KTAASLLLLL
	10	20	30	40	50	60
a794.pep	ASLAHALDT	GRIPQNEIAV	YVQELDSGKV	IIDHRSDVP	VNPASTMKLV	TFAAFKTFGS
m794	ASLAHALDT	GRIPQNEIAV	YVQELDSGKV	IIDHRSDVP	VNPASTMKLV	TFAAFKTFGS
	70	80	90	100	110	120
a794.pep	NYRWATEFKS	NGTVNDGTL	DNLWAGSGD	PVFNQENLL	AVQRQLREQ	GIRNITGHLMLD
m794	NYRWATEFKS	NGTVNDGTL	DNLWAGSGD	PVFNQENLL	DAQQLREQ	GILNITGHLMLD
	130	140	150	160	170	180
a794.pep	HSLWGEVGS	PDDFEADSG	SPFMTPPNP	TMLSAGMVM	VRAERNAAD	STDILTDPPLPHIFA
m794	HSLWGEVGS	PDDFEADSG	SPFMTPPNP	TMLSAGMVM	VRAERNAAG	STDILTDPPLPHIFA
	190	200	210	220	230	240
a794.pep	QNNLKITASQ	AACPSIKKLM	RASFSDNTL	KLGRNIPES	CLGKPVGVR	MFALDELIRQSFT
m794	QNNLKITASQ	AACPSIKKLM	RASFSDNTL	KLGRNIPES	CLGKPVGVR	MFALDELIRQSFT
	250	260	270	280	290	300
a794.pep	NHWLLGGGRI	SDGIGISDTP	PEGAQTLVA	HSKPMKEIL	TDNMKRSNLI	ARSVFLKLGGD
m794	NHWLLGGGRI	SDGIGISDTP	PEGAQTLVA	HSKPMKEIL	TDNMKRSNLI	ARSVFLKLGGD
	310	320	330	340	350	360
a794.pep	NHWLLGGGRI	SDGIGISDTP	PEGAQTLVA	HSKPMKEIL	TDNMKRSNLI	ARSVFLKLGGD
m794	NHWLLGGGRI	SDGIGISDTP	PEGAQTLVA	HSKPMKEIL	TDNMKRSNLI	ARSVFLKLGGD

1281

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|||||:|||||:|||||:|||||:|||||:
m794      NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTDNKRSDNLIARSVFLKLGGD
           310      320      330      340      350      360

           370      380      390      400      410      420
a794.pep   GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m794      GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
           370      380      390      400      410      420

           430      440      450      460      470      480
a794.pep   QDFIDLPIAGTDGTLRNRFKQSGGLRLKTGT LNNVRALAGYWLGDKPMVAVVVIINSGR
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m794      QDFIDLPIAGTDGTLRNRFKQSGGLRLKTGT LNNVRALAGYWLGDKPMVAVVVIINSGR
           430      440      450      460      470      480

           490      500      510
a794.pep   AVSLLPDLDNFVANNIISGGDGWLD AKLMCKERRAX
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m794      AVSLLPDLDNFVANNIISGGDGWLD AKLMCKERRAX
           490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2699>:

```

g900.seq
1   ATGccgTCTG AAATGCCGTC TGAAACGTGG CAGGCGGAGG TTCGGACGGC
51  ATTGGGTTTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
101 AACAAATCGC GCGCTTCTTT GCGCGCTTTT TGCGCGcctg cctGCAAAAT
151 CTCTTCGATT TCGGAAGGAT TAGAGGTCAA TCGGTTGTAG CGTTCGCGCA
201 GTTCTGCCAA TTCGGCGTTG ATTTTCGCCG CCGAAAGTTT TTTCGCCTCG
251 CCCCAGGCA AGCCGTCGGC AAGCATTTCG GTAAATTCCG CCGTTTCAGA
301 CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
351 GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
401 TTTTGGGTTT TTTTGTCTGT TTCCCAAAGC GGAATGGTAT TGCCGTAGGA
451 TTTGGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTCG ACGTTTTCTG
501 CGATTTTCAC TTCGGGCagg GTGaagagtt cTTGGAaacc gtgggtgaa
551 gggccggcAa tgtcgcgcgc cATTTCgacg tgttgGATTT GGTCCGCCCC
601 GACGGGGACT TCGTTGGCGT TGAACATCAA AATGTCGGCA GTCATCAGAA
651 TCGGATAACT GAACAAACCC ATTTCCACAC CGAAATCGGG GTCTTCTGTC
701 CCGTTTTCCG CATTTGGCTG AACGGCGGCT TTGTAGGCGT GGGCGCGGTT
751 CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
801 CTTCGGGAAT GTCGCTTTGG CGGTAGAAGG TGGTGCGCTC GGGGTCCAGT
851 CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tgGGTGGATT GGTGAATCAT
901 CTCTTGCTCG TGGCATTGA TGATGCCGTG GTAATCGGCG AGGAAGAGGA
951 AGGATTTCGT ATCGGGGTTT TCGCCCGCGC GGACGGCGGG GCGGATGCGC
1001 CCGACGTAGT TGCCCAGATG CGGGGTGCCG GTGGTGGTTA CGCCGGTCAG
1051 AACTCGTTTT TTGCTCATAA AAATGTCCTT ACGGCAGCAA TGCCGTCTGA
1101 AAGGGAAaA. gatgcgCCGA TTATACCCGA TTGCCACAT ACATCCAGCC
1151 GacaACagaC TTTTCCATAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng>

```

g900.pep
1   MPSEMPSETW QAEVRTALGL FQRADADRIA YFIQQFARFF ARFLRACLQN
51  LFDLRRIRGQ CVVAFQAQFCQ FGVDfRRRKf FRLAPSQAVG KHLRKfRRfR
101 RRGEgFIDfK QRAfVGLfRL ARLfHVGNdf VDRfLGfFFvV fPKRNGIaVg
151 FGHfASVQTD QEFdVfVdFh FGQGEeFLET VGEaAGNVAR HFDvLDLVaP
201 DGDFVgVEHQ NVGSHQNRIT EQTHfHTEIG VFLpVfFRIGL NGGfVgVGaV
251 HQTlGGDaGQ NPVQLHHfGN VALAVEGGaL GVESaGKPSG GNGLGGLVNh
301 LLLVAFDDaV VIGEEeEGfG IGVLRRADGG ADGaDVVaQM RGAGGGYAGQ
351 NSFFaHKNVL TAAMPsEREK DAPIIPDLPH TSSRQQTfPY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

```

m900.seq
1   ATGCCGTCG AAACGCGGCA GGCGGAGGTT CGGACGGCAT CGGGTTCATT
51  TCAACGGGCG GATGcCGACC GCATCgG.TA CTTGTGCCAA TAATTGCGCT
101 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTCGATTTG

```

1282

```

151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CGGCGTTGAT TTTCGCCGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATCCACC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATT TTGGGTTTTT
401 tTGTCGTTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CGGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGGCGATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCC GTTTTCTGCA
701 TTTGCCTGCA CGGCGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCTT
751 GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTGAGTCC GCAGGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGT
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTGCGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGG GGATGGCGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCGGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

```

m900.pep
  1 MPSETRQAEV RTASGSFQRA DADRIXFVQ *FACFFTRFR RACLQNLFDL
 51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPCR NGVAVGFHF
151 ASVQTDQEFV VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTAIRVFLP VFCICLHGGF VGMGAVHQTL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHRLRV
301 AFDDTVVIGE EEEFGGIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QQTFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

```

m900/g900

      10      20      30      40      50
m900.pep  MPSETRQAEVRTASGSFQRADADRIGYFVQXFACFFTRFRACLQNLFDLRRVGGQ
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g900      MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGQ
          10      20      30      40      50      60

      60      70      80      90     100     110
m900.pep  LVVAFARFGEFGVDFFRQKFFGFTPRQAVGKHFRKFHRFRRRGEFGVDFKQWAFVGLFRL
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g900      CVVAFQAQFCQFGVDFRRRKFFRLAPSAVGKHLRKFRRFRRRGEGFIDFKQRAFVGLFRL
          70      80      90     100     110     120

      120     130     140     150     160     170
m900.pep  ARLFHIGDDFVDRFLGFFVFPKRNGVAVGFGHFASVQTDQEFVDFIDFHFGQGEEFPEA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g900      ARLFHVGNDFVDRFLGFFVFPKRNGIAVGFGHFASVQTDQEFVDFVDFHFGQGEEFLET
          130     140     150     160     170     180

      180     190     200     210     220     230
m900.pep  VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFICIL
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g900      VGEAAGNVARHFDVLDLVAPDGDVVGVEHQNVGSHQNRITEQTHFHTAIGVFLPVFRIGL
          190     200     210     220     230     240

```


1283

	240	250	260	270	280	290
m900.pep	HGGFVGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	: : : : : :					
g900	NGGFVGVGAVHQTLGGDAGQNPVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	250	260	270	280	290	300
	300	310	320	330	340	350
m900.pep	LRLVAFDDTVVIGEEEEFGFIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVL					
	:					
g900	LLLVAFDDAVVIGEEEEFGFIEVLRRADGGADGADVVAQMRGAGGGYAGQNSFFAHKNVL					
	310	320	330	340	350	360
	360	370	380			
m900.pep	AASMPSEREKDVPIIPDLPTSSRQQTFFPYX					
	: :					
g900	TAAMPSEEREKDAPIIPDLPTSSRQQTFFPYX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2703>:

a900.seq (partial)

```

1   GAGGTTCCGA CGGCATTGGG TTTATTTCAA CGGGCGGATA CCGACCGCAT
51  CACGTACTTT GCCCAATAAT TCGCGTGCTT CTTTACGCGC TTTTTCGCGC
101 CCTGCCTGCA AAATCTCTTC GATTTGCGAA GGGTCGCGCG TCAGCTCGTT
151 GTAGCGTTCG CGCGGTTCCG CGAGTTCGGC GTTGATTTTC GCCGCCAAAA
201 GTTTTTTTGC CTCGCCCAA GCCAAGCCGT CGGCAAGCAT TTTCGTAAT
251 TCTGCCGTTT CAGACGCGCT GGAGAAAGCT TTGTAGATTT CAAACAGAGG
301 GCTTTCGTCG GGCTTCTTCG GCTCGCCCGG CTCTTTCATA TTGGTGATGA
351 TTTTGTGAC  CGATTTTGGG GTTTTTTTGT CGTTTCCCA AAGCGGAATG
401 GTGTTGCCGT AGGATTGGGA CATTTTGCGT CCGTCCAAAC CAACCAAGAG
451 TTCGACGTTT TCGTCGATTT TCACTTCGGG CAGTGTGAAG AGTTCCTGGA
501 AGCGGTGGTT GAAGCGGCCG GCAATATCGC GTGCCATTTT AACGTGTTGG
551 ATTTGGTCGC GACCGACTGG AACTTCATGG GCATTGAACA TGAGAATGTC
601 GGCAGTCATG AGGATAGGGT AGCTGTACAA ACCCATTTCC ACGCCGAAAT
651 CGGGGTCTTC CTGCCCGTTT TCCGCATTG  CCTGCACGGC GGCTTTGTAG
701 GCGTGGGCGC GGTTTCATCA ACCCTTGCGG GTGATGCAGG TCAGAAATCCA
751 GTTCAATTCC ATCACTCGG GAATGTCGCT TTGACGGTAG AAGGTGGTGC
801 GCTCGGGGTC GAGTCCGCAG GCAAGCCAAG TGGCGGCAAC GGCTTGGGTG
851 GATTGGTGAA TCATCTCCGG CTCGTGGCAT TTGATGATAC CGTGTAATC
901 GGCAGAGGAG AGGAAGGATT CGGTATCAGG GTTTTGCGCC GCGCGGACGG
951 CGGGGCGGAT AGCACCAGC TAGTTGCCCA GATGCGGGAT GCCGTGGTG
1001 GTTACGCCGG TCAGAACTCG TTTTGTGCTC ATAAAAATGT CCTGCGGCA
1051 TCAATGCCGT CTGAAAGGGA AAAAGATGCG CCGATTATAC CCGATTGACC
1101 ACCTACATCC AGCCGACAAC AGACTTTTCC ATATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2704; ORF 900.a>:

a900.pep (partial)

```

1   EVRTALGLFQ RADTDRITYF AQ*FACFFTR FLRAQLQNLFLDLRRVGGQLV
51  VAFARFGEFG VDFRRQKFFC LAPSQAVGKH FRKFCRFRRR GESFVDFKQR
101 AFVGLLRRLAR LFHIGDDFVD RFLGFFVVFV KRNGVAVGFG HFASVQTNQE
151 FDFVDFHFG  QCEEFPEAVV EAAGNIACHF NVLDLVATDW NFMGIEHENV
201 GSHEDRVAVQ THFHAIEGVE LPVERICLHG GFVGVGAVHQ TLGGDAGQNP
251 VQFHHFGNVA LTVEGGALGV ESAGKPSGGN GLGGLVNHRL LVAFDDTVVI
301 GEEEEFGFIR VLRRADGGAD STDVVAQMRD AGGGYAGQNS FFAHKNVLAA
351 SMPSEREKDA PIIPDLPTS SRQQTFFPY*

```

m900/a900 88.4% identity in 378 aa overlap

	10	20	30	40	50	60
m900.pep	MPSETRQAEVRTASGSFQRADADRIXFYVQXFACFFTRFRRACLQNLFLDLRRVGGQLVVA					
	: : :					
a900	EVRTALGLFQRADTDRITYFAQXFACFFTRFLRAQLQNLFLDLRRVGGQLVVA					
	10	20	30	40	50	
	70	80	90	100	110	120

1284

```

m900.pep    FARFGEFGVDERRQKFFGFTPRQAVGKHFRKFHRRRRGEGFVDFKQWAFVGLFRLARLF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        FARFGEFGVDERRQKFFCLAPSQAVGKHFRKFHRRRRGESFVDFKQRAVGLLRLARLF
              60          70          80          90          100         110

              130         140         150         160         170         180
m900.pep    HIGDDFVDRFLGFFVFPKRNGVAVGFGHFASVQTDQEFDFIDHFGQGEFFPEAVVEA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        HIGDDFVDRFLGFFVFPKRNGVAVGFGHFASVQTNQEFDFVDFHFGQCEFFPEAVVEA
              120         130         140         150         160         170

              190         200         210         220         230         240
m900.pep    AGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICLHGGF
||::| ||:||||| |::|:|||||:|||||:|||||:|||||:|||||:|||||
a900        AGNIACHFNVLDLVATDWNFMGIEHENVGSHEDRVAVQTHFAEIGVFLPVFRICLHGGF
              180         190         200         210         220         230

              250         260         270         280         290         300
m900.pep    VGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNLRLV
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        VGVGAVHQTLGGDAGQNPVQFHHFGNVALTVEGGALGVESAGKPSGGNGLGGLVNLRLV
              240         250         260         270         280         290

              310         320         330         340         350         360
m900.pep    AFDDTVVIGEEEEFGFIEVLRRADGGADGVVAQMRDAGGGYAGQNSFFAHKNVLAASM
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        AFDDTVVIGEEEEFGFIRVLRADGGADSTDVVAQMRDAGGGYAGQNSFFAHKNVLAASM
              300         310         320         330         340         350

              370         380
m900.pep    PSEREKDVPIIPDLPTSSRQQTFFPYX
|||||:|||||:|||||:|||||
a900        PSEREKDAPIIPDLPTSSRQQTFFPYX
              360         370

```

g901.seq not found yet

g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

```

m901.seq
1  ATGCCCGATT TTCGATGTC CAATTGGGCC GTTGCCCTTT CCATCACATT
51  GGCTGCCCGT TTGTTTACCG TATTAKGyAG TGGCTTGGTG ATGTTTTCCTA
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTTG GTTTGGCGTT TGCCGGCGGT
151 GCGATGGTAT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
251 CATTTTGGC CGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
351 ACGCGCCCAT ATCGCGCGAG TCGGCATGAT GGCGGCGTTT GCGATTACTG
401 CGCACAATTT CCCGAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAT
451 CCAGCAGTCG GGATGCCCTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGGCCAC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTGGGG
601 GCGGCTTTGG GCTATTTGGT TTTCAGCCG TTTTGTGCG CTGCCGTGTT
651 TGGTTCGGTA TTCGCGGTGA TAGCCGGTGT GATGGTGT TTGGCGTTG
701 ACGAGCTGnt GCCGCTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT
751 TACGGCCTGA CAACGGGTAT GCGCGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

```

m901.pep
1  MPDFSMSNLA VAFSITLAAG LFTVLXSGLV MFSKTPNPRV LSFGLAFAGG
51  AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP

```

1285

101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELXPAA KRYSDGHETV
 251 YGLTTGMAVI AVSLVLFHF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq

1 ATGCCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCCTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTCCA
 101 AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTTGGCATT TGCCGGCGGT
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTCGCGCG GCGACCATGG
 251 CATTTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
 301 AACC CGCATG AAAC TTTAGA CGCGCAAGAC CCGTCGTTT C AAGAAAGCAA
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGCGCGTTT GCGATTACTG
 401 CGCACAATT CC CGAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT
 451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
 501 GGAGGGCATT TCCATCGCG CGCGGTTTA TTTTGGCCAC CGCAGCCGTA
 551 AGAAAACGCT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTGGGG
 601 GCGGCTTTGG GCTATTTGGT TTTGCAGCCG TTTTGTGCGC CTGCCGTGTT
 651 TGGTTTCGTA TTCGGCGTGA TAGCCGCTGT GATGGTGTTT TTGGCGTTGG
 701 ACGAGCTGCT GCCGCTGCC AAACGCTATT CAGACGCCA TGAAACCGTT
 751 TACGGCCTGA CAATGGGCAT GCGGTGATT GCCGTCAGCC TGGTATTGTT
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep

1 MPDFSMSNLA VAFSITLAAG LFTVLGSGLV MFSKTPNPRV LSFGLAFAGG
 51 AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP
 101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
 251 YGLTMGMAVI AVSLVLFHF*

m901/a901 98.9% identity in 269 aa overlap

	10	20	30	40	50	60
m901.pep	MPDFSMSNLA VAFSITLAAG LFTVLGSGLV MFSKTPNPRV LSFGLAFAGG AMVYVSLTEI					
a901	MPDFSMSNLA VAFSITLAAG LFTVLGSGLV MFSKTPNPRV LSFGLAFAGG AMVYVSLTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m901.pep	FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP NPHE TLDAQD PSFQESKRRH					
a901	FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP NPHE TLDAQD PSFQESKRRH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m901.pep	IARVGMMAAF AITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
a901	IARVGMMAAF AITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
	130	140	150	160	170	180
	190	200	210	220	230	240
m901.pep	RSRKKTWVAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELXPAA					
a901	RSRKKTWVAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA					
	190	200	210	220	230	240
	250	260	270			
m901.pep	KRYSDGHETV YGLTMGMAVI AVSLVLFHF					
a901	KRYSDGHETV YGLTMGMAVI AVSLVLFHF					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

g902.seq

```

1  ATGCCGTCGG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTGATTTC
151 ACGCCGCGCC TGTTGCGCGT GGGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GGCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTtgcggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTTGGT CTCGcgatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TGCGTGcgcG CGcgcgcgtg aacggcaaGg
551 gcggcaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgctcgtcg tgccaaccca AacggGTTTt GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCCTGC
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTTCttgg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgcgg
801 catCCGCCAT CtgttcggGG TCGCTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCTT
901 GAGCGTCGGA TCGCTGGCCA GCATTTcGCA CACCGCCAA CcTGCGCCAA
951 ACGCCCGACA GAGGCGGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCGA TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

g902.pep

```

1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQON GGS AFCQTQG
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAaIF GDFGDGGQVL
201 IVVVPQTGF EGNgyARRLD HRLQNGGNQR LVLHORATGL DVAHFLGGAA
251 HIDVDDLrPE SDVVTRRIRH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

m902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51  CGCACGCCCA ACTGTGCGTT TTTTCGGCAA GTCTTTCaAG ATAACCTGCA
101 AGCATGTCTG ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TgTCTgTTCG CCGTcGGGCA TTTCTGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG TATGGCGCGG
251 ATGTGGTTCA AAATAGCGGC GGCGCATTCT GCCAAACTCA AGGCAGGCGG
301 CAAAAACACG TGTTGCGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGGCGGC GGTtTGTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGCG GATGAGTTCT TAACGCGCTT
501 CGCCTTTGTA CATTGCGTA CGCGTGCCTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTGCGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CcTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTGCGCTG GTCAGCATTT CGCACACCGC CCAACCTGCG CCAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGcGCaAGT
1001 GCGATGGGGT TGTGATAAAA ATAGCCGCGG ATGTGCATAA TGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

m902.pep
 1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
 51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFCQTQGRR
 101 QNTVFGIMFQ IAEEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
 151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAIFGD FGDDGQVLMV
 201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV
 251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSISER
 301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRKCDGVVDK IAADVHNGSA
 351 FQKSTPLYIF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

m902.pep	10	20	30	40	50
	LHFQRIIKCS	EGIWAVGARP	TVGFFGKSFK	ITCKHVVLRR	RTVQAVDFTT
g902	10	20	30	40	50
	MPSEPERRHGNTALPFP	IAARPTVGFGSGKPF	KITGKCVLRRR	RIVQAVDFTPRL	FAVGHF
m902.pep	60	70	80	90	100
	VDVPAYVFACDAHTGG	VAVKRVYGADVQNSG	GAFCQTQGRRQNT	TVFGIMFQIAEEPR	PA
g902	60	70	80	90	100
	ADVPAVFACDAHTDGL	TIKRVHGADVQNGGS	AFCQTQGRRXNAV	FGIMLQIAEKPR	PA
m902.pep	120	130	140	150	160
	LRAAPYHNAVGGGLF	EDGLGFLRRSNVAVD	PDRDVQTAFGFGD	EFVTRFAFVHLR	TRASV
g902	120	130	140	150	160
	LRAAPYHNAVGGGLF	EDGGFLRRSDVAVD	PGRDVQTAFGLG	DEFVTRLAFVHL	RARAPV
m902.pep	180	190	200	210	220
	DGKGGDAIFGDFGDD	GQVLMVVVPTQTGF	EGNGYACRTDDG	FQNGGNQRLV	LHQRATGL
g902	180	190	200	210	220
	NGKGGNAIFGDFGDD	GQVLIVVVPTQTGF	EGNGYARRLDHRL	QNGGNQRLV	LHQRATGL
m902.pep	240	250	260	270	280
	DIADFFSGTAHV	DVDKLRPKADV	VTRGIRHLLRIAS	GNLHGNNAAFI	GKIAAVQGFSSIS
g902	240	250	260	270	280
	DVAHFLGGAHIDV	DDLRPESDVVTR	RIHFLGVAAGNL	HGNDAAFI	GKITAVQGFSGIP
m902.pep	300	310	320	330	340
	ERRVAGQHFAHRPT	CAKISAKSAERFV	GNARHRRKCDG	VVDKIAADVHN	GSFAFQKSTPLY
g902	300	310	320	330	340
	ERRIAGQHFAHRPT	CAKRPTEAEGFV	GNARHRRKCDG	VVDKITADVHN	GPFAFQKSAPLY
m902.pep	360				
	IFX				
g902	360				
	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

1 TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
 51 CGCACGCCCA ACTGTCGGTT TTTCGGCAA GTCTTTCAG ATAACCTGCA

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101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTCG CCGTCGGGCA TTTCTGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAAACTCA AGGCAGGCGG
301 TAAAACACCG TGTTCGGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTTTGTTTG
401 AGGACGGCTT GGGCTTTTTC CGGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTTGCGTG CGCGTGCCTC CGTGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCCGCCGCTT
651 TGACCACCGC CTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCTT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATTG CGCACACCGC CCAACCTGCG CCAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

```

a902.pep
1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLR RTVQAVDFTT
51 CLFAVGHEVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGRR
101 *NTVFGVMFQ IAEPRSALR AAPYHNAVCG GLFEDGLGFL RRGNAVDPDP
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGNAAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNAHR RRCDDGVVDK IADVHNGSA
351 FQKSTPLYIF *

```

m902/a902 94.7% identity in 360 aa overlap

	10	20	30	40	50	60
m902.pep	LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRTVQAVDFTTCLFAVGHEVD					
a902	LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRTVQAVDFTTCLFAVGHEVD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m902.pep	VPAYVFACDAHTGGVAVKRVYGADVQNSGGAFQCQTQGRRNQNTVFGIMFQIAEPRPALR					
a902	VPAYVFACDAHTGGVAVKRVHGSDDVVQNSGGTFCQTQGRRNQNTVFGVMFQIAEPRSALR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m902.pep	AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASVDG					
a902	AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFGFGNQVVSRAFAFVHLRARASVDG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m902.pep	KGGDAAI FGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGLDI					
a902	KGGNAAIFGDFGDDGQVLMVVVPTQTGFEGNGYARRFDHRLQNGGNQRLVLHQRATGLDI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m902.pep	ADFFSGTAHVDVDKLRPKADVTRGIRHLLRIASGNLHGNNAFIGKIAAVQGFSSISER					
a902	ADFFSGTAHVDVDKLRPKADVTRGIRHLLRIASGNLHGNNAFIGKIAAVQGFSSISER					
	250	260	270	280	290	300
	310	320	330	340	350	360
m902.pep	RVAGQHFAHRPTCAKISAKSAERFVGNAHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF					

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          |||
a902      RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
          310      320      330      340      350      360

m902.pep      X
                |
a902           X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
51  TCCTATTTCT GAGGTGGAaT TGGTGGGTGA aGaaacggct aAATTCGGgt
101 tTGCCTTcaa ccaTGCCTTG tggcAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAatcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAAccctga tggcggGCTA TctgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTT CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTTGGA ACAAGGACTG GAAAACTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgtttc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAc GTCTGCTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTc AGCCCTTTTc
751 GGTAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTCCG CTTCAACCGC CTGTTGTATC GTGATGCCAA ACCGAAAACC
901 TATCTCAGTG TAAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAAGTg ACTGTACAAC GGCGTAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTCGAGTA CGGCAGATTT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCTTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAAACTGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTTAAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGGTTATCGG GCCAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGGCA GATAAAGCTT GGCGGCAACC TGCAATTACG TATATTTACC
1501 GGCCGTGCAT TGAAAAAGCC cgaatatttt cAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTtGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51  LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAFQ NKFPTRSNDL LNLRLDLEOGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMNDSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHRKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQAVSG LSEVYDYNK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRE TKSVIDDAEL TVQRRKTTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTFPQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGKY WRNDLSWQFK
451 PGHQLYLAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKWVTGFO VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAATGT
51  CCGTTTCGAG CAACCATTGG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

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151 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTG GGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCAATC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTTCTAATC TTCGCGATGT AGAGCAGGGC TTGGAAGAAC TCGCTCGTTT
501 GCCCGAGTGT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCAGT
601 ATCGGTATAG ATGATGCCGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTtTATG
701 TTTCATATGG ACGCGGTTTG GCGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAG CTGAAAGCGG ATCCAGAAAG TACAGCGTGC ATTATTCCGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCCAGGTA CATCTCGTAT GAAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AyTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTTCG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTCATCCG ACCATCAGTT CTATCTCGGT GCGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

m903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI
101 QPQNMDGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NNFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTAT
251 GTETESGSR S YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNGKQ
301 YQSSLA AERM LWRNRLHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHAYLN RWQLDGKLSY KRGTMGRQSM PAPEENGDDI LPGTSRMKII
401 TASLDAAAPF XLGKQFFYA TAIQAQWNKT PLVAQDKLSI GSRVTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

              10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL
              |||  |||  |||  |||  |||  |||
g903      MATQVGGANSDEASPCFPISEVELVGEETAKFRFALNHA
              10      20      30

              70      80      90      100     110     120
m903.pep  MKETAFKTMCLGSNNLSRLQKAAQILIVRGYLTSAIIQPQNMDSGILKLRVSAGEIG
              :  :  |  :  |  ||  :  :  :  :  :  ||  ||  ||  :  :  ||  :  :  |  :
g903      LCQTHFVSGKCLHAGDINQIMSLAQNALIGRYTTTRILAAPQDLNSGKQLTLMPGYLR
              40      50      60      70      80      90

```


[illegible]

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTTAAC TG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTCTTCC	TTCTGTGCTC	ATGAAAAGAA	CAGCTTTTAA
201	AAGTGGGATG	TGTTTAGGTT	CCAATAATT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGGCTACC	TCACTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTC	GGGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGGCAGTAT	TAGTGCATTC	AATAACAAAT	TTCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TTCCGCATGT	AGAGCAGGGC	TTGGA AAAAC	TGCGTCGTTT
501	CGCGAGTGTT	AAAACAGATA	TTCAGATTAT	ACCGTCCGAA	GAGAAGGCCA
551	AAAGCGATTG	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTTCAGT

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601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTTATG
701 TTTCATATGG ACGCGGTTTG GTGCACAAA CGGACTTGAC TGATGCCACC
751 GGTACGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCCGAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAAATCATA
1201 ACCGCCGGAT TGGATGCAGC GGCCCCGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTA
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NNKFLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 QTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSLAERM LWRNRFHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRLAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGSGT IPGTSRMKII
401 TAGLDAAPF MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

m903/a903 98.4% identity in 547 aa overlap

	10	20	30	40	50	60
m903.pep	MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL					
a903	MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL					
	70	80	90	100	110	120
m903.pep	MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG					
a903	MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG					
	130	140	150	160	170	180
m903.pep	DIRYEEKRDG KSAEGSISAF NNKFLYRNK ILNLRDVEQG LENLRLPSV KTDIQIIPSE					
a903	DIRYEEKRDG KSAEGSISAF NNKFLYRNK ILNLRDVEQG LENLRLPSV KTDIQIIPSE					
	190	200	210	220	230	240
m903.pep	EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL					
a903	EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL					
	250	260	270	280	290	300
m903.pep	AHKTDLT DATGTETESGSR SYSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ					
a903	VHKTDLT DATGTETESGSR SYSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ					

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	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKT SVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHRAYLN					
a903	YQSSLAERMLWRNRFHKT SVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHRAYLN					
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQQFFYA					
a903	RWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQQFFYA					
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTNTVYG					
	550	560	570	580	590	600
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

```

g904.seq
1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCG CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGTAATGCA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGCGGCGAT
351 CAAACCAGCC GCAGCGGCGC GCGCGGCCG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAATT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTGACGATG CCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGC GCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTTCGTTCAA CACGCGggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTGTCTTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCTG
901 GCCGATTTTG CTTTGCCGCG GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCGAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAAGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTGCGCGCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

```

g904.pep
1  MMQHNRRFAV GAGGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADSRFAP

```

1294

```

51 AGHGFVNRFA GFHRIARTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
101 HTGNAVDLDG AFQGGGIKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS RAGETVGRGN EGVSAVVDVQ
201 QRTLRAFKQQ FFAVFVFFVQ HAGHVGNNHRR NARRDFFDNR HHVFRFNRSR
251 VMQVLELDVV IGKDGIIQFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF AGLVERDVVR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGNDNART DEAIQSFVQD TARNQAQNGF FAADDQGMAR IVAALEAHDA
401 AGFFRQPVND FTFTLVAPLC ADYNNIFSHS HITRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

```

m904.seq
1 ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCGgTG GAGACGATGG
51 CGACCGGCGC GCCGCGAGCT TCTTCAATCC GTTTCAAATA TGCTTTGGCG
101 TTTTCGGGCA ATGCGCCGTA GTCTTCACG CCGAAAGTGG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTTCCACC GCATCGGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC ATAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TAGTAATACA
301 CATAACCGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGCGCT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAAACCTAC GCCTACTTCG TCGAACAATT CCGTCGGGAA
451 CGGGCCCCGAA CCGACGCGCG TGGTATAGGC TTGACGATG CCAAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC TGCGCCCGCC
551 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCGG TTTTGTGTTT
651 TCTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGCTCGGC
751 ATTGTGCAGA TGTTGCAGTT GGACATGTGA ATAGGCAAGG ACGGCATCCA
801 GTTTTTTCACG CAGTTTytCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CCGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 CCGGATTTTG CTTTGTCCGC GCG.ATcTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAAACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACCAcGCC
1201 CCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTaT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

```

m904.pep
1 MMQHNRFFSV GAGGDDGDRR AADFFNPFOI CFGVFGQCAV VLHAESGFAP
51 AGHGFVNRFA GFHRIARTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVSAFCQTY AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS CARQTVGRGN EGISAVVDVQ
201 QRTLRAFKQQ FFAVFVFLVQ HAGHVGNNHRR NARRDFFDNR HHVFRFNRLG
251 IVQMLQLDIV IGKDGIIQFFT QFXRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAAXIF AGLVERDVVR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMR IVAALEAHHA
401 AGFFRQPVND FTFTLVAPLC ADXYNIFSHS HITRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

```

m904/g904
10 20 30 40 50 60
m904.pep MMQHNRFFSVGAGGDDGDRRAADFFNPFOICFGVFGQCAVVLHAESGFAPAGHGFVNRFA
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g904 MMQHNRFFAVGAGGDDGDRRAADFFNPFOICFGIGRQCVVAFHADS RFAPAGHGFVNRFA
10 20 30 40 50 60
70 80 90 100 110 120

```

1295

m904 . pep	GFHRIGTARQDVGFAAVGGQFIADADIDGFNAVHYIEFSNTHTGNAVDLDGAFQGGGIKPA
g904	GFHRIRTARQDVGFAAAWQFVADADIDGFNAVHYIEFGNAHTGNAVDLDGAFQGGGIKPA
	70 80 90 100 110 120
m904 . pep	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
g904	AAARAAGYRTEFVSALRQTCAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
	130 140 150 160 170 180
m904 . pep	CARQTVGRGNEGISAVVDVQORTLRAFQKQFFAVFVFLVQHAGHVGHNHRRNARRDFFDNR
g904	RAGETVGRGNEGVSAVVDVQORTLRAFQKQFFAVFVFFVQHAGHVGHNHRRNARRDFFDNR
	190 200 210 220 230 240
m904 . pep	HHVFRFNRLGIVQMLQLDIVIGKDGIIQFFTFQFXRMQIGGANGAACHFVFVGRADAAAGR
g904	HHVFRFNRSQVMQVLELDVIGKDGIIQFFTFQFXRMQIGGANGAACHFVFVGRADAAAGR
	250 260 270 280 290 300
m904 . pep	ADFAFAARIFAGLVERDVVRQDQRAGRRDFQTAFDVFHACRVQLVDFQAQGGFGGDDNART
g904	ADFAFAARCFAGLVERDVVRQDQRAGRRDFQTAFDVFHACRVQLVDFQAQGGFGGDDNART
	310 320 330 340 350 360
m904 . pep	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVAALAHHAAGFFRQPVNDFTFTLVAPLC
g904	DEAIQSFVQDTARNQAQNGFFAADDQGMARIVAALAHDAAGFFRQPVNDFTFTLVAPLC
	370 380 390 400 410 420
m904 . pep	ADXYNIFSHSHITYRYX
g904	ADYYNIFSHSHITYRYX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

1	ATGATGCAGC	ACAATCGTTT	CTTCGCGGTC	GGGGCCGGTG	GAGACGATGG
51	CGACCGGCGC	ACCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCA
101	TTGGCAGGTA	ATGCGTCGTA	GCTTTTCACG	CCGAAAGTGG	ATTCGCTCCA
151	ACCGGGCATG	GTTTCGTAA	TCGGCTTGCA	GGCTTCTACC	GCATCAGAGC
201	CGCAAGGCAG	GATGTCGGTT	TTGCCGCCGT	CGGGCAATTC	GTAGCCGACG
251	CAGATATTGA	TGGTTTCAAC	GCCGTCCATT	ACATCGAGTT	TGGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGGATGGA	GCGTTTCAGG	GCGGCGGCAT
351	CAAACAGCC	GCAGCGGCGT	GCGCGTCCGG	TTACCGAACC	GAATTCGTGT
401	CCGCGTTCTG	CCAAACCTGC	TCCGACTTCG	TCGAACAATT	CGGTCGGGAA
451	CGGGCCCGAA	CCGACGCGCG	TGGTATAGGC	TTTGACGATG	CCCAAAACAT
501	AATCCAGCAT	TTGAGGGCCT	ACGCCGCGC	CTGCCGAAGC	CGCGCCGGCG
551	AGGCAGTTGG	ACGAAGTAAC	GAAGGGGTAA	GTGCCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAAACAGCAG	TTTTTCGCCG	TTTTTGTFTT
651	TTTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGGCGT	AATGCGCGGC
701	GCGACTTTT	CGATAACCGC	CATCAGCTCT	TCCGCTTTCA	CCGACTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGACGTTGTA	ATAAGCAAAG	ACGGCATCCA
801	GTTTTTCACG	CAGTTTTTCA	GGATGCAGCA	AATCGGCGGC	GCGAATGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCCGC	GGCCGGTCGT
901	GCCGATTTTG	CCTTTGCCGC	GCGATGCTTC	TCGGGCTTGG	TCGAGCGCGA

1296

```

951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGAAGC GCACCACGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

a904 . pep

```

1 MMQHNRFFAV GAGGDDGDRR TADFFNPFQI CFGIGR*CVV AFHAESGFAP
51 TGHGFVNRLA GFYRIRAARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVLDLG AFQGGGIKPA AAACASGYRT EFVSAFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFHRLG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF SGLVERDVIR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQMTR IVAALEAHHA
401 SGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

	10	20	30	40	50	60
m904 . pep	MMQHNRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA					
a904	MMQHNRFFAVGAGGDDGDRRTADFFNPFQICFGIGRXCVAFAHAESGFAPTGHGFVNRLA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m904 . pep	GFHRIGTARQDVGFAAVGQFIADADIDGFNAVHYIEFSNTHGTNAVLDLGAFFQGGGIKPA					
a904	GFYRIRAARQDVGFAAVGQFVADADIDGFNAVHYIEFGNTHGTNAVLDLGAFFQGGGIKPA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m904 . pep	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNIQHRLTYARACRS					
a904	AAACASGYRTEFVSAFCQTCSDFEVQFGRERARTDARGIGFDDAQNIQHRLRAYARACRS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m904 . pep	CARQTVGRGNEGISAVVDVQRTLRAFQKQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR					
a904	RAGEAVGRSNEGVS AVVDVQRTLRAFQKQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m904 . pep	HHVFRFNRLGIVQMLQLDIVIGKDGIOFFTQFXRMQQIGGANGAACHFVFGRADAAAGR					
a904	HHVFRFHRLGIVQMLQLDVVISKDGIOFFTQFFRMQQIGGANGAACHFVFGRADAAAGR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m904 . pep	ADFAFAAXIFAGLVERDVVRQDQRAGRRDFQTAFDVFHACRVQLVDFAQQGGGDDNART					
a904	ADFAFAARCF SGLVERDVIRQDQRAGRRDFQTAFDVFHACRVQLVDFAQQGGGDDNART					
	310	320	330	340	350	360
	370	380	390	400	410	420
m904 . pep	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVNDFFTLVAPLC					
a904	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVNDFFTLVAPLC					
	370	380	390	400	410	420

1297

```

m904.pep      ADXYNIFSHSHITYRYX
              || ||||| ||||| |||
a904          ADYYNIFSHSHITXRYX
              430

```

g906.seq not found yet
g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
51  GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFGG FKPNPWDAAS FWELKNYANP YPGSASAALD
51  QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPYENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTgcaAC GCCGCCGCCT
51  GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGCA AGATTCTGCC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAQREETL ADDVASVMRS
51  SVGSVNPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51  GTTGTGTGCC GCCGGTGCCT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGCA AGGTTCTGCC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGTTAT GCCGTkTGG AAAAActACA TCGGCAAAACC GGCGACAAC
451 TGTTCGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MRKPTDTLPV NLQRRRLCA AGALLLSPLA HAGAQREETL ADDVASVMRS
51  SVGSVNPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVA RGLMQVMPXW KNYIGKPAHN

```

1298

151 LFDIRTNLRY GCTILRHRYN LEKGNIVRAL ARFNGLSGSN KYPNAVLGAW
201 RNRWQWR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907.pep	MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	:	:	:	:	:	:
m907	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
g907.pep	VFDNPKEGERWLSAMSARLARFVPEDEGERRLLVNIQYESSRAGLDTQIVLGLIEVESGY					
	:	:	:	:	:	:
m907	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	70	80	90	100	110	120
g907.pep	RARIIS					
m907	RQYAIISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHRYNLEKGNIVRAL					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

```

1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGCAAC GCCGCCGCTT
51  ATTGTGTGCT GCCGGCGCGC TGTGTGCTCAG CCCGCTGGCA CAAGCCGGCG
101 CGCAACGTGA AGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGC
151 TCTGTCGGCA GCATAAATCC GCCGAGGCTG GTGTTCGACA ATCCGAAAGA
201 GGGCGAGCGT TGGCTGTCCG CGATGTCTGC TCGGTTGGCA AGGTTCGTCC
251 CCGATGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTTGG AAAAATAACA TCGGCAAACC GGCGCACAA
451 CTGTTCGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCACTC GCCCGTTTTA
551 ACGGTAGCCT CGGCAGCAAT AAATATCCGA ACGCCGTTTT GGGCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

```

1  MKKPTDTLPV NLQRRRLCA AGALLSPLA QAGAQREETL ADDVASVMRS
51  SVGSINPPRL VFDNPKEGER WLSAMSARLA RFVPDEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAIISGVA RGLMQVMPFW KNYIGKPAHN
151 LFDIRTNLRY GCTILRHRYN LEKGNIVRAL ARFNGLSGSN KYPNAVLGAW
201 RNRWQWR*

```

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	:	:	:	:	:	:
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAQREETLADDVASVMRSSVGSINPPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	:	:	:	:	:	:
a907	VFDNPKEGERWLSAMSARLARFVPEDEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

1299

	70	80	90	100	110	120
	130	140	150	160	170	180
m907.pep	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
a907	RQYAISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180
	190	200				
m907.pep	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
a907	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1  ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTTCGCA GGTGTAAGT CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTTAT
151 CAAAACGGTC CGCATTTAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatT TTagcttcgc tgaaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPTQTAT LFPIIREQVK PDSIVYTDY RSYDVLVDSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAGT CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTTGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTATATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1  MRKSRLSQYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPTQTAT LFPIIREQVK PDSIFYTDY RSYDVLVDRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

```

g908/m908
10      20      30      40      50      60
g908.pep  MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRLXLIYQNGPHLEMF

```

	: : : : :
m908	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAYYFHRLLLIYQNSPHLEMF
	10 20 30 40 50 60
	70 80 90 100 110 120
g908.pep	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNTQTATLPFIIREQVK
m908	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTVPNTQTATLPFIIREQVK
	70 80 90 100 110 120
	130 140 150 160
g908.pep	PDSIVYTD CYRSYDVL DVSEFSHFSFAETSFSYSQSQHTFCRTTKPYX
m908	PDSIFYTD CYRSYDVL DVREFSHFSFAETSFSYSQSQHTFCRTTKPYX
	130 140 150 160

a908.seq					
1	ATGAGAAAAA	GTCGTCTAAG	CCAGTATAAA	CAAAATAAAC	TCATTGAGCT
51	ATTTTGTCGA	GGTGTAAC TG	CAAGAACGGC	AGCAGAGTTA	GTAGGCGTTA
101	ATAAAAATAC	CGCAGCCTAT	TATTTTTCATC	GTTTACGATT	ACTTATTTAT
151	CAAACAGTC	CGCATTTGGA	AATGTTTGAT	GGCGAAGTAG	AAGCAGATGA
201	AAGTTATTTT	GGCGGACAAC	GCAAAGGCCAA	ACGCGGTCGC	GGTGCTGCCG
251	GTAAGATCGC	CGTATTCGGT	CTTTTGAAGC	GAAATGGTAA	GGTTTATACG
301	GTTACAGTAC	CGAATACTCA	AACCGCTACT	TTATTTCCCTA	TTATCCGTGA
351	ACAAGTGAAA	CCTGACAGCA	TTGTTTATAC	GGATTGTTAT	CGTAGCTATG
401	ATGTATTAGA	TGTGCGCGAA	TTTAGCCATT	TTAGCTTCGC	TGAAACTTCG
451	TTTTCGTATC	AATCACAGCA	CACATTTTGC	CGAACGACAA	AACCATATTA
501	A				

a908.pep

1	<u>MRKSRLSQYK</u>	<u>QNKLIELFVA</u>	<u>GVTARTAAEL</u>	VGVNKNTAAY	YFHRRLRLLIY
51	QNSPHLEMF	GEVEADESYF	GGQRKGKGR	GAAGKVAVFG	LLKRNGKVYT
101	VTVPNTQTAT	LFPIIREQVK	PDSIVYTDCY	RSYDVLDVRE	FSHFSFAETS
151	FSYQSQHTFC	RTTKPY*			

	10	20	30	40	50	60
m908.pep	MRKSRLSQYKQXKLI	ELFVTGVTARTAAEL	LVGVNKNTAAYYF	HRLRLLIYQNSP	HLEMFD	
		:				
a908	MRKSRLSQYKQNKLI	ELFVAGVTARTAAEL	LVGVNKNTAAYYF	HRLRLLIYQNSP	HLEMFD	
	10	20	30	40	50	60
	70	80	90	100	110	120
m908.pep	GEVEADESYFGGQ	RKGKRGGAAGKV	AVFGLLKRNGKV	YTVTVPNTQTAT	LFPIIREQVK	
a908	GEVEADESYFGGQ	RKGKRGGAAGKV	AVFGLLKRNGKV	YTVTVPNTQTAT	LFPIIREQVK	
	70	80	90	100	110	120
	130	140	150	160		
m908.pep	PDSIFYTDCYRSY	DVLDVREFSHFS	FAETSFSYSQSQ	HTFCRTTKPYX		
a908	PDSIVYTDCYRSY	DVLDVREFSHFS	FAETSFSYSQSQ	HTFCRTTKPYX		
	130	140	150	160		

```
g909.seq (partial)
      1  atgcgtaaaa ccgtacttat cCTgaccatc tccgcgcgcc ttttgtcggg
     51  ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
    101  caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcqgctca
```

151 aaaaaggttg actgcgacga gtacggtggc gaacgcggg ccgtgttgcg
201 caaccaaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa
301 acgggggaag qgaagcgatc ggcgaag. .

q909.pep (partial)

1 MRKTVLILTI SAALLSGCTW ETYQDGS GKT AVRACSTGT PLCWQDGRGS
51 KKVDCDEYGG ERRAVLNRNQ RGKPTRRAA TLGKPSFRAR DGGGRVNRAE
101 TGEGKRSAR..

m909.seq

1	ATGCGTAAAA	CCTTCCTCTT	CCTGACCGCT	GCCGCCGCC	TTTTGTGCGG
51	CTGCGCGTGG	GAACTTATC	AAGACGCAA	CGGCAAGACC	GCCGTCCGTC
101	AAAAATATCC	CGCCGGCAGC	CCCGTTTATT	ACCAAGACGG	CAGTCTACTCG
151	AAAAATATGA	ACTACAACCA	ATACCGTCCC	GAACGCCATG	CCGTGTTACC
201	CAATCAAACC	GGCAACAACG	CCGACGAAGA	GCATCGCCAA	CACTGGCAAA
251	AACCAAGTT	TCAAAACCGA	TAA		

m909.ppt

1 MRKTFLFLTA AAALLSGCAW ETYQDGNGKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQ T GNNADEEHRQ HWQKPKFQNR *

Homology with a predicted ORF from *N. gonorrhoeae*

m909/q909

	10	20	30	40	50	60
m909.pep	MRKTF	FLFLTA	AAALLSG	CAWETYQ	DGNGKTA	VRQKYPAG
g909	MRKTV	LILTI	SAALLSG	CTWETYQ	DGSGKTA	VRAKCSTG
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVL	PNQ	TGNNAD	EEHRQ	HWQKPK	FQNRX
g909	ERRAVL	RNKR	GRGKPA	TRRAAT	LGLKPS	FRARDGG
	70	80	90	100		

a909.seq

1	ATGCGTAAAA	CCTTCTTAT	CCTGATGACT	GCCGCCGCC	TTTTGTGCGG
51	CTGCGCGTGG	GAACTTTATC	AAGACGGCAA	CGGCAAGACC	GCCCTGCCGT
101	AAAAATATCC	CGCGCGCAGC	CCCGTTTATT	ACCAAGACGG	CAGCTACTCG
151	AAAAATATGA	ACTACAACCA	ATACCGTCCC	GAAGGCCATG	CCGTGTTACC
201	CAACCAAAAC	GGCAACAACG	CCGACGAAGA	GCATCGCCAA	CACTGGCAAA
251	AGCCCAAAAT	TCAAAACCGA	TAA		

a909.pap

1	MRKTFLILMT	AAALLSGCAW	ETYQDGNKGT	AVRQKYPAGT	PVYYYQDGSYS
51	KNMNYNOYRP	ERHAVLPNOT	GNNADEEHRO	HWQKPKFQNR	*

	10	20	30	40	50	60
m909.pep	MRKTF	FLFL	TAAALL	SGCAW	ETYQD	GNKGK
	TA	VRQKY	PAGTP	PVYYQ	DGSYS	SKNMN
	NYNQY	RP				
		:	:			
a909	MRKTF	LI	MTAA	ALLSG	CAWET	YQDGN
	KTAV	RQKY	PAGTP	PVYYQ	DGSYS	SKNMN
	NYNQY	RP				
	10	20	30	40	50	60

1302

	70	80	90
m909.pep	ERHAVLPNQTGNNADEEHRQHWQPKPFQNRX		
a909	ERHAVLPNQTGNNADEEHRQHWQPKPFQNRX		
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.pep
1  MKKLLLLAAVV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCCG
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.pep
1  MKKLLLLAAVV SLSAAAFAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

g910/m910

	10	20	30	40	50	60
g910.pep	MKKLLLLAAVVSLNAATAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDYW					
	: :					
m910	MKKLLLLAAVVSLSAAAFAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDDHW					
	10	20	30	40	50	60
	70	80	90			
g910.pep	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
m910	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAAACAGCG CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

a910.pep

1303

1 MKKLLLVAVV SLAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
51 VHDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLA	AVVSLS	AAAFAG	DSAE	RQIYGD	PHFEQNRTKAVKMLEQRGYQVYD
a910	MKKLLLV	AVVSLS	AAATAF	AGDSAE	RQIYGD	PYFEQNRTKAVKMLEQRGYQVHDVDADDDHW
	10	20	30	40	50	60
	70	80	90			
m910.pep	GKPVLE	VEAYKD	GREYDI	VL	SYPDLK	IIKEQLDRX
a910	GKPVLE	VEAYKD	GREYDI	VL	SYPDLK	IIKEQLDRX
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq
1 ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCTTGATCGG
51 CGCGGCGGCG GTTGCCCTTTC TCGCTTTCG CGTGGCGGGC GGCGCGGCGT
101 TCGGCGGTTC GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG
201 GCGGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTTGATTT GGACGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
351 CGGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAAGTT
401 CTGCAATGGT TCTGGAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC
451 GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcag aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDDGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq
1 ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG
51 CGCGGCGGCG GTTGCCCTTTC TCGCTTTCG CGTGGCGGGC GGTGCGGCGT
101 TCGGCGGTTC GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG
201 GCGGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTT GGACGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAAGTT
401 CTGCAATGGT TCTGGAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGCC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDDGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10 20 30 40 50 60

1304

```

g911.pep      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
|||||
m911          MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
              10      20      30      40      50      60

              70      80      90      100     110     120
g911.pep      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
|||||
m911          SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              70      80      90      100     110     120

              130     140     150     160
g911.pep      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNAEKNAEKAEX
|||||
m911          ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1   ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGAAGTTCG TCCTGATTGG
51  CGCGCGGCG GTTGCCTTTC TCGCTTCCG CGTGCGCGG GGTGCGCGCT
101 TCGGCGGTTT GGACAAACT TACGCCGTT ATGCCGATT CGGCACATC
151 GCGCGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGC TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTG GGACGGCAAG TATCAGTTC GCAGCGACG TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGC TGCAGCAGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACAGTT
401 CTGCAATGGT TCTGAAAAC CTTATCGGCA AATTCATGAC GAGTTTTGCC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCCGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1   MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFFGGSDKT YAVYADFGDI
51  GGLKVNAPVK  SAGVLVGRVG AIGLDPKSYQ ARVRDLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

              10      20      30      40      50      60
m911.pep      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
|||||
a911          MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
              10      20      30      40      50      60

              70      80      90      100     110     120
m911.pep      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
|||||
a911          SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              70      80      90      100     110     120

              130     140     150     160
m911.pep      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
|||||
a911          ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1   gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

```

151 CGCCCAAAG CCGAAGCCTA TCGGTTCCC TATTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG TACCGCGTCC GACGCGCAAA
251 AACAAAGCGT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTCAA AAACGCGACC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAGGGCGGCA AGGAAATCGT CGTCCGTGCC GAAGTCGGCA
401 TCCCCGGTCA GAAGCCCGTC AATATGGACT TTACCACCTA CCAAAGCGGC
451 GGCAAATACC GTACCTACAA CGTCGCCATC GAAGGCACGA GCCTGGTTAC
501 CGTGTAACGC AACCAATTCG GCGAAATCAT CAAAGCCAAA GGCATCGACG
551 GGCTGATTGC CGAGTTGAAA GCCAAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2760; ORF 912.ng>:

```

g912.pep
  1 VKKSSFISAL GIGILSIGMA FASPADAVGQ IRQATQVLT ILKSGDAASA
 51 RPKAEAYAVP YDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTY
101 GTMLKFKNAT VNVKDNPIVN KGGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTVYR NQFGEI IKAK GIDGLIAELK AKNGGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2761>:

```

m912.seq
  1 ATGAAAAAAT CCTCCCTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
 51 CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAGCCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA ACGGCGATGC CAACACCGCT
151 CGCCCAAAG CCGAAGCCTA TCGGATTCCC TATTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
251 AACAAAGCGT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGTAACGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGTGGACG
551 GACTGATTGC CGAGTTGAAA GCCAAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:

```

m912.pep
  1 MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRQATQVLS ILKNGDANTA
 51 RQKAEAYAIP YDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTY
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTVYR NQFGEI IKAK GVDGLIAELK AKNGGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

```

g912/m912
      10      20      30      40      50      60
g912.pep  VKKSSFISALGIGILSIGMAFASPADAVGQIRQATQVLTILKSGDAASARPKAEAYAVP
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m912      MKKSSLISALGIGILSIGMAFAAPADAVSQIRQATQVLSILKNGDANTARQKAEAYAIP
          10      20      30      40      50      60

      70      80      90     100     110     120
g912.pep  YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKFKNATVNVKDNPIVN
          |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m912      YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN
          70      80      90     100     110     120

      130     140     150     160     170     180
g912.pep  KGGKEIVVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTVYRNQFGEI IKAK
          |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m912      KGGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTVYRNQFGEI IKAK
          130     140     150     160     170     180

      190
g912.pep  GIDGLIAELKAKNGGKX

```

1306

```

m912      | : | | | | | | | | | | | | | |
          GVDGLIAELKAKNGGKX
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

```

a912.seq
1  ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTGAGCAT
51  CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAACCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
151 CGCCAAAAAG CCGAAGCCTA TGCGATTCCC TATTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAT AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGATCCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GGCGTGGACG
551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

```

a912.pep
1  MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA
51  RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYR NQFGEI IAK GVDGLIAELK AKNGSK*

```

m912/a912 98.0% identity in 196 aa overlap

```

m912.pep      10      20      30      40      50      60
              MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP
              | | | | : | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | | | | |
a912           10      20      30      40      50      60
              MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNATQVLSILKSGDANTARQKAEAYAIP
              10      20      30      40      50      60

m912.pep      70      80      90      100     110     120
              YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a912           70      80      90      100     110     120
              YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN
              70      80      90      100     110     120

m912.pep      130     140     150     160     170     180
              KGGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNVQFGEI IAK
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a912           130     140     150     160     170     180
              KGGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNVQFGEI IAK
              130     140     150     160     170     180

m912.pep      190
              GVDGLIAELKAKNGGKX
              | | | | | | | | | | | | | |
a912           190
              GVDGLIAELKAKNGSKX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

```

g913.seq
1  atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTG GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCTT
151 GCCGCGCGCG GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTTAACAACC TGCGCGACGT GGTCAGTTTC GGCAGCAATA
251 TCTTGCGTTT GGAcatCAAA cgcgcaAGcg aAGACctcgT CCGcgtcggc
301 atCAATACCA CCTTCGGTTT GGgcgGGCTC ATTGATATTG CCGGcgGgGg
351 cggcggttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctgGAAAaa cagcaATTAT TTCGTgttgG CCGtcttagg cccgtccacc

```



```

451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
501 tatcgttttc cataccctg ccggacgctg GGgcacgact gCCGCTGCCG
551 CCGTcagtac gcgcgaaggc ctctctgatt tgaccgacag TCtggacgaa
601 gccgccatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
751 CCCGCCGTTC ACGAAGATTC CGTATCCGAA ACACAGGCAG AAGCAGCAGG
801 GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

g913.pep

```

1 MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
51 AARGYRKVTP KPVVRAGVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGVP DNKNTLGDTF ASWGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYPPKNIVF HTPAGRWGTT AAAAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDIDEL VESAETGAAE
251 PAVHEDSVSE TQAEAAGEAE TQPGTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

m913.seq

```

1 ATGAAAAAAA CCGCCTATGC CTTCTCTCTG CTGATCGGGT TCGCTTCCGC
51 CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTC AAC GACCAAGCCG ACCGCTACAT TTTCCGCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTACAGTTC GGCAGCAATA
251 TCTTGCCTT GGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGC
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTGGG CGACAGTTT GCCTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTGTC CCGTCTTAGG GCCGTCCACC
451 GTCGCGGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCAGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTgCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGgtACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

m913.pep

```

1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
51 AARGYRKVAP KPVVRAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETO PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

g913/m913

	10	20	30	40	50	60
g913.pep	MKKTAYAILLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVTP					
	:					
m913	MKKTAYAFLLLLIGFASAPAF AETRPADPYE GYNRAVFKFNDQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g913.pep	KPVVRAGVSNFFNNLRDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGVP					
m913	KPVVRAGVSNFFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
	70	80	90	100	110	120

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	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT					
m913	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPAVHEDSVSETQAEAAGEAETQPGTQPX					
m913	VESAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

```

a913.seq
1  ATGAAAAAAA CCGCCTATGC CTTCTCTCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGCGGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCACTTC GGCAGCAATA
251 TCTTGCGCTT AGACATCAAA CGCGCAAGCG AAGACCTGT CCGCTCGGT
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCTTCGTGGG
401 GATGGAAGAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCTG TCGGACGCTG GGGCAGCACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGC GCGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGGCGGAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

```

a913.pep
1  MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
51  AARGYRKVAP KPVRAVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPVLPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDSLDE
201 AADKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*

```

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAPAARGYRKVAP					
a913	MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVRAVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG INTTFGLGGL IDIAGAGGIP					
a913	KPVRAVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG INTTFGLGGL IDIAGAGGIP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
a913	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCG GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCTG
451 taggctTCGA CGATTTTTCG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTTGT TCGGGCGTGg tgTtttGcgC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAg cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAFAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLW
201 SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCTAGT GTGTTCTGCC
451 GATTCGTAGG CTTTCGACGAT TTTTTCGACC AAAGGATGCC GGACAACGTC
501 TTCGCCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTGTATGT TTTTGGGCAG GTCGATTGTTG
601 CTGGTGTGCG CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGGGGTCAG
651 GAACATTTTC ATTTGTTCGG GCGTGGTGTG TTGCGCTTCG TCGAGGATGA
701 TGATGCGGCC GTTGAGCGTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEDA
101 IRCRKFDXCI GWTDKETDTD TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

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151 DSXASTIFCT KGCRTTSSPV KVKYSPSTL CSFSRASFP DLMFLGRSIW
 201 LVSPVMTAFA PKPMVRNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPAFADRISDLLEARLAQLEHRVAVLESGGNTVKIDLFSGNSTMYVC					
m914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFSGNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEDEAIRCRKFDXCIGWTDKETDTD					
	70	80	90	100	110	120
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSLPDFPCIGFQTALEQCSCSADSXASTIFCTRGCRRTSSPVKVKYSPATP					
m914	TELGFRLCFSLPDFPCIGFQTALEQCSCSADSXASTIFCTKGCRTTSSPVKVKYSPSTL					
	130	140	150	160	170	180
	180	190	200	210	220	230
g914.pep	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
	240					
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

1	ATGAAAAAAT	GTATTTTGGG	CATTTTGACC	GCGTGTGCCG	CCATGCCTGC
51	ATTTGCCGAC	AGAATCGGCG	ATTTGGAAGC	ACGTCTGGCG	CAGTTGGAAC
101	ACCGTGTCCG	CGTATTGGAA	AGCGGCAGCA	ATACCGTCAA	AATCGACCTT
151	TTCGGTTCAA	ATTCCACCAT	GTATGTATGC	AGCGTTACGC	CTTTTCAGAA
201	GACGTTTGAG	GCAAGCGATC	GGAATGAAGG	CGTGGCGCGG	CAGAAAGTGC
251	GTCAGGCGTG	CAACCGCGAA	ACTTCGGCAA	TGTTTTCGGA	AGATGAGGCA
301	ATCCGATGCA	GAAAATTCGA	TGATGTATC	GGTTGGACGG	ATAAAGAAAC
351	GGATACGGAG	CTTGGCTTCC	GTATCTGTTT	TTCTCTGCCC	GATTTTCCAT
401	GCATCGGGTT	TCAGACGCA	TGGAATGTC	AGTCGTGTTT	TGCCGATTCTG
451	TAGGCTTCGA	CGATTTTTTG	CACCAAAGGA	TGCCGACAA	CGTCTTCGCC
501	GGTAAAGGTG	TGGAAATACA	GCCCTTCCAC	GCCGTGCAGT	TTCTCACGCG
551	CATCTTTTAA	TCCCCGATTG	ATGTTTTTGG	GCAGGTCGAT	TTGGCTGGTG
601	TCGCCGGTAA	TGACGGCTTT	CGCGCCGAAG	CCGATGCGGG	TCAGGAACAT
651	TTTCATTTGT	TCGGGCGTGG	TGTTTTGCGC	TTCGTCGAGG	ATGATGTATG
701	CGCCGTTGAG	CGTCCTGCCG	CGCATATAG		

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

1	MKKCILGILT	ACAAMPAFAD	RIGDLEARLA	QLEHRVAVLE	SGSNTVKIDL
51	FGSNSTMYVC	SVTPFQKTFE	ASDRNEGVAR	QKVRQACNRE	TSAMFCDEA
101	IRCRKFD*CI	GWTDKETDTE	LGFRICFSLP	DFPCIGFQTA	LECQSCSADS
151	*ASTIFCTKG	CRTTSSPVKV	WKYSPSTPCS	FSRASFPDL	MFLGRSIWLV
201	SPVMTAFAPK	PMRVRNIFIC	SGVVFCASSR	MMYAPLSVLP	RI*

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m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914.pep	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
a914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD					
a914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--					
	70	80	90	100	110	
	130	140	150	160	170	180
m914.pep	TELGFRICFSLPDFPCIGFQTALECSQSCSADSXASTIFCTKGCRTTSSPVKVKYSPSTL					
a914	TELGFRICFSLPDFPCIGFQTALECSQSCSADSXASTIFCTKGCRTTSSPVKVKYSPSTP					
	120	130	140	150	160	170
	190	200	210	220	230	240
m914.pep	CSFSRASFPDLMLGRSIWLSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
a914	CSFSRASFPDLMLGRSIWLSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	180	190	200	210	220	230
m914.pep	LPRIX					
a914	LPRIX					
	240					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915.seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915.pep

```

1  MKKTLLAIVA VFALSACROA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915.seq

```

1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGC.tG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCcCGGCAG ATTAGCGACC
101 GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG

```

1312

451 GTTGTGCGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

```

m915.pep
  1 MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

```

m915/g915
      10      20      30      40      50      60
m915.pep MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g915      MKKTLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          10      20      30      40      50      60

      70      80      90     100     110     120
m915.pep DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g915      DQPVWFSTVKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWIDAKKAFYVIDS
          70      80      90     100     110     120

      130     140     150     160
m915.pep GFIGGGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
g915      GFIGGGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

```

a915.seq
  1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCAGAG TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG
451 GTTGTGCGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

```

a915.pep
  1 MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

m915/a915 99.4% identity in 164 aa overlap

```

      10      20      30      40      50      60
m915.pep MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a915      MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          10      20      30      40      50      60

      70      80      90     100     110     120
m915.pep DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
a915      DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS

```

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFFIGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
a915	GFFIGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1 ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc tgcttgacgc
51 gtgcGGCGGT Tcggacaaac cgcctgcccga Aaaaccggca ccggcgGaAA
101 accaaAacgt atTgAAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCCG
251 GTTACGACAT TGTGCGCCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCACTG
501 GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCGG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GCGCGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CCGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGG ATTTGGGTGG
851 ATTCTTTGCT GATTCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTG ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCGGCCGCG GCATTGAAGT TTATGGTGCG
1101 CCAAGTGCAG GATGTGAAGG CCGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1 MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51 TVADFEKKNG IKVTYDVYDS DETLESKVL T GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FNPEYTFKLK QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGD LNTAKRR AEEAGGKEKI RVMPKKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1 ATGACCAAAC ATCTGCCCTT GGCCGTCCTG ACTGCTTTGC TGCTTGACGC
51 GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTGCGCCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCACTG
501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCGG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

```

1314

```

751  GGCGGCGATT  TGAACATCGC  CAAACGCCGT  GCCGAAGAAG  CGGGCGGCAA
801  GGAAAAATC   CGCGTGATGA  TGCCCAAAGA  GGGCGTGGGG  ATTTGGGTGG
851  ATTCTTTCGT  GATTCCGAAA  GATGCGAAAA  ACGTCGCCAA  CGCGCACAAA
901  TACATCAACG  ACTTCCTCGA  CCCGGAAGTG  TCGGCGAAAA  ACGGCAATTT
951  CGTTACTTAC  GCGCCTTCGA  GCAAGCCTGC  GCGTGAGCTG  ATGGAAGACG
1001 AATTAAAAAA  CGACAATACG  ATTTTCCCAA  CCGAGGAGGA  TTTGAAAAAC
1051 AGCTTTATCA  TGGTGCCAT  CCAGCCGCG  GCATTGAAGT  TTATGGTGCG
1101 CCA GTGGCAG  GATGTGAAG  CGGGGAAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

m917.pep

```

1  MTKHLPLAVL  TALLLAACGG  SDKPPAEKPA  PAENQNVLKI  YNWSEYVDPE
51  TVADFEKNG  IKVTYDVYDS  DETLESKVL  T  GKSGYDIVAP  SNAFVGRQIK
101 AGAYQKIDKS  LIPNYKHLNP  EMMRLMDGVD  PGHEYAVPFY  WGTNTFAINT
151 ERVKALGTD  KLPDNQWDLV  FDPEYTSKLK  QCGISYLD  SAEIYPMVLNY
201 LGKNPNSSNT  EDIREATALL  KKNRPNIKRF  TSSGFIDDLA  RGDTCVTIGF
251 GGDLNIAKRR  AEEAGGKEKI  RVMPKKEG  VGIWVDSFV  IPKDAKNVANAHK
301 YINDFLDPEV  SAKNGNFVTY  APSSKPAREL  MEDEFKNDNT  IFPTEEDLKN
351 SFIMVPIQPA  ALKFMVRQWQ  DVKAGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLK					
g917	EMMRLMDGVDPDHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTFKLK					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLD SAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
g917	QCGISYLD SAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKKEGVGIWVDSFVIPKDAKNVANAHK					
g917	RGDTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKKEGVGIWVDSFVIPKDAKNVANAHK					
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPSGEDLKNSFIMVPIRPA					
	310	320	330	340	350	360

370

1315

m917.pep ALKFMVRQWQDVKAGKX
 |||||
 g917 ALKFMVRQWQDVKAGKX
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq
 1 ATGACCAAAC ATCTGCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACAG
 51 GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA
 101 ACCGAAACGT ATTGAAAATT TACAACTGGT CGGAATACGT CGATCCGGAA
 151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
 201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAACTCG
 251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAAG
 301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
 351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
 401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
 451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCACTG
 501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
 551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACATAT
 601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
 651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCTG
 701 GCTTTATCGA TGATTTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
 751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CCGGCGGCAA
 801 GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
 851 ATTCTTTCGT GATTCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
 901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
 951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
 1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTGAAAAAAC
 1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
 1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep
 1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
 51 TVADFEKKNG IKVTYDVYDS DETLESKVL T GKSGYDIVAP SNAFVGRQIK
 101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
 151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY
 201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
 251 GGDNLNIAKRR AEEAGGKEKI RVMPKEGVG IWDVSFVIPK DAKNVANAHK
 301 YINDFLDPEV SAKNGNFVY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
 351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

m917/a917 99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m917.pep	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
a917	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m917.pep	QCGISYLSAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					

1316

```

a917      QCGISYLDAAEIYPMVLNLYLGNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTCVTIGFGGDLNIAKRRRAEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      RGDTCVTIGFGGDLNIAKRRRAEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVITYAPSSKPALEMEDEFKNDNTIFPTEEDLKNSFIMVFIQPA
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      YINDFLDPEVSAKNGNFVITYAPSSKPALEMEDEFKNDNTIFPTEEDLKNSFIMVFIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWQDVKAGKX
           ||||||||||||||
a917      ALKFMVRQWQDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

g919.seq

```

1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGCG cgtGGCaggT tgcaggcaAC GGAAGcCTTG
401 CaggtaaggT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCCG ACCTCTCCCG ATTCCCACATC ACCGCGCGCA CAACGGeaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCGcgcTT GACGGCAAag cccCCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAACCcG tccggcaaat acatCCGCAt cggATacgcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGetaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGcatc aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

g919.pep

```

1  MKKHLRSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIROTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGPVGALG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

This corresponds to the amino acid sequence <SEQ ID 2792; ORF 919>:

1	<u>MKKYLFRAL</u>	<u>YGIAAAILAA</u>	<u>CQSKSIQTFF</u>	<u>QPDTSVINGP</u>	<u>DRPVGIPDPA</u>
51	<u>GTTVGGGGAV</u>	<u>YTVVPHLSLP</u>	<u>HWAAQDFAKS</u>	<u>LQSFRLCGAN</u>	<u>LKNRQGWQDV</u>
101	<u>CAQAFQTPVH</u>	<u>SFQAQDFFSF</u>	<u>YFTPWQVAGN</u>	<u>GSLAGTVTGY</u>	<u>YEPVLKGGDR</u>
151	<u>RTAQARFPIH</u>	<u>GIPDDQFIVER</u>	<u>LPAGLRSGKA</u>	<u>LVRNIQTGKN</u>	<u>SGTIDNTGGT</u>
201	<u>HTADLSRFPI</u>	<u>TARTTAIKGR</u>	<u>FEGSGRFLPYH</u>	<u>TRRQINGGAL</u>	<u>DGKAPILGYA</u>
251	<u>EDPVELFFMH</u>	<u>IQGSGRLKTP</u>	<u>SGKYIRIGYA</u>	<u>DKNEHPVSI</u>	<u>GRYMADKGYL</u>
301	<u>KLGGTSMQGI</u>	<u>KSYMRQNPQR</u>	<u>LAELVLQGNPS</u>	<u>YIFFRELAGS</u>	<u>SDNGPVGALG</u>
351	<u>TPLMGEYAGA</u>	<u>VDRHYITLGA</u>	<u>PLFVATAHPV</u>	<u>TRKALNRLIM</u>	<u>AQDTGSAIKG</u>
401	<u>AVRVDFYWG</u>	<u>DEAGEALAGK</u>	<u>QKTTGYVWQL</u>	<u>LPNGMKPEYR</u>	<u>P*</u>

m919/g919

	10	20	30	40	50	60
m919.pep	MKKYLFRAALYGIAAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
	: : :					
g919	MKKHLLRSALYGIAAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER					
	:					
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER					
	70	80	90	100	110	120

1318

	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLAGTVTGYEYVPLKGDGRRRTAQARFPIYGIPDDFISVPLPAGLRSGKA					
	:					
g919	YFTPWQVAGNGSLAGTVTGYEYVPLKGDGRRTERARFPIYGIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	:					
g919	LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
g919	DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA					
	:					
g919	KLGQTSMQGIKAYMRNPQRLAEVLGQNPSYIFFRELAGSGNEGVPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFYFWGYGDEAGELAGK					
	:					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFYFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
g919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCGG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGGCGGCGG CGGGGCGGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAACCC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTCCAT TCGGTTTCA GAAACAGTT
351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACTC CGGTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCGCTCT
801 GAAAACCCCG TCCGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCCG CGCACTGGGC
1051 ACGCCGCTGA TGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAG

```

1319

1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
 1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGGACGAAG CCGGCGAACT
 1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCAACG
 1301 GTATGAAGCC CGAATACCGC CCGTAA

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

      1 MKKYLFRAAAL CGIAAAILAA CQSKSIQTFF QPDTSVINGP DRPVGIPDPA
     51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
    101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
    151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
    201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
    251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
    301 KLGQTSMQGI KAYMQQNQR LAEVLQNPNS YIFFRELTS SNDGPVGALG
    351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
    401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
           10      20      30      40      50      60
m919.pep  MKKYLFRAAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
           |||||
a919       MKKYLFRAAALCGIAAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
           10      20      30      40      50      60

           70      80      90     100     110     120
m919.pep  YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFQAKQFFER
           |||||
a919       YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER
           70      80      90     100     110     120

           130     140     150     160     170     180
m919.pep  YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
           |||||
a919       YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
           130     140     150     160     170     180

           190     200     210     220     230     240
m919.pep  LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
           |||||
a919       LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
           190     200     210     220     230     240

           250     260     270     280     290     300
m919.pep  DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
           |||||
a919       DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
           250     260     270     280     290     300

           310     320     330     340     350     360
m919.pep  KLGQTSMQGIKSYMQRNPQRLAEVLQNPNSYIFFRELTSNDGPVGALGTPLMGEYAGA
           |||||
a919       KLGQTSMQGIKAYMQQNQRLEAEVLQNPNSYIFFRELTSNDGPVGALGTPLMGEYAGA
           310     320     330     340     350     360

           370     380     390     400     410     420
m919.pep  VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
           |||||
a919       VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
           370     380     390     400     410     420

           430     440
m919.pep  QKTTGYVWQLLPNGMKPEYRPX
           |||||
a919       QKTTGYVWQLLPNGMKPEYRPX
           430     440

```

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTTCGGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCTT GGAAATCGTC
301 CCGCTGGACA ATCccgcgca caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacggcctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaagtgg acatcatCCC
501 CTTGcgcmaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAttccc
551 CCGATcaaAG CCTGTGccga AAACAggcgA ACTACaCaac TTtaaccttc
601 caaatcgccc attetCacca tTaa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTAEY OPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCACGCC CACCGmGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCCTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTCTCT TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGCACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YOPTFWSKXK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```

1321

201 SDRSKTHXXE AQAFSDSTDD KGEVDIIXLR QGFWKANVEH KTDFPDQSVC
 251 QKQANYSTLT FQIGHSHH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng) from *N. gonorrhoeae*:

g920/m920

				10	20	30
g920 . pep				PMQLVTEKGKENMIQRGT	YNYQYRSNRPVK	
m920	GGEYLKADLGYGEFPELEPIAKDRLHIFSKPMQLVTEKGKENMIQRGT	YNYQYRSNRPVK				
	40	50	60	70	80	90
g920 . pep	DGSYLVTAIEYQPTFRSKNKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT					
m920	DGSYLVIAIEYQPTFWSKXKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT					
	100	110	120	130	140	150
g920 . pep	KPVGQNLEIVPLDNPADIVHVGXRFKVRVLFERGEPLNPATVTATFDGFDTSDRSKTHKTEA					
m920	KPVGQNLEIVPLDNPANIHVGERFKVRVLFERGEPLNPATVTATFDGFDTSDRSKTHXXEA					
	160	170	180	190	200	210
g920 . pep	QAFSDTTDGEGEVDIIPLRQGFWKASVEYKADFPDQSLCRKQANYTTTLTFQIAHSHHX					
m920	QAFSDSTDDKGEVDIIXLRQGFWKANVEHKTDFFPDQSVCQKQANYSTLT FQIGHSHHX					
	220	230	240	250	260	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2799>:

a920 . seq

1	TGAAAGAAAA	CATTGACACT	GCTCGCCGTT	TCCGCCCTAT	TGCGCGCATC
51	CGCCACGCC	CACCGCGTCT	GGGTGGAAC	CGCCACACG	CACGGCGGCG
101	AATACCTTAA	AGCCGACTTG	GGCTACGGCG	AATTTCCTGA	ACTCGAACCC
151	ATCGCCAAAG	ACCGCCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAAGGC	AAGGAAAAACA	TGATTCAACG	CGGCACATAC	AACTACCACT
251	ACCGAAGCAA	CCGTCCCGTT	AAGGACGGCA	GTTACCTCGT	CATCGCCGAA
301	TATCAGCCTA	CTTCTGGTC	AAAAACAAC	GCAGGCTGGA	AACAGGCGGG
351	CATCAACAA	ATGCCTGACG	CAAGCTATTG	CGAACAAACC	CGAATGTTTCG
401	GCAAAACAT	CGTCAACGTC	GGACACGAAA	GCGCGGACAC	CGCCATCATC
451	ACCAAACCGG	TCGGACAAAA	CTTGGAAATC	GTCCCGCTGG	ACAATCCCGC
501	CAACATTAC	GTAGGCGAAC	GCTTCAAAGT	CCGCGTTCTG	TTCGGTGGCG
551	AACCGCTGCC	CAATGCCACC	GTACCGCCA	CCTTTGACGG	CTTCGACACC
601	AGCGACCGCA	GCAAAACGCA	CAAAACCGAA	GCACAGGCTT	TCTCCGACAG
651	CACAGACGAC	AAAGGCGAAG	TGGACATCAT	CCCCTTGCGC	CAAGGCTTCT
701	GGAAAGCCAA	TGTCGAACAC	AAAGCCGACT	TCCCGGATCA	AAGCGTGTGC
751	CAAAACAGG	CGAACTACTC	GACTTTAACC	TTCCAAATCG	GCCATTTCGCA
801	CCATTAA				

This corresponds to the amino acid sequence <SEQ ID 2800; ORF 920.a>:

a920 . pep

1	*KKTLLTLLAV	SALFAASAHA	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDLRHIFS	KPMQLVTEKG	KENMIQRGT	NYQYRSNRPV	KDGSYLVIAE
101	YQPTFWSKNK	AGWKQAGIKQ	MPDASYCEQT	RMFGKNIVNV	GHESADTAII
151	TKPVGQNLEI	VPLDNPANIH	VGERFKVRVL	FRGEPLNPAT	VTATFDGFDT
201	SDRSKTHKTE	AQAFSDSTDD	KGEVDIIPLR	QGFWKANVEH	KADFPDQSVC
251	QKQANYSTLT	FQIGHSHH*			

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLLSVS	SALFATS	SAHAHRV	VWVETAHT	HGGEY	LKADLGYGEFPELEPIAKDRLHIFS
a920	XKKTLLAVS	ALFAASA	HAHRVWV	ETAHTHG	GEY	LKADLGYGEFPELEPIAKDRLHIFS
	70	80	90	100	110	120
m920.pep	KPMQLVTE	KENMIQR	GTNYQY	RSNRPV	KDGSYL	VIAEYQPTFWSKXKAGWKQAGIKE
a920	KPMQLVTE	KENMIQR	GTNYQY	RSNRPV	KDGSYL	VIAEYQPTFWSKNKAGWKQAGIKQ
	130	140	150	160	170	180
m920.pep	MPDASYCE	QTRMFG	KNIVNV	GVGHES	ADTAII	ITKPVGQNLEIVPLDNPANIHVGERFKVRVL
a920	MPDASYCE	QTRMFG	KNIVNV	GVGHES	ADTAII	ITKPVGQNLEIVPLDNPANIHVGERFKVRVL
	190	200	210	220	230	240
m920.pep	FRGEPLPN	ATVTAT	FDGFDTS	DRSKTH	XEAQAF	SDSTDDKGEVDIIXLRQGFWKANVEH
a920	FRGEPLPN	ATVTAT	FDGFDTS	DRSKTH	KTEAQAF	SDSTDDKGEVDIIPLRQGFWKANVEH
	250	260	269			
m920.pep	KTDFPDQS	VQCQKQ	ANYSTLT	TFQIGH	SHHX	
a920	KADFPDQS	VQCQKQ	ANYSTLT	TFQIGH	SHHX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA  CATTGACACT  GCTCGCcggt  TcCGCACTAT  TTGCCACATc
51  cgCaCACCCC  CACCgCGTCT  GGGTCGAAAC  CgcccCACAg  cAegGCGGCG
101 AATACCTTAA  AGCCGACTTG  GGCTACGGCG  AATTCCCCGA  ACTCGAACCC
151 ATCGccAAAG  ACCgccTGCA  CATCTTCAGC  AAACCGATGC  AGCTGGTTAC
201 CGAAAAAGGT  AAGGAAAACA  TGATTCAACG  CGGCACATAC  AACTACCAAT
251 ACCGCAGCAA  CCGTCCCGTC  AAAGACGGCA  GCTACCTCGT  TACCGCCGAA
301 TATCAGCCTA  CTTCCCGGTC  AAAAAACAAA  GCAGGCTGGA  AACAGGCTGG
351 CATCAAGAA  ATGCCTGACG  CAAGCTATTG  CGAACAAACC  CGTATGTTCT
401 GTAAAAACAT  TGTCAACGTG  GGACACGAAA  GCGCGGACAC  CGCCATCATC
451 ACCAAACCGG  TCGGACAAAA  CTTGGAATC  GTCCCGCTGG  ACAATCCCGC
501 CAACATTCA  GTAGGCGAAG  GCTTCAAAGT  CCGCGTTCTG  TTCCGTGGCG
551 AACCGCTGCC  CAATGCCACC  GTTACCGCTA  CATTTGACGG  CTTTCGACAC
601 AGCGACCGCA  GCAAAACGCA  CAAAACCGAA  GCCCAAGCCT  TCTCCGACAC
651 CACCGACGGC  AAAGGCGAAG  TGGACATCAT  CCCCTTGC  CAAGGCTTTT
701 GGAAAGCGAG  TGTGGAATAC  AAAGCGGATT  TCCCCGATCA  AAGCCTGTGC
751 CAAAAACAGG  CGAACTACAC  AACTTTAACC  TTCCAAATCG  GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLLLAV  SALFATS  AHP  HRVWVETAHT  HGGEY  LKADL  GYGEFPELEP
51  IAKDRLHIFS  KPMQLVTEK  KENMIQRGT  NYQYRSNRPV  KDGSYLVTAE
101 YQPTFRSKNK  AGWKQAGIKE  MPDASYCEQ  RMFGKNIVNV  GHESADTAII
151 TKPVGQNLEI  VPLDNPANIH  VGERFKVRVL  FRGEPLPNAT  VTATFDGFD
201 SDRSKTHKTE  AQAFSDT  TDG  KGEVDIIPLR  QGFWKASVEY  KADFPDQSLC
251 KQQANYTTLT  FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA  CATTGACACT  GCTCGCCGTT  TCCGCCCTAT  TTGCCACATC
51  CGCCACGCC  CACCGCGTCT  GGGTCGAAAC  CGCCACACG  CACGGCGGCG
101 AATACCTTAA  AGCCGACTTG  GGCTACGGCG  AATTTCCCGA  ACTCGAACCC
151 ATCGCCAAAG  ACCGCCTGCA  CATCTTCAGC  AAACCGATGC  AGCTGGTTAC
201 CGAAAAAGGC  AAGGAAAACA  TGATTCAACG  CGGCACATAC  AACTACCACT
251 ACCGAAGCAA  CCGTCCCGTT  AAGGACGGCA  GTTACCTCGT  CATCGCCGAA

```


1323

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGC GC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GTCATTCGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

```

m920-1.pep
1 MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFFDQSV
251 QKQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
g920-1						
	10	20	30	40	50	60
	70	80	90	100	110	120
m920-1.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE					
g920-1						
	70	80	90	100	110	120
	130	140	150	160	170	180
m920-1.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIIKTPVGQNLEIVPLDNPANIHVGERFKVRVL					
g920-1						
	130	140	150	160	170	180
	190	200	210	220	230	240
m920-1.pep	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
g920-1						
	190	200	210	220	230	240
	250	260	269			
m920-1.pep	KTDFFDQSVCKQKQANYSTLTFQIGHSHHX					
g920-1						
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

```

a920.seq
1 TGAAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51 CGCCCACGCC CACCGCGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGC GC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GCCATTTCGCA
801 CCATTAA

```

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This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

```

a920.pep
1  *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIORGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDSTDD KGEVDIPLR QGFWKANVEH KADFPDQSV
251 QKQANYSTLT FQIGHSHH*

m920-1/a920 98.9% identity in 267 aa overlap

m920-1.pep      10      20      30      40      50      60
m920-1.pep      MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
a920             KKKTLTLLAVSALFAASAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
m920-1.pep      70      80      90      100     110     120
m920-1.pep      KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE
a920             KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKQ
m920-1.pep      130     140     150     160     170     180
m920-1.pep      MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNL EIVPLDNPANIHVGERFKVRVL
a920             MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNL EIVPLDNPANIHVGERFKVRVL
m920-1.pep      190     200     210     220     230     240
m920-1.pep      FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIPLRQGFWKANVEH
a920             FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIPLRQGFWKANVEH
m920-1.pep      250     260     269
m920-1.pep      KTDFPDQSVCKQKQANYSTLTFQIGHSHHX
a920             KADFPDQSVCKQKQANYSTLTFQIGHSHHX

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

```

g921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51  Ccagtctatt tatGtgccca cattgacggA aatccccgTg aatccccatca
101 ataCCgtcaa aacggaagCA CTGCAAAAG GTTTTCGCCT CGCCCCCTCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGCTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggAA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

```

g921.pep
1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFR LAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
101 YEIYLRSADV SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMMQMP LK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

```

m921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA

```

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```

251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGATAGAC AGCCAGCGGG GCGCAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

m921.pep

```

1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
51  HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
151 FLMEVMKMOP LK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng) from *N. gonorrhoeae*:

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLAPSHWADVAKISD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	:					
g921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAVDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMOPPLKX					
	:					
g921	SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMOPPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

a921.seq

```

1  ATGAAAAAAT ACCTTATCCC TCTTTCATT GTGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACGCTCAA AACGGAAGCA CCTGCAAAAG GTTCCGCCT TGCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGATAGAC AGCCAGCGGG GCGCAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

a921.pep

```

1  MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
51  HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
151 FLMEVMKMOP LK*

```

m921/a921 99.4% identity in 162 aa overlap

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
a921	MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1   ATGGAAGAAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAC CGGTATCCGA CAGCGGGTTT GCCGCCAATG CAAATGTCCG
201 CCGTTTTGTG GACGATGAAG TCGGGAAAAG GGATTTTCC CAGGCGGAAT
251 GGCAGGATTT TTTTGACAAA GCGGCTTACA AGCGGCACAT CGTCAAGATt
301 ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtggttcc gCacggGAAa
351 ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
401 gcgcggttat cgatgatgtg gcgCAAAAt acggcgGCC TGCCGAGCTT
451 ATCTGGCGA TTATCGGGAT TGAAACGAAT TACGGCAAAA ATACGGGCAG
501 TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551 GCGCCGGGTT TTTCCAAAAA GAATTGGTCG AGCTTTTAAA GCTGGCAAAA
601 GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651 GGGTATGCCG CAATTTATGC CTTCGAGCTA CCGGAAATGG GCGGTGGATT
701 ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
751 gcatcggTTG CCAATTAtat gaagCAGCAC GGTGGCGCA Cgggcggtaa
801 AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CAggcAATCA
851 TTGGCGAAAA AACCGCCCTG ACGCGGACGG TGGCGGATTT GAaggCGTAc
901 ggcacatccc ccggggaaaC GCTCGCAGAT GATGAAAAGg cgGTTTGTGTT
951 CAAACTGGAA ACCGCACCCG CCGTGTGTTGA ATATTATTTG GGCTTGAACA
1001 ATTTTATAC GGTATGGCAG TACAACCACA GCCGGATGTA TGTAAcggcg
1051 gtcaggGACA TTGCCAATTC GTCGGCGGCG CCGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1   MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KESRPAFDA
51  AAVPVSDSGF AANANVRRFV DDEVGKGDFS QAEWQDFFDK AAYKADIVKI
101 MHRPSTSRPW YVFRGTNSGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151 IVAIIGIETN YGKNTGSFRV ADALATLGFD YPRRAGFFQK ELVELLKLAK
201 BEGGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251 ASVANYMKQH GWRTGGKMLV SATLAPGADV QAIIGEKAL TRTVADLKAY
301 GIIPGETLAD DEKAVLFKLE TAPGVFEYYL GLNNFYTVWQ YNHSRMYVTA
351 VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1   ATGAAAAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTTCCTG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACGCCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAAATT CCGGCAAGGC GAAATTTCCG GCGCGCGGCC
401 GTTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCTCG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CGGCAAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCGC GCCGGGTTTT TCCAAAAAGA ATTGGTCGAG

```

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```

601 CTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTTCG CCTTTAAAGG
651 CAGCTATGCG GGC GCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AACGTCGGCG ATGTCGCGGC ATCGGTTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAAA TGCTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GGCGAAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTTGA AGGCGTACGG CATCATCCCC GGCGAAGAGC TTGCAGATGA
951 TGAAAAGGCG GTTTTGTTCA AACTGGAAAC CGCACC GGCG GTGTTTGAAT
1001 ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTTCG TTGGCGGCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

m922.pep

```

1 MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KKERPAFDA
51 AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDfsraew QDFFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASVA NYMKQHGWR TGGKMLVSATL APGADVQAI IGEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

m922.pep	10	20	30	40	50	60
	MKKRKILPLAICLAALSACTAMEARPPRANEAAQAPRAVEMKKESRPAPFDAAAVFDAAAVP					
g922	MEKRKILPLAICLAALSACTAMEARTPRANEAAQAPRADEMKKESRPAPFDAA-----AVP					
	10	20	30	40	50	
m922.pep	70	80	90	100	110	120
	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
g922	VSDSGFAANANVRRFVDDEVGKGDFSQAQEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
	60	70	80	90	100	110
m922.pep	130	140	150	160	170	180
	TGNSGKAKFRGARRFYAENRALIDDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
g922	TGNSGRAKFGARRFYAENRAVIDDDVAQKYGVPaelivaiIGIETNYGKNTGSFRVADAL					
	120	130	140	150	160	170
m922.pep	190	200	210	220	230	240
	ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
g922	ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
	180	190	200	210	220	230
m922.pep	250	260	270	280	290	300
	DGDGHRDIWGNVGDVAASVANVMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
g922	DGDGHRDIWGNVGDVAASVANVMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
	240	250	260	270	280	290
m922.pep	310	320	330	340	350	360
	ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI					
g922	ADLKAYGIIPGETLADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI					

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	300	310	320	330	340	350
		370				
m922 . pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922 . seq
1  ATGAAAAACA  GAAAAATACT  GCCGCTGGCA  ATTTGTTTGG  CGGCTTTGTC
51  TGCCTGTACG  GCGATGGAGG  CACGCCCGCC  CCGGGCAAAT  GAAGCCCAAG
101 CCCCCCGCGC  GGATGAAATG  AAAAAAGAAA  GCCGCCCGCG  GTTTGACGCG
151 GCAGCCGTAT  TTGACGCGGC  AGCCGTACCG  GTATCCGACA  GCGGGTTTGC
201 CGCCAATGCA  AATGTCCGCC  GTTTTGTGGA  CGATGAAGTC  GGGAAAGGGG
251 ATTTTTCCTG  GCGGAATGG  CAGGATTTT  TTGACAAAGC  GGCTTACAAG
301 GCGGACATCG  TCAAGATTAT  GCACCGCCCC  TCCACATCGC  GTCCGTGGTA
351 TGTGTTCCGC  ACGGGAAAT  CCGGCAAGGC  GAAATTTTCG  GGCGCGCGCC
401 GGTTTTATGC  GGAACCCGC  GCGCTTATCG  ATGATGTGGC  GCAAAAATAC
451 GGCGTGCCTG  CCGAACTTAT  CGTGGCGGTT  ATCGGGATTG  AAACGAATTA
501 CGGCAAAAAT  ACGGGCAGTT  TCCGTGTGGC  GGACGCATTG  GCGACCTTAG
551 GCTTTGATTA  CCCCCGCCGC  GCCGGGTTTT  TCCAAAAGA  ATTGGTCGAG
601 CTTTAAAGC  TGGCAAAAGA  AGAAGCGGCG  GATGTTTTTC  CCTTTAAAGG
651 CAGCTATGCG  GCGCAATGG  GGATGCCGCA  ATTTATGCCT  TCGAGCTACC
701 GGAAATGGGC  GGTGGATTAT  GACGGGGACG  GACATCGGGA  CATATGGGGC
751 AATGTTGGCG  ATGTCGCGGC  ATCGATTGCC  AATTATATGA  AGCAGCACGG
801 TTGGCGCACG  GCGGGGAAAA  TACTGTGTGC  TGCAACATTG  GCGCCGGGTG
851 CGGATGTTCA  GGCAATCATT  GGCAGAAAAA  CCGCCCTGAC  GCGGACGGTG
901 GCGGATTGTA  AGGCGTACGG  CATCATCCCC  GGCGAAGAGC  TTGCCGATGA
951 TGAAAAGGCG  GTTTTGTTC  AACTGGAAAC  CGCACCCGCG  GTGTTTGAAT
1001 ATTATTTGGG  CTTGAACAAT  TTTTATACGG  TATGGCAGTA  CAATCACAGT
1051 CGGATGTATG  TAACGGCGGT  CAGGGACATT  GCCAATTCGC  TTGGCGGCCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922 . pep
1  MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KKE SRPAFDA
51  AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGD FSRAEW QDFFDKAAKY
101 ADIVKIMHRP STSRP WYVFR TGN SGKAKFR GARRFYAENR ALIDDDVAQKY
151 GVP AELIVAV IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLK LAKEEGG DVFAFKGSYA GAMGMPQFMP SSKRWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHGWR TGGKILVSATL APGADVQAI GEK TALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEY YLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922 . pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAAPRAVEMKKE SRPAFDA AAVFDAAAVP					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAAPRADEM KKE SRPAFDA AAVFDAAAVP					
	10	20	30	40	50	60
m922 . pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAAYKADIVKIMHRPSTSRP WYVFR					
a922	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAAYKADIVKIMHRPSTSRP WYVFR					
	70	80	90	100	110	120
m922 . pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAAYKADIVKIMHRPSTSRP WYVFR					
a922	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAAYKADIVKIMHRPSTSRP WYVFR					
	70	80	90	100	110	120
m922 . pep	TGN SGKAKFRGARRFYAENRALIDDDVAQKYGVP AELIVAVIGIETNYGKN TGSFRVADAL					
a922	TGN SGKAKFRGARRFYAENRALIDDDVAQKYGVP AELIVAVIGIETNYGKN TGSFRVADAL					
	130	140	150	160	170	180
m922 . pep	TGN SGKAKFRGARRFYAENRALIDDDVAQKYGVP AELIVAVIGIETNYGKN TGSFRVADAL					
a922	TGN SGKAKFRGARRFYAENRALIDDDVAQKYGVP AELIVAVIGIETNYGKN TGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

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```

m922.pep    ATLGFDYPRRAGFFQKELVELLKLAKKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922        ATLGFDYPRRAGFFQKELVELLKLAKKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
            190      200      210      220      230      240

            250      260      270      280      290      300
m922.pep    DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEKTALTRTV
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922        DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEKTALTRTV
            250      260      270      280      290      300

            310      320      330      340      350      360
m922.pep    ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSMYVTAVRDI
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922        ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSMYVTAVRDI
            310      320      330      340      350      360

            370
m922.pep    ANSLGGPGLX
            |||||||||
a922        ANSLGGPGLX
            370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1   ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTCTGTCT
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTAC GCAATATTGT
101 CCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGCGG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTGTGTCGG
201 CGGTTGGACG GGCGCATACT TGGGTAGTAG GATGTTTCAAG CATAAAACGG
251 CGAAAAAGCG TTTTGTGTGT CTGTTCCGTC TGAAGTTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTT GTTCCGCCCG AACTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1   MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRRAVR
51  GKRRIPRHRL LLPALFGGWT GAYLGSRMFR HKTAKKRFV LFRLLTVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1   ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTCTGTCT
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTAC GCAATATTGT
101 CCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GGCAGCAT TCGGCAGCAT GACATTCAA CATAAGACAG
251 CGAAAAAGCG TTTTGTGTGT CTGTTCCGTC TGAAGTTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGA TTAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTGCCGTA CTATTTGTAC TGTCTGCGGC TTCGTGCGCT
401 TGTCTGATT TTTGTTAATC CACTATAT T ATTTTGTCCC GCCTGAATTT
451 TTCGTAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1   MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCRIR
51  GQRRIPRHRL LLPALLGGWV GAYFGSMTFK HKTAKKRFV LFRLLTVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HXYFVPPPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

1330

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

	10	20	30	40	50	60
g923 .pep	MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRRIPEHRL					
m923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100		
g923 .pep	LLPALFGGWTGAYLGSRMFRHKTAKKRFFVLFRLTVSGNVLATCILID-----					
m923	LLPALGGWVGAYFGSMTFKHKTAKKRFFVLFRLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			110	120		
g923 .pep	-----YFVPPELFVKLGQHLX					
m923	PCRTICTVCGFVALSXFLLIHYIYFVPPEFFVKLGQNTX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923.seq

1	ATGAAGCGGC	AGGCTTTCTT	CAAACTGATG	GCGTGTGCGG	CATTTCTGTC
51	TGCCGTTTCG	CTGCGCCTCC	CCGTATTGGG	CGCGTGTTAC	GCAATATTGT
101	CCCTCTATGC	GTTTGCACTT	TACGGCATCG	ACAAACGGCG	TGCCGTGCGG
151	GGAAAACGCC	GCATTCCCGA	ACACCGCCTG	CTGCTGCCTG	CCTTGTTCGG
201	CGGTTGGGCG	GGCGCATACT	TGGGCAGCAG	GATATTCAGG	CATAAAACGG
251	CGAAAAAGCG	TTTTGTTGTG	CTGTCCGTC	TGACTGTTTC	GGGCAATGTC
301	CTGGCGACCC	TCATCCTGAT	TTATAGTGGA	TTAAATTTAA	ACCAGTACGG
351	CGTTGCCTCG	CCTTA.GCTC	AAAGAGAACG	ATTCTCTAAG	GTGCTGAAGC
401	ACCAAGTGAA	TCGGTTCCGT	ACTATTTGTA	CTGTCTGCGG	CTTCGTCGCC
451	TTGTCCTGAT	TTTTGTTAAT	CCACTAT.AT	TATTTTGTCC	CGCCTGAATT
501	TTTCGTAAAA	CTCGGCAGA	ATACCTGA		

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923.pep

1	MKRQAFFKLM	ACAAFLSAVS	LRLPVLGACY	AILSLEYAFAL	YGIDKRRRAVR
51	GKRRRIPEHRL	LLPALFGGWA	GAYLGSRIFR	HKTAKKRFFV	LFRLTVSGNV
101	LATLILIIYS	GNLNQYGVAS	PXAQRERFSK	VLKHQVNRFR	TICTVCGFVA
151	LS*FLLIHYX	YFVPPEFFVK	LGQNT*		

m923/a923 84.6% identity in 175 aa overlap

	10	20	30	40	50	60
m923 .pep	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
a923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m923 .pep	LLPALGGWVGAYFGSMTFKHKTAKKRFFVLFRLTVSGNVLATLILIIYSGNLNLNQYGVAS					
a923	LLPALFGGWAGAYLGSRIFRHKTAKKRFFVLFRLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			130	140	150	159
m923 .pep	PC-----RTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
a923	PXAQRERFSKVLKHQVNRFRITICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

g925.seq

```

1  ATGAAACAAA TGCTTTTGGC cgtcggcggtg ggcgcggtgt TGGCGGGCTG
51  CGGCAaggat gcCGGCGGtt acgagggtTA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

g925.pep

```

1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51  KINVTGKKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQTA QAYLDARNAL PSNOTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

m925.seq (partial)

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTAATTCCTT

```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

m925.pep (partial)

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGLSINTGIGEIPKLSDDGKELYVERRRYVKTDAMKDKIIAHQKKCGQT				
	60	70	80	90	100
	110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

g925-1.seq

```

1  ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51 KINVFTGKEE SLLSEKDG LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKGQTA QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGCGCTG GTGGCGGTGT TGGCGGGCTG
51 CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTTCA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAG
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

m925-1.pep..

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL
51 NKIHVVTKGE ESLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAAAMKDKI IAHQKKGQT AQAYRDARNA LPSNQTYQQH LAAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTKGE					
	: : : : : : : : :					
g925-1	MKQMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE					
	10	20	30	40	50	
	70 80 90 100 110 120					
m925-1.pep	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKGQT					
	: : : : : : : : :					
g925-1	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKGQT					
	60	70	80	90	100	110
	130 140 150 160 170					
m925-1.pep	AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX					
	: : : : : : : : :					
g925-1	AQAYLDARNALPSNQTYQQRQAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

a925-1.seq

```

1  AATAAAATCA ACGTGTTCAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51 AAAAGACGGC GCGCTTTTCA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAG
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

a925-1.pep

```

1  NKINVFTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51 KTDAAAMKDKI IAHQKKGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
101 FEAEFDELEK EIKCNGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

	10	20	30
a925-1.pep	NKINVFTGKEESMLLSEKDGALSINTGIGE		
	: : : : : : : :		
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTKGEESLLSEKDGALSINTGIGE		
	30	40	50
	60	70	80
	40	50	60
	70	80	90

1333

```

a925-1.pep  IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQTAQAYLDARNALPSNQTYQQH
              |||
m925-1      IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQTAQAYRDARNALPSNQTYQQH
              90      100      110      120      130      140

              100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
              |||
m925-1      LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX
              150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGTTGGCAG TCAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGacAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAactGC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GGCGGGCGCG CCTtaccGCA
401 TCCGTTcAGA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcCGACAGT GGGGGGCaag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGTTGGCAG TGAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAAAGT
301 GCGGAAGAAAT TGAGCAGGCA GCTGGTCGGT TTCAAactGC CAATCCAATA
351 TCTGCATATC TGGGCGAGAT GCAGGCGTGT GGCGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACCC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCAGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWVGR
151 ADSGGQVRTL QLNNGNLNIR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

              10      20      30      40      50      60
g926.pep  MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              |||
m926      MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              10      20      30      40      50      60

              70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGGKGNVYQAEGETEDLSRQLVGFKLPIQYLHI
              |||
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGGKGNVYQAESEELSRQLVGFKLPIQYLHI
              70      80      90      100     110     120

              130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEQYGTWIGQNCRQWGASPNVATE

```

1334

|||||
m926 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
130 140 150 160 170 180

a926.seq

```

1 ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGGCG
51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
101 GCAGTTTCAC GCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GCGGGGCGCG CTTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CCGCAGAACC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATT
501 GAACATCAGG CTGGTTTTC ACGAGATTGG TATGCCGTCT GAAACCGAAA
551 CCAAGAACA ATGCGCGGCA CGCATACAGT AA

```

a926.pep

```

1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEKGK
51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGLAVD GKGNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
151 ADGGQVRTL QLNNGNLNR LVFTEIGMPS ETETQEQQAA RIQ*

```

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASVILLTACAQLPQNNENLWQPSSEHISFSAEGRRLAVKAEKGKSYANFDWTYQ					
a926	MKHTVSASVILLTACAQLPQNNENLWQPSSEHTRSFTAEGRLAVKAEKGKSYANFDWTYQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m926.pep	PPVETININTPLGSTLGQLCQDRDGLAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI					
a926	PPVETININTPLGSTLGQLCQDRDGLAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
	130	140	150	160	170	180
	190					
m926.pep	ETETPERCAARTRX					
a926	ETETQEQQARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

g927.seq

```

1 atgaaaacct acGCACAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
51 CAGCCCcgca GCcgatTcaa accaTCCGTC CGGAcAaAAT GCCCCGGCCA
101 ATACCGAATC cgacGgaaAA AACATtaccC TGctcaatgc cTcgtagcat
151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcggaaCATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCCACGGCG
251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCCTACA

```

1335

```

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATAACGT TACGGTCTGA
551 AAGCCAACAA CGGcaaCGAG CAGGAAGCCC AAAAAGCTCGT CGCATCCATC
601 CTCAAAAACA CACCCGTTTT TGAAAACGGC GGACGCGC.C CGCCGCCACC
651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
701 agCcaactac gtCAGCAAAA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

```

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VTRYFYKEYD HLFVGTYSQE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV
101 VTMMQSSDID LLEKXGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIAKTSN GRYAFLGAYG YGLKANNGNE QEAQKLVASI
201 LKNTVPVFENG GRXPPPPSH NATSATYSSL LKTKPTTSAK N*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

```

1 ATGAAACCTT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
51 CAGCCCCGCA GCGGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGCCA
101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
151 GTGGCACGGG ATTTTACAA AGAATACAAC CCCTTATTTA TCAAAACATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCCAA ACAGATCCGC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
501 CAAACCTCG GGCAACGGAC GCTACGCTT CCTCGGCGCA TACGGTTACG
551 GTCTGAAAC CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
601 TCCATCCTCA AAAACACCCC CGTTTTTGAA AACGGCGGAC GCKCgCCACC
651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTTGAAAA
701 CGAAGCCAAC TACGTCAGC AAAAActGA

```

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

```

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
101 VTMMQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
201 SILKNTVPFE NGGRXPPPPS HNATSATYSS LLKTKPTTSA KN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
m927	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
g927.pep	HLFVGTYSQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMMQSSDIDLLEKXGLVEK					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMMQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
g927.pep	HLFVGTYSQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMMQSSDIDLLEKXGLVEK					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMMQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
g927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGNRYAFLGA					
m927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA					
	130	140	150	160	170	
g927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGNRYAFLGA					
m927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA					
	130	140	150	160	170	180

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	180	190	200	210	220	230
g927.pep	YGYGLKANNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTS					
	::					
m927	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPP-SHNATSATYSSLLKTKPTTS					
	190	200	210	220	230	

	240
g927.pep	AKNX
m927	AKNX
	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1  ATGAAACCT  ACGCACGGC  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATCAA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTTTCCTT  GTCCGAAAAA  ACAACCCCAA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAAACCTCG  GGCAACGGAC  GCTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAAC  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTTGAAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAAAGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1  MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  FLFIKTYQSE  HPGTSVSIQQ  SHGSSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTPVFE  NNGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*
  
```

m927/a927 99.2% identity in 242 aa overlap

	10	20	30	40	50	60
m927.pep	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
a927	MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60

	70	80	90	100	110	120
m927.pep	PLFIKTYQSEHPGTSVSIQQSHGSSSKQALSVANGLQADVVTMNQSSDIDLEKKGLVEK					
a927	PLFIKTYQSEHPGTSVSIQQSHGSSSKQALSVANGLQADVVTMNQSSDIDLEKKGLVEK					
	70	80	90	100	110	120

	130	140	150	160	170	180
m927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNLAKDGVNIVIANPKTSNGNGRYAFLGA					
a927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNLAKDGVNIVIANPKTSNGNGRYAFLGA					
	130	140	150	160	170	180

	190	200	210	220	230	240
m927.pep	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA					
a927	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA					
	190	200	210	220	230	240

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m927.ppep KNX
 III
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GCGGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTTGGAAGAA AAACgctggg CATCGGTTAC AGTCTCGCTC
 401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
 451 GCGCGCATT TACATCcgat TATGCagtcg attgCcggCA GttacggctC
 501 caatCCCACA AAAGGCACag aaggcaagat gggtAAATAT TtggcTtgg
 551 tcaattaTCA TTCcaatCCC atttcgctcg ctAtggctat taCTGcaact
 601 gCCCCcaacc CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag
 651 ttcccgctCTT Tcttgggggg cgTGGGcgtg ggcaaTGGCT Gttccccggc
 701 ttatcgctt TtctgTTATG CTTTGATTTT TATATTTTTT GTATCCGCCT
 751 GAAATTAAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGTCGAG
 801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
 851 GTATCTTGCT GCTGTTGTGG GCAGATGTTC CCGCCCTTAT TACCGGCAAT
 901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT
 951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAA
 1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATGATTAT GATGGCCGCA
 1051 TTTTtaAATA Aactcggact gattaaatGG TTCTCCGAG TGTGGCGGA
 1101 AagtgtcggC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
 1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
 1201 ATTACCGCTA TGTCGGCGC ATTTCTCGCT GCTGCCGTTT CACTGAATGC
 1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
 1301 TGACCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCCGCTCG
 1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTTA TCATGAGCGT
 1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTGG TGGAAAGTTC
 1451 TGGGATATTG GTAA

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep
 1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
 51 VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
 101 SRGLLTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
 151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMAITAT
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
 251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMPASTTAH
 401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
 451 GYTTMGEWWK AGFIMSVVNF LIFSIVIGSIW WKVLGYW*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GCGGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
 401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

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```

451  GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501  CAATCCCAGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551  TCAACTATCA TTCCAATCCC ATTTTCGTCGG CTATGTTTAT TACTGCAACT
601  GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651  TTCCGCTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701  TTATCGCCTT TTTCGTTATG CCTTTGATTT TATATTTwyT GTATCCGCCT
751  GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801  GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851  GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901  CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951  GCTTTTGCTT TCCGGTGTAT TGA CTGTTGGG CGATGTTTGT AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGCGCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGGCGGA
1101 AAGTGTGGCG GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGGCG ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTTCG
1351 GGTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

```

m929.pep
1  MKLGFKPIPL AIAAVLCALV LALVPDGVK PQAWTLLAMF VGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNVQ FAKDRLEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASTTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng)

from *N. gonorrhoeae*:

g929/m929

```

          10      20      30      40      50      60
g929.pep  MKLGFKPIPLAIAAVLCALVLALVPDGVKPAWTLLAMFVGVIAAIIGKVMPLGALSII
          |||
m929       MKLGFKPIPLAIAAVLCALVLALVPDGVKPAWTLLAMFVGVIAAIIGKAMPLGALSII
          10      20      30      40      50      60

          70      80      90      100     110     120
g929.pep  AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV
          |||
m929       AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV
          70      80      90      100     110     120

          130     140     150     160     170     180
g929.pep  FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY
          |||
m929       FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY
          130     140     150     160     170     180

          190     200     210     220     230     240
g929.pep  LALVNYHSNP ISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM
          |||
m929       LALVNYHSNP ISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM

```


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	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLSEMGKMSADEIIMAVIFGILLLLWADV PALITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTAHTAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTAHTAMFGAFAAAVSLNAPAM					
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

```

a929.seq
1  ATGAAATTGG  GTTTCAAACC  GATACCCCTC  GCCATTGCCG  CAGTATTGTT
51  CGCCTTGGTT  TTGGCACTGC  CCGTACCCGA  CGGGGTCAAG  CCTCAGGCTT
101  GGACGCTGCT  GGCCATGTTT  ATCGGTGTGA  TTGCCGCCAT  TATCGGCAAG
151  GCCATGCCGT  TGGGTGCGCT  GTCGATTATT  GCCGTGCGGT  TGGTCGCAGT
201  AACCGGCGTA  ACCGCCGACA  AACCGGTGTC  GGCGATGAGC  GATGCGTTGA
251  GTGCGTTCGC  CAATCCGTTG  ATTTGGCTGA  TTGCCATCGC  AGTTATGATT
301  TCGCGCGGTT  TGCTCAAAAC  AGGGCTGGGG  ATGCGTATCG  GATATTTGTT
351  TATCGCCGTT  TTTGGAAGAA  AAACGCTGGG  CATCGGTTAC  AGTCTCGCTC
401  TTTCCGAACT  GCTGCTGGCT  CCCGTTACCC  CTTCCAATAC  CGCGCGCGGC
451  GCGCGCATTA  TACATCCGAT  TATGCAGTCG  ATTGCCGGCA  GTTACGGCTC
501  CAATCCCGCA  AAAGGCACAG  AAGGCAAGAT  GGGTAAATAT  TTGGCTTTGG
551  TCAACTATCA  TTCCAATCCC  ATTTGCTCGG  CTATGTTTAT  TACTGCAACT
601  GCCCCCAACC  CTTTAATCGT  CAACTTGATT  GCCGAAAATT  TAGGCAGTAG
651  TTTCCGTCTT  TCTTGGGGGG  CGTGCGCGTG  GGCAATGGCT  GTTCCCGGCG
701  TTATCGCCTT  TTTCGTTATG  CCTTTGATTT  TATATTTTTT  GTATCCGCCT
751  GAAATTAAAG  AAACGCCCAA  TGCCGTTCAA  TTTGCCAAAG  ACCGTCTGAG
801  GGAGATGGGT  AAAATGTCGG  CAGACGAAAT  CATTATGGCG  GTCATTTTCG
851  GTATCTTGTT  GCTGTTGTGG  GCAGATGTTC  CCGCCCTTAT  TACCGGCAAT
901  CACGCTTTTA  GTATCAACGC  CACCGCCACC  GCATTTATCG  GATTAAGCCT
951  GCTTTTGCTT  TCCGGTGTAT  TGACTTGGGA  CGATGTTTTG  AAAGAAAAAA
1001  GCGCGTGGGA  TACGATTATT  TGGTTTGGCG  CATTGATTAT  GATGGCCGCA
1051  TTTTAAATA  AACTCGGACT  GATTAAATGG  TTCTCCGGAG  TGTGGCGGGA
1101  AAGTGTCGGC  GGTTCGGGCG  TTAGCGGCAC  GGCTGCGGGC  GTAATCCTCG
1151  TGCTTGCTTA  TATGTATGCG  CATTATATGT  TTGCCAGTAC  TACTGCACAT
1201  ATTACCGCTA  TGTTCCGGCG  ATTTTTCGCT  GCTGCCGTTT  CACTGAATGC
1251  CCCGGCGATG  CCGACCGCGC  TGATGATGGC  GGCCGCATCT  AACATTATGA
1301  TGACCCTCAC  TCATTATGCG  ACCGGTACTT  CGCCTGTGAT  TTTCCGGTTCG
1351  GGCTACACCA  CAATGGGAGA  ATGGTGGAAG  GCGGGTTTAA  TCATGAGCGT
1401  AGTCAATTTT  CTGATTTTTT  TCGTTATCGG  CAGCATTTGG  TGGAAAGTTC
1451  TGGGGTATTG  GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```
a929.pep
  1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
 51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101  SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151  GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201  APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYFP
251  EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301  HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351  FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMEASTTAH
401  ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451  GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*
```

m929/a929 99.6% identity in 487 aa overlap

	10	20	30	40	50	60
m929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPQAWTLLAMFVGIVIAAIIGKAMPLGALSII					
a929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPQAWTLLAMFIGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m929.pep	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRI					
a929	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m929.pep	FGRKTLGIGYSLALSELLLPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
a929	FGRKTLGIGYSLALSELLLPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m929.pep	LALVNYHNSPISAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
a929	LALVNYHNSPISAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m929.pep	PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVPALITGN					
a929	PLILYFLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVPALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
a929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
m929.pep	FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFFAAAVSLNAPAM					
a929	FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFFAAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
m929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
a929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
m929.pep	WKVLGYWX					

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a929 WKVLGYWX

g930.seq not found yet
g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```

1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTGT GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAC GAAAGGGTGT TGGAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWLVEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```

1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCTGAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAGG
201 ACGTATTGCA GCATTCCAAA ACAAAATTTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 AAGTGATGTC GTGGTGCAAT GGGCGTAACG TCTGTGCCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGAAGTGTG ATATGTTCTA
501 TGTAAATTTT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCGGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTCCGG TCAACCGGCC TGTGTATATG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACGAGGGAAA CAAAAAGTTA
801 CATTGATGAT GCCGAACCTG CTGTACAACG GCGTAAACCC ACAGGTTGGT
851 TGGCAGAACT TTCCACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGGCATG AAAGATGCTC TGCGCGCGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GGCAGCAACG TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTTATCGGG CCAAACTCTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGGTTATTC GTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```

1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQLTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKLCP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGTFPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYSVSKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FGEGTSRMKI WTASADVNTF FQIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGMESLPAER GWYWRNDLSW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGQ 1KLGGNLDHYD

```

451 IFTGRALKKP EYFQTKKWVT GFQVGYSF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```
1 ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51 CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTT TGCCATTAAC GAAGTGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTTT CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTGGA ACAAGGACTG GAAAATCTCA AACGTCTCCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAACC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGCTGTGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAATAAT TGGACGTTTC ATTGGCGGTA CGCCCGATGA GGAAAGTTTT
901 GACGGCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCTTTTC GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAAACTGTG GATGAGGGAA ACAAAAAGTT
1151 ACATTGATGA TGCCGAACTG ACTGTACAAC GGCGTAAAC TGCGGGTTGG
1201 TTGGCAGAAC TTTCCACAAA AGAATATATC GGTCGAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAAACGCG GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAGC CTTTGGCGAA GGCACGTCAC GTATGAAAAA TTGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTTCAAATC GGTAACAGC TATTTCCTTA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAAACTGGC TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTAAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTACGACA ATCCGCCAAA TGGTTATCGG GCCAAACTCT ATCGGCGACA
1651 GCAATTGGGA TACGCGGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA
1701 TATATTACC GGCCGCGCAT TGA AAAAGCC CGAATTTTTC CAATCAAGGA
1751 AATGGCAAG CGGTTTTCAG GTAGGCTATA CGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```
1 MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNPAEIRM QODIQQRQRE
51 EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFO NKFPTSRNDL
201 LNLRLDLEQGL ENLKRLLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDNSGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGHRRKGGSN NYAVHYSAPF GKWTWAFNHN GYRYHQAVSG LSEVVDYNGK
351 SYNTDFGFNR LLYRDAKRKT YLGVKLMWRE TKSYYIDDAEL TVQRKRTAGW
401 LAELSHKEYI GRSTADFKLK YKRGTGMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTFFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWY WRNDSLWQFK PGHQLYLGAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*
```

m930-1/g930-1 95.4% identity in 478 aa overlap

```
90      100      110      120      130      140
m930-1.pep AINEVVLEGEHHRFQFALKRALRETGFQAGKCLHAGNINQIMSLAQNALIGRGYTTTRI
g930-1.pep      |||||:|||||
                GKCLHAGDINQIMSLAQNALIGRGYTTTRI
                        10      20      30

150      160      170      180      190      200
m930-1.pep LAAPQDLNSGKLQTLTIPSYLRSIRIDRSNDDQTHAGRIAAFNKFPTSRNDLLNLRDLE
g930-1.pep      |||||:|||||
                LAAPQDLNSGKLQTLMPGYLRSIRIDRSNDDQTHAGRIAAFNKFPTSRNDLLNLRDLE
                        40      50      60      70      80      90

210      220      230      240      250      260
m930-1.pep QGLENLKRLLPTAEADLQIVPVEGEPNQSDVVVQWRQRLPYRVSVGMDNSGSEATGKYQG
                ||||| ||||| ||||| ||||| ||||| |||||
```

a930-1.pep not yet found

q931.seq

1	ATGAAACCCA	AATTCAAAC	CGTTTAAAC	GCGCTGCTT	TGGCGGTTT
51	CTGCGCTT	ATGGCGGCA	CCGCGCTCT	GATGGAACC	GATATGGGA
101	ATATCCGTT	GGTTTGGAC	AATCCAAAG	CCTCAAAAC	CGTTGCCAA
151	TTCTGTGCT	ATGCCGAAA	AGGCTTTAC	GACCAACGA	TTTTCCACC
201	CGTcatCGC	GGCTTCGTCA	TCCAAGGCGA	CGGATTGACC	GAGGACTTGG
251	TGCAAAAGGC	AACCGATAAG	GCCGTTGCCA	ACGAATCCGG	caacgCTTG
301	AAAAACCGC	TCGGCACCAT	CGCAATGGCG	CGGACGGCA	CCCCGATTC
351	CGCCGCCCGC	CAATTCTTTA	TCAATCTGGC	GGACAACGTT	TCGCTCGACT
401	ACAAAAACGG	ACAATACGGC	TACACCGTTT	TCGGCAGGGT	AGAAAGCGGA
451	ATGGACACCG	TTTCCAAAAT	CGCCCGCGTC	AAAACCGCCA	CGCGCGGCTT
501	TTATCAAAAC	GTACCCGTAC	AGCCCGTCAA	AATCCGTCGC	GTTGTTGTCTG
551	GGCAGTAACA	GCAGACAGA	CGTTCAGACG	GCGTCGCCCG	TTTCCCAAAA
601	AACGCGTTT	AA			

q931.pep

1 MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKTVAN
51 FVRVYARKGFI DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGO*

1344

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

m931.seq

```

1  ATGAAACCCA AATTCAAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201 CGTTATCGAC GGTTTTGTTA TCCAGGGCGG TGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTGCGCA ACGAATCCGG CAACGGCTTG
301 AAAAAACACCG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
351 CGCCACCAGC CAATTCCTTA TCAATCTGGC GGACcA.kCT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

m931.pep..

```

1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

	10	20	30	40	50	60
g931.pep	MKPKFKTVLTALLLAVSLPSMAATRVLMDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
g931.pep	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNPVPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVPVKIRR					
	130	140	150	160	170	180
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNPVPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

a931.seq

```

1  ATGAAACCCA AATTCAAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CACCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTGCGCA ACGAATCCGG CAACGGCTTG
301 AAAAAACTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTC
351 CGCCACCAGC CAATTCCTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC

```

1345

451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
 501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep
 1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLT	ALLLAVSLPS	MAATHVLMET	DMGNIRLVLD	ESKAPKTVAN	FVRYARKGFY
a931	MKPKFKTVLT	ALLLAVSLPS	MAATHVLMET	DMGNIRLVLD	ESKAPKTVAN	FVRYARKGFY
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVID	GFVIQGGGLT	EDLAQKASDK	AVANESGNGL	KNTAGTIAMART	TAPDSATS
a931	DNTIFHRVIG	GFVIQGGGLT	EDLAQKASDK	AVANESGNGL	KNTVGTIAMART	ADPDSATS
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	QFFINLADXX	SLDYKNGQYG	YTVFGRVESG	MNTVSKIARV	KTATRGFYQN	VPVQPVKIRR
a931	QFFINLVDND	SLNYKNGQYG	YTVFGRVESG	MNTVSKIARV	KTATRGFYQN	VPVQPVKIRR
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51 GTTTGGGGGA TTTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep
 1 MKYIVSISLA MGLAACSFGG FKPWPDAAS FWELKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPENK
 101 KYEWPREEGK TK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCACCGC

g934 . pep

1	MKKIIASALI	ATFALTACQD	DTQARLERQQ	KQIEALQQQL	AQQADDTVYQ
51	LTPEAVKDTI	PAQAQANGNN	QGPVTGKRRA	AVYLRPIDRK	LAAAKPDWRG
101	GRRVYRQAG	KQIHTGGQPR	QPRRPSRACC	LPSVRTPQCA	HQOGFEHAQP
151	PCKTTGGAGA	ALPPDNAPAR	QLPPSRYARF	RQKAVNPARQ	CRLKGFQTAF
201	LYLLGALLCC	RLIFFRRHFVS	KRLMSGWOF*		

m934.seq (partial)

1	CGGCTCGAAC	AGCAGCAGAA	ACAGATTGAA	GCCCTGCAAC	AGCAGCTCGC
51	ACAGCAGGCA	GACGATACGG	TTTACCAACT	GACTCCCAGAA	GCAGTCAAAG
101	ACACCATTCC	TGCCGAAGCA	CAGGCAAAACG	GCAACAACgG	GCAACCCGTT
151	ACCGGTAA. A	GACGGGCAGC	AGGTATATTTA	CGACCAATTG	ACAGGAAGCT
201	GGCTGCTGCA	AAGCCTGGTC	GGCGCGGCGG	CAGGCGCGTT	TATCGGCAAC
251	GCGCTGGCAA	ACAAATTAC	ACGGGCAGGC	AACCAAGACA	GTCCGTCGCG
301	CCGGCGCGCG	CGTGACACCT	ACCATCAGTC	CGCACGCCCC	AATGCGCGCA
351	yCAGCAGGGA	TTTGAACCG	CGCAGCTCC	GTGCAAAAAC	ACAGGCGGCG
401	CAKCGCGAGC	GTTACGCCCC	GACAAACGCG	CCG _s CCG _s CA	ATTACGCCCG
451	CCCCGCTATG	CGCGTTTTCG	GCAGGAGGCG	GTAACCCCGG	CGCGCCAATG
501	CGGTCTGAAG	AGCTTTTCAGA	CGGCATTnT	GCATTTGTTA	GGGACATTGT
551	TATGTTTGCC	TTTGATTTC	AGACGGCATT	TTGTTTCCAA	CGGTTTGATG
601	TCGGGATGGC	AATTCTGA			

m934.pep (partial)

```

1      .RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAE  QANGNNGQPV
51     TGXRRAAVYL  RPIDRKLAAA KPGRRGRRV  YRQRAQKQIH TGRQPRQSRR
101    PARACSLPSV  RTPQCAHQQG  FEHAQPCKT  TGGAAXALPP DNAPXRQLPP
151    PRYARFRQEA  VNPARQCRLK  SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201    SGWF*

```

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/q934

[illegible]

1347

```

m934.pep  QSRRLPARACSLPSVRTPQCAHQQGFQHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
           |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g934      QPRRPSRACCLPSVRTPQCAHQQGFQHAQPPCKTTGGAGAALPPDNAPARQLPPSRYARF
           130      140      150      160      170      180

           160      170      180      190      200
m934.pep  RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
           ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g934      RQKAVNPARQCRLKGFQTAFLYLLGALLCCRLIFRRHFVSKRLMSGWQFX
           190      200      210      220      230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2869>:

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCGCCGC
51  CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGGCAAA
201 CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGG TCGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGAG
351 GCAACCAAGA CAGTCCCGTC GCCCGGCGCG CGCGTGCCGC CTACCATCAG
401 TCCGCACATC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TGCGCGGTTT CGGCAGAAGG
551 CGGTAAATCC GCGGTGCCAA TGCCGTCTGA AGGGCTTCA GACGGCATT
601 TTGTATTGTG TAGGGACATT GTTATGTTGC CGTTTGATT TTAGACGGCA
651 TTTTGTTC AAGAGTTTGA TGTCGGGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2870; ORF 934.a>:

```

a934.pep
1  MKKIIASALI ATFALAACQD DAQARLEQQQ KQIEALQQQL AQQADDTVYQ
51  LTPEAVKDTI PAEAQANGNN GQPVTX*RRR AVYLRPIDRK LAAAKPGRRG
101 GRRVYRQAG KQIHTGRQPR QSRRLPARACR LPSVRTSQCA HQQGFQHAQP
151 PCKTTGGAGA ALPPDNAPAR QLPPPRHARF RQKAVNPACQ CRLKGFQTA
201 LYLGLTLLCC RLIFRRHFVS KSLMSGWQF*

```

m934/a934 94.1% identity in 205 aa overlap

```

           10      20      30
m934.pep  RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a934      MKKIIASALIATFALAACQDDAQARLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
           10      20      30      40      50      60

           40      50      60      70      80      90
m934.pep  PAEAQANGNNGQPVGTGXRRRAVYLRPIDRKLAAPKGRRGRRVYRQAGKQIHTGRQPR
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a934      PAEAQANGNNGQPVTXRRRAVYLRPIDRKLAAPKGRRGRRVYRQAGKQIHTGRQPR
           70      80      90      100     110     120

           100     110     120     130     140     150
m934.pep  QSRRLPARACSLPSVRTPQCAHQQGFQHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a934      QSRRLPARACRLPSVRTSQCAHQQGFQHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF
           130     140     150     160     170     180

           160     170     180     190     200
m934.pep  RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
           ||:||||| ||||| ||||| ||||| ||||| ||||| |||||
a934      RQKAVNPACQRLKGFQTAFLYLLGTLCCRLIFRRHFVSKSLMSGWQFX
           190     200     210     220     230

```

g935.seq not found yet

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAATC
801 AGCTTATGAC GACGGGTTTC GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAACAAAA CGGGTAAACA ACCGCCCGCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCAAAA CCGGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTGTG CGGTTGTGTC CGAAACGCGA AACGGTGGCG
1201 GCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTT ATGCCGCTG
1251 GCGCGCAGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTTCGCGCT
1301 CTTATGCCCG CCGCAACTAT AAGGCGGTTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

a935.pep

```

1 MLYFRYGFV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51 KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGHGVGVQL SHYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPIYA KRRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

	10	20	30	40	50	60
m935.pep	MLYFRYGFVWVWCAAGVSAA YGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
a935	MLYFRYGFVWVWCAAGVSAA YGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
	10	20	30	40	50	60
m935.pep	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
m935.pep	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAAKLDLPAPVLENVGRF					
a935	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
m935.pep	RKKTEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
a935	RKKAEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
	190	200	210	220	230	240
m935.pep	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGAGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGCCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGAAGGCCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGTG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAA
551 CCGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAAGTGTCA GCCGGGCGGA GCGGGCGGCA GGGTTGAATT
701 ATGAAATCGA GCGGAAAAAG CTGACGCCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCG GTAAAAAATC
801 AGCTTATGAT GACGGGTTTCG GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCGGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
1001 ACCGCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CCGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CCGTTTGTGC CGAAACCGGA AACGGTGGGC
1201 GCGCGCGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGTTG
1251 GCGCAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCC CCGCAACTAT AAGGGCATTG CCGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVENDAPRVV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP ABAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAAKLDLP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNRRLLPPY MLAGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEV FVS
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGAGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGAAGGCCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGTG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCCGAGG CGGAAAAATT
501 GGATTTGCCG GCGCCGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAG
551 CCGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1350

	310	320	330	340	350	360
m935.pep	GSDGFD AKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFD AKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFVVPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFVVPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSASYARRNYKGIAAFSTE AQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSASYARRNYKGVA AFSTE AQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNV PYAKRRNSEVFVSADWRFX					
a935	GRTESNV PYAKRRNSEVFVSADWRFX					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGCGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGcgcgAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGT
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVS AVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTA...

```

1351

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from *N. gonorrhoeae*:

m936/g936

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
	: : : : : : : : : : : :					
g936	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAASVIDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	: : : : : : : : : : : :					
g936	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
	130					
m936.pep	VASLPRTAXXX					
g936	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

a936.seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTGCCG	CCGTCCTCAG
51	CCTTGCCCTC	GGCGGCTGCG	TCAGCGCAGT	CGTCGGCGGC	GCGGCGGTCG
101	GCGCGAAATC	CGCCGTCGAC	CGCCGAACCA	CCGGCGCGCA	AACCGACGAC
151	AACGTAATGG	CGCTGCGTAT	CGAAACCACC	GCCCGCTCCT	ATCTGCGCCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCCCCA	AATCTCCGTT	GTCGGCTACA
251	ACCGCCACCT	GCTGCTGCTC	GGACAAGTCG	CCACCGAAGG	CGAGAAACAG
301	TTCGTCGGTC	AGATTGCACG	TTCCGAACAG	GCCGCCGAAG	GCGTGTACAA
351	CTACATTACC	GTCGCCTCCC	TGCCGCGCAC	TGCCGGCGAC	ATCGCCGGCG
401	ACACTTGGA	CACATCCAAA	GTCCGCGCCA	CGCTGTTGGG	CATCAGCCCC
451	GCCACACAGG	CGCGCGTCAA	AATCGTTACC	TACGGCAACG	TAACCTACGT
501	TATGGGCATC	CTCACCCCGG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCACCACCGT	CGGCGTACAA	AAAGTCATCA	CCCTCTACCA	AAACTACGTC
601	CAACGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

a936.pep

1	MKPKPHTVRT	LTAAVLSLAL	GGCVSAVVGG	AAVGAKSVD	RRTTGAQTDD
51	NVMALRIETT	ARSYLQNNQ	TKGYTPQISV	VGYNRHL	LLLGQVATEGEKQ
101	FVGQIARSEQ	AAEGVYNYIT	VASLPRTAGD	IAGDTWNTSK	VRATLLGISP
151	ATQARVKIVT	YGNVTYVMGI	LTPEEQAQIT	QKVSTTVGVQ	KVITLYQNYV
201	QR*				

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
	: : : : : : : : : : : :					
a936	MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAVGAKSVDRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	: : : : : : : : : : : :					
a936	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936.pep	VASLPRTA					

1352

```

          |||||
a936      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

```

g936-1.seq
1  ATGAAACCCA AACACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGccgAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACCTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

```

g936-1.pep
1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

```

m936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51 CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCCGCGCAC ATCGCCGGCG
401 ACACCTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

```

m936-1.pep
1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIV YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

m936-1/g936-1 95.5% identity in 202 aa overlap

```

          10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAKSVDRRTTGAQTDDNVMALRIETT
          10      20      30      40      50      60

          70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLQGVATEGEKQFVGQIARSEQAAEGVYNYIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLLLQGVATEGEKQFVGQIARSEQAAEGVYNYIT
          70      80      90      100     110     120

          130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1353

```
g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180
              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```
a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51  CCTTGCCTCT GCGGCTGCGC TCAGCGCAGT CGTCGGCGGC GCGGCGGTCTG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACCTTGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```
a936-1.pep
1  MKPKPHTVRT LTAAVLSLAL GGCVSAVVG AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GOVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*
```

a936-1/m936-1 97.0% identity in 202 aa overlap

```
              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAVGAASAVDRRTTGAQTDDNVMALRIETT
              ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a936-1      MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAGVGAASAVDRRTTGAQTDDNVMALRIETT
              10      20      30      40      50      60
              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLGOVATEGEKQFVGQIARSEQAAEGVYNYIT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLLLGOVATEGEKQFVGQIARSEQAAEGVYNYIT
              70      80      90      100     110     120
              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180
              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```
g937.seq
1  atGAAAAATA TTCTCTTAgt ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51  CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAactGGA AACTTccctt acctacctga acaGCGAAAA cagCCGCGCC
151 GCACTTGCCT CACCGGTTTA CATTcAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGAccg GCAataccga CATTTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACCTCGacg GCAACGGCAA
```

q937.ppt

1	<u>MKNILLVFVS</u>	<u>FVPLCVRTDL</u>	<u>PLNIEDIMTD</u>	<u>KGKWKLETSL</u>	<u>TYLNSSENSRA</u>
51	<u>ALASPVYIQT</u>	<u>GSASFIPVPT</u>	<u>EIQENGSTND</u>	<u>MLAGTLGLRY</u>	<u>GLTGNTDIYG</u>
101	<u>SGSYLWHEER</u>	<u>KLDGNGKTRN</u>	<u>KRMSDISAGI</u>	<u>SHTFLKDGKN</u>	<u>PALIAFLEST</u>
151	<u>VYEKSRNKAS</u>	<u>SGKSWLIGAT</u>	<u>TYKAIDPIVL</u>	<u>KTAAAYRING</u>	<u>SKTLSDDVKY</u>
201	<u>KAGNYWMLNP</u>	<u>NISFAANDRI</u>	<u>SLTGGIQWLQ</u>	<u>KQPDRIIDGKK</u>	<u>ESARNTSTYA</u>
251	<u>HCGAGGFETK</u>	<u>TAALNASARF</u>	<u>NVSGOSSSEL</u>	<u>KLQVOHTF*</u>	

m937.seq

1	ATGAAGCGCA	TCTTTTGGCC	CGCCTTGCCC	GCCATCTGCG	CTTTATCCAC
51	TTATGCCGAC	CTGCCCTTGA	CGATTGAAGA	CATAATGACC	GACAAGGGAA
101	AATGGAAACT	GGAAACTTCC	CTTACCTACC	TGAACAGCGA	AAACAACCGC
151	GCCGAACCTG	CCGCAACGGT	TTACATTCAA	ACCGGCGACA	CCTCGTTTA
201	CCCCATTCCG	ACCGAAATCC	AgaAAAaCGG	CAGCAATAAC	GATATGCTCG
251	TCCGCACGCT	CGGTTTGGCG	TACGGACTGA	CCGGGAATAC	CGACATTTAC
301	GGCAGCGGCA	GCTATCTGTG	GCACGAAGAA	CGCAAACCTC	ACGGCAACAG
351	CAAAACCCGC	AACAAACGGA	TGTCCGACGT	ATCCCTCGGC	ATCAGCCACA
401	CTTTCCTTAA	AGACGACAAA	AACCCCGCCC	TAATCAGCTT	TCTTGAAAGC
451	ACGGTTTACG	AAAAATCGCG	CAACAAGCG	TCGTCCGGGA	AATCCTGGCT
501	CATCGGCGCC	ACCACCTACA	AAGCCATAGA	TCCGATTGTC	CTTTCCCTCA
551	CGCCCGCCTA	CCGCATCAAC	GGCAGCAAAA	CCCTTTCAGA	CGGCATCCGC
601	TACAAATCGG	GCAACTACCT	GCTGCTCAAC	CCCAACATCT	CATTTGCTGC
651	CAACGACAGA	ATCAGCCTGA	CCGGAGGCAT	CCAATGGCTG	GGCAGGCAGC
701	CCGACCGGAC	GGACGGCAAA	CGGGAATCCT	CCAGAAACAC	ATCCACCTAC
751	GCCCATTTCG	GCGCAGGTTT	CGGTTTCACC	AAAACCACGG	CTTTAAACGC
801	ATCCGCACGT	TTCAACGTTT	CAGGGCAAAG	CAGTTCGGAA	CTGAAATTTG
851	CGGTACAGCA	TACATTTTAA			

m937.pep..

1	<u>MKRIFLPALE</u>	<u>AILPLSTYAD</u>	<u>LPLTIEDIMT</u>	<u>DKGKWKLETS</u>	<u>LTYLNSENNRR</u>
51	<u>AELAAPVYIQ</u>	<u>TGATSFPIPI</u>	<u>TEIQENGSNR</u>	<u>DMLVGTLGLR</u>	<u>YGLTGNTDIY</u>
101	<u>GSGLYLWHEE</u>	<u>RKLDGNSKTR</u>	<u>NKRMSDVSGL</u>	<u>ISHTFLKDDK</u>	<u>NPALISFLES</u>
151	<u>TVYEKSRNKA</u>	<u>SSGKSWLIGA</u>	<u>TTYKAIDPIV</u>	<u>LSLTAAYRIN</u>	<u>GSKTSLSDGIR</u>
201	<u>YKSGNYLLLN</u>	<u>PNISFAANDR</u>	<u>ISLTGGIQWL</u>	<u>GRQPDRTDGC</u>	<u>RESSRNTSTY</u>
251	<u>AHFGAGYFGFT</u>	<u>KTTALNASAR</u>	<u>FNVSGQSSSE</u>	<u>LKFGVQHTF*</u>	

Homology with a predicted ORF from *N.gonorrhoeae*

q937/m937

	10	20	30	40	50	59
g937.pep	MKNILL-VFVSFVPLCVRTLPLNIEDIMTDKGKWKLETSLTYLNSENRAALASPVYIQ					
	: :: :: : : : : : : : : :					
m937	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	60	70	80	90	100	119
g937.pep	TGSASFIPVPTEIQENGSENTDMLAGTLGLRYGLTGNTDIYSGSYLWHEERKLDGNGKTR					

[illegible]

```
a937.seq
1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACG GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACTTACC TGAACAGCCA AAACAACCGG
151 GCCGAACCTG CCGCACC GGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCAGCT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCGGA AACAAACGGA TGTCCGACGT ATCCCTCGG ATCAGGCCAA
401 CTTCTCTTAA AAGACGACAA AACCCTGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCGTCGTC CTCTCATTTA
551 CCGTGCTCTA CCGTATCAAC GGCAGCAAAA CCTTTCAAG CAACACCAA
601 TACAAGCAG GCAATTACTG GTGCTGAAT CCCAATATCT TCTTCGCGCG
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTG CGCGAGGTTT CGGTTTCACC AAACACCGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTAA
```

```
a937.pep
1 MKRIFLPALP AILPLSAYAD LPTIEDIMT DKGKWKLETS LTYLNSENN
51 AELAAPVYIQ TGATSFIP PTEIQENGST DMLVGTGLR YLGTGNTDIY
101 GSGSYLWHEE RKL DGNKTR NKRMSDVLG ISHTFLKDDK NPALISFES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSNNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDARDGK KESARNTSTY
251 AHFGAGYFET KTTALNASAR FNVSGQSSSE LKFGVOHTF*
```

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTKGKWKLETSLTYLNSENNRAELAAPVYIQ					
a937	MKRIFLPALPAILPLSAYADLPLTIEDIMTKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m937.pep	TGATSFIFIPIPTETQENGSTNDMLVGLTGLRYGLTGNTDIYSGSGSYLWHEERKLDGNSKTR					
a937	TGATSFIFIPIPTETQENGSTNDMLVGLTGLRYGLTGNTDIYSGSGSYLWHEERKLDGNGKTR					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m937.pep	NKRMSDVSLSGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVSLSGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGGK					
a937	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
a937	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TCGCATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHOTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TCGCATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CCGTGAAGCC AATCCTAAGG AAAATCCCAG
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CCGGTATGCC GGGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTGAGCATC AGGCATATAT
501 TGTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGGAGATAT TGCAAACCGT ATGTCTGAAG AAGATTTGAA AGCGGTTCGGC
601 AACTTTATCC AAGGTTTGCG TTAA
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHOTIGIRD GKRTGSAAV MKPVVMNLSQ QDILNVSAFY
101 AKQPKSGEA NPKENPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAIVIEQ MNAYKSGQRK NTIMEDIANR MSEDLDKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.p	MKRLTLLAFVLAAGAVSASP KADVEKGKQVAATVCAACHAADGNSGIAMY PRLAAQHTAY					
a939	MKRLTLLAFVLAAGAVSASP KADVEKGKQVAATVCAACHAADGNSGIAMY PRLAAQHTAY					

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```

              10      20      30      40      50      60
              70
m939.pep      IYHQTIGIRDVNAP
              |||||
a939          IYHQTIGIRDGKRTHGSAAVMKPVVMNLSDDILNVSAFYAKQPKSGEANPKENPELGA
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCGGC GCCGTGTCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGC GGCG CATCCAAATC TGCCGAAGGT TCGTGC GGCG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAAGCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGC GGCG CGGCTGCTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

```

              10      20      30      40      50
m950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----
              |||||
g950          MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCGASKSAEGSCGASKSAEG
              10      20      30      40      50      60

              60      70      80      90      100
m950.pep      ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |:|||||
g950          SCGAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGC GGCG CGGCTGCTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

1358

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a950.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
m950	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a950.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m950	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCTACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCGG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGGTGTTC ACCTGTGTGG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTGGAACG CACAAAATCC
301 CCGGAAGTGT CCGAACGCGC CTTGGAAATG GCCGTGTCGC TGAACGCGTT
351 TGAACAGGCG GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG GCGGGGTGGC TCGGGAACGT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CGGGTTGGA GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGTCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTCG CCGTGCAGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CCGTGTTCGG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAATA TTGCCCCCA CTTTAATGAC GTTGCCTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAAATT ATGAATCTGG
851 TTTCCCTGCG TAAGCCGGAT GATGCCTATG CGCGTTTGA CTTGCTGTGTG
901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATGGCGGC
951 AAACCGAAAA GAAGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTCGA CAAAGGCGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCGGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACCTTC GGCAGCGGGA
1351 AGCACGGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTTACGA
1401 ACAGTTCCGC AAACGGGGAA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAAATC AACCCGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAG ACGACCCCGA GCCCGAAGTT GCCGCCATT TGGCGAAGT
1701 GTTGTGGGCA TTGGCGAAC GCGATCAGGC GGTGACGTA TGGACGAGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GCGGGGAGAC GCTCAAACGC
1801 TACGAATCG CTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MIMLPARFTI LSVLAAALLA GOAYAAGAAD VELPKEVGKV LRKHRRYSEE
```

1359

```

51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWROI EPIPGEAQKR AGWLRNVLRE
151 GGNQHLDGLE EVLAQSDDVQ KRRIFLLLVQ AAVQQGGVAQ KASKAVRRRAA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFFEQTDTON LSAVWOEMEI MNLVSLRKP DAYARLNVLL
301 EHNPNANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLKKVS APEYLFDKGV LAAAAAELD GGRAALRQIG
401 RVRKLPEQQG RYFTADNLSK IQMLALSCLP DKREALIGN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQTAYQI NPDDTAVNDS IGWAYYLLKG AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLLR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1 ATGATTATGT TACCTAACCG TTTCAAAATG TTAAGTGTGT TGACGGCAAC
51 CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTTCA GAAAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTGCGGCAGC TGGGCGAGCG
201 GGTTAATCAG ATATTACGT TGCTGGGAGG GGAAACCGCC TTGCAAAAGG
251 GGCAGCGGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCCG TGTCGCTGAA
351 CGCGTTTGAA CAGCGGAAA TGATTATCA GAAATGGCGG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAGAGG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GGCAGACGAA GGACAGAACC GCAGGGTGT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTG GCGCAAAAG CATCGAAAGC GGTTCGCCCG
601 GCGCGTGTGA AATATGAACA TCTGCCCGAA GCGGCGGTG CCGATGTGGT
651 GTTCAGCGTA CAGGGACGCG AAAAGGAAAA GGCAATCGGA GCTTTGCAGC
701 GTTTGGCGAA GCTCGATACG GAAATATTGC CCCCCACTTT AATGACGTTG
751 CGTCTGACTG CACGCAATA TCCGAAATA CTGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTTT CGGCCGCTG GCAGGAAATG GAAATTATGA
851 ATCTGGTTTC CCTGCACAG CTGGATGATG CCTATGCGCG TTTGAACGTG
901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTCAGG CAGCGATATT
951 GCGCGCAACG CGAAAGAAG GTGCTTCCGT TATCGACGGC TACGCCGAAA
1001 AGGCATACGG CAGGGGACG GAGGAACAGC GGAGCAGGC GCGCTAACG
1051 GCGGCGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAAG TCAGGCAAGT
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CCGCTGCGGC GGCTGTGCGG TTGGACGGCG GCAGGGCGGC TTTGCGGCAG
1201 ATCTGGCAGG TGCGGAAACT TCCGAAACAG CAGGGGCGGT ATTTACGGC
1251 AGACAATTTG TCCAAAATAC AGATGCTCGC CCTGTGGAAG CTGCCCGATA
1301 AACGGGAGGC TTTGAGGGGG TTGGACAAGA TTATCGAAAA ACCGCCGTGC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTCAAGTTG
1401 TTACGATCGG CTTGGCAAGC GGAATAAAT GATTTCAGAT CTTGAAAGGG
1451 CGTTCAGGCT TGCACCCGAT AACGCTCAGA TTATGAATAA TCTGGGCTAC
1501 AGCCTGTCTG CCGATTCCAA ACGTTTGGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGGCATA CAAATCAACC CCGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGGCGTA TTACTGAAA GCGCAGCGCG AAAGCGCGCT GCCGTATCTG
1651 CCGTATTCTG TTGAAAACGA CCCCAGCGCC GAAGTTGCCG CCCATTGCGG
1701 CGAAGTGTGG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 GCGAGCGGCG ACACCTTACG GGAGACAAGA AAATATGGCG GGAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCAACCT TCCCGAAAC CTCGGAAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1 MIMLPNRFKM LTVLTATLIA GQVSAAGGGA GDMKQPEVGV KVFRRQQRYS
51 EEEIKNERAR LAAVGERVNO IFTLLGGETA LQKGQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQKWR QIEPIPGKAQ KRAGWLRNVL
151 RERGNQHLDG LEEVLAQADE GQNRVFLLL AQAAVQDGL AQKASKAVRR
201 AALKYEHLP EAAVADVFSV QGREKEKAIG ALQRLAKLDT EILPPTLMTL
251 RLTKYPEI LDGFFEQTD TQNL SAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAILAAN RKEGASVIDG YAEKAYGRGT EEQRSRAALT
351 AAMMYADRRD YAKVRQWLKK VSAPEYLFDK GVLA AAAAVE LDGGRALRLQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALS LDPKREALRG LDKIIEKPPA
451 GSNTLQAEAL LVQSVVYDR LGKRKKMISD LERAFRLAPD NAQIMNNLGY
501 SLLTDSKRLD EGFALLQTAY QINPDDTAVN DSIWAYYLLK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDQAV DVWTQAAHLT GDKKIWRETL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

	10	20	30	40	50	60
m951.pep	MIMLPNRFKMLTVLTATLIAGQVSAAGGAGDMKQPKVEGKVKFRKQQRYSSEEEIKNERAR					
g951	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGKVLKRRYSSEEEIKNERAR					
	10	20	30	40	50	
	70	80	90	100	110	120
m951.pep	LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPVAERALEMAVSLNAFE					
g951	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPVAERALEMAVSLNAFE					
	60	70	80	90	100	110
	130	140	150	160	170	180
m951.pep	QAEMIQKWRQIEPIPGKAKRAGWLRNVLRERGNQHLGEEVLAQADEGQNRVFLLL					
g951	QAEMIQKWRQIEPIGKAKRAGWLRNVLRERGNQHLGEEVLAQSDDVQKRRI FLLL					
	120	130	140	150	160	170
	190	200	210	220	230	240
m951.pep	AQAAVQQDGLAQKASKAVRRAALKYEHLPAAVADVFSVQGREKEKAIGALQRLAKLDT					
g951	VQAAVQQGGVAQKASKAVRRAALKYEHLPAAVADVFGVQGREKEKAIEALQRLAKLDT					
	180	190	200	210	220	230
	250	260	270	280	290	300
m951.pep	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLHRLDDAYARLNV					
g951	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLRKPD DAYARLNV					
	240	250	260	270	280	290
	310	320	330	340	350	360
m951.pep	LLERNPNADLYIQAILAANRKEGASVIDGYAEKAYGRGTEEQRSRAALTAAMMYADRRD					
g951	LLEHNPNANLYIQAILAANRKEGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD					
	300	310	320	330	340	350
	370	380	390	400	410	420
m951.pep	YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRKLPEQQGRYFTADNL					
g951	YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRKLPEQQGRYFTADNL					
	360	370	380	390	400	410
	430	440	450	460	470	480
m951.pep	SKIQMLALS KL PDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD					
g951	SKIQMLALS KL PDKREALIGLNNIIAKLSAAGSTEPLAEALQRSIIYEQFGKRGKMIAD					
	420	430	440	450	460	470
	490	500	510	520	530	540
m951.pep	LERAFRLAPDNAQIMNNLGYSL L TDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	LETALKLTPDNAQIMNNLGYSL L TDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
	480	490	500	510	520	530
	550	560	570	580	590	600
m951.pep	GDAESALPYLRYSFENDPEPEVA A HLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL					
g951	GDAESALPYLRYSFENDPEPEVA A HLGEVLWALGERDQAVDVWTQAAHLRGDKKIWRETL					
	540	550	560	570	580	590
	610					
m951.pep	KRHGIALPQPSRKPRK					
g951	KRYGIALPEPSRKPRKX					
	600	610				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCCGTTTCAC CATTTTATCT GTGCTCGCGG CAGCCCTGCT
51  TGC CGG CAG GCGTATGCCG CCGGCGCGGC GGATGCGAAG CCGCCGAAGG
101 AAGTCGGAAG GGTTTTCAGA AAGCAGCAGC GTTACAGCGA GGAAGAAATC
151 AAAAACGAAC GCGCACGGCT TGC GGCAGTG GGCAGCGGG TTAATCAGAT
201 ATTTACGTTG CTGGGAGGGG AAACCGCCTT GCAAAAGGGG CAGGCGGGAA
251 CGGCTCTGGC AACCTATATG CTGATGTTGG AACGCACAAA ATCCCCCGAA
301 GTCGCGGAAC GCGCCTTGGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GCGGGAATG ATTTATCAGA AATGGCGGCA GATTGAGCCT ATACCGGGTA
401 AGGCGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGCTGAG GGAAGAGGA
451 AATCAGCATC TAGACGGA CTGAGGAGTG CTGGCTCAGG CCGACGAAGG
501 ACAGAACCGG AGGGTGT TTTT TATTGTTGGC ACAAGCCGCC GTGCAACAGG
551 ACGGGTTGGC GCAAAAAGCA TCGAAAAGCG TTCGCCGCGC GGCCTTGAGA
601 TATGAACATC TGCCCGAAGC GGC GGTGCC GATGTGGTGT TCAGCGTACA
651 GGGACGCGAA AAGGAAAAGG CAATCGGAGC TTTGCAGCGT TTGGCGAAGC
701 TCGATACGGA AATATTGCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGCAATATC CCGAAATACT CGACGGCTTT TCGAGCAGA CAGACACCCA
801 AAACCTTTCG GCGCTCTGGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGCACAGGCT GGATGATGCC TATGCGCGTT TGAACGTGCT GTTGAACGC
901 AATCCGAATG CAGACCTGTA TATTCAGGCA GCGATATTGG CGGCAAAACCG
951 AAAAGAAAGG GCTTCCGTTA TCGACGGCTA CGCCGAAAAG GCATACGGCA
1001 GGGGACGGG GGAACAGCGG GGCAGGGCGG CAATGACGGC GGCATGATA
1051 TATGCCGACC GAAGGGATTA CACCAAAGTC AGGCAGTGGT TGAAAAAAGT
1101 GTCGCGCGCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTCGCGCGG
1151 CTGTCGAGTT GGACGGCGGC AGGGCGGCTT TCGGCGAGAT CGGCAGGGTG
1201 CGGAACCTTC CCGAACAGCA GGGCGGTAT TTTACGGCAG ACAATTTGTC
1251 CAAAATACAG ATGTTGCGCC TGTGGAAGCT GCCCGACAAA CGGGAGGCTT
1301 TGAGGGGGTT GGACAAGATT ATCGAAAAAC CGCCTGCCGG CAGTAATACA
1351 GAGTTACAGG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGGCAAGCGG AAAAAAATGA TTTAGATCT TGAAAGGGCG TTCAGGCTTG
1451 CACCCGATAA CGCTCAGATT ATGAATAATC TGGGCTACAG CCTGCTTTCC
1501 GATTCCAAAC GTTTGGACGA AGGCTTCGCC CTGCTTCAGA CGGCATACCA
1551 AATCAACCCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACCTGAAAGG CGACGCGGAA AGCGCGCTGC CGTATCTGCG GTATTCGTTT
1651 GAAACGACC CCGAGCCCGA AGTTGCCGCC CATTGGGCGC AAGTGTGTTG
1701 GGCATTGGGC GAACGCGATC AGGCGGTTGA CGTATGGACG CAGGCGGCAC
1751 ACCTTACGGG AGACAAGAAA ATATGGCGGG AAACGCTCAA ACGTCACGGC
1801 ATCGCATTGC CCCAACCTTC CCGAAAACCT CGGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAAALLAGO AYAAGAADAK PPKEVGKVFR KQORYSEEEI
51  KNERARLAAY GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEM IYQKWRQIEP IPGKAQKRAG WLRNVLRERG
151 NOHLDGLEEV LAQADEGQNR RVFLLLAQAA VQDGLAQKA SKAVRRAALR
201 YEHLPEAAVA DVVFSVQGRE KEKAIGALQR LAKLDTEILP PTLMTLRLTA
251 RKYPEILDGF FEQTDTONLS AVWQEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNADLYIQA AILANRKEG ASVIDGYAEK AYGRGTGEOR GRAAMTAAMI
351 YADRRDYTKV RQWLKVSAP EYLFDKGVL AAAAAVELDGG RAALRQIGRV
401 RKLPEQQGRY FTADNLSKIQ MFALSKLPDK REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLSS
501 DSKRLDEGFA LLQTAYQINP DDTAVNDSIG WAYYLLKGD AE SALPYLRYSF
551 ENDEPEEVAA HLGEVLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRHG
600 IALPQPSRKP RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```

10      20      30      40      50
a951.pep  MLPARFTILSVLAAALLAGQAYAAAG--AADAKPPKEVGKVFRKQORYSEEEIKNERAR
          ||| || :|:|:|:|:|:|: ||| | :| | | | | | | | | | | | | | | | |
m951      MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPPKEVGKVFRKQORYSEEEIKNERAR
          10      20      30      40      50      60

60      70      80      90      100     110
a951.pep  LAAGGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
```

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m951      |||||
          LAAVGERVNQIFTLGGETALQKQGAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
          70      80      90      100     110     120

a951.pep  120      130      140      150      160      170
          QAEMIYQKWROIPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
          |||||

m951      130      140      150      160      170      180
          QAEMIYQKWROIPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL

a951.pep  180      190      200      210      220      230
          AQAAVQQDGLAQKASKAVRRRAALRYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
          |||||

m951      190      200      210      220      230      240
          AQAAVQQDGLAQKASKAVRRRAALKYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT

a951.pep  240      250      260      270      280      290
          EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
          |||||

m951      250      260      270      280      290      300
          EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV

a951.pep  300      310      320      330      340      350
          LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
          |||||

m951      310      320      330      340      350      360
          LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRSRAALTAAMMYADRRD

a951.pep  360      370      380      390      400      410
          YTKVRQWLKKVSAPEYLFDKGVLA AAAA AVELDGGRAALRQIGRVRKLPQQGRYFTADNL
          |||||

m951      370      380      390      400      410      420
          YAKVRQWLKKVSAPEYLFDKGVLA AAAA AVELDGGRAALRQIGRVRKLPQQGRYFTADNL

a951.pep  420      430      440      450      460      470
          SKIQMFALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
          |||||

m951      430      440      450      460      470      480
          SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD

a951.pep  480      490      500      510      520      530
          LERAERLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
          |||||

m951      490      500      510      520      530      540
          LERAERLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK

a951.pep  540      550      560      570      580      590
          GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
          |||||

m951      550      560      570      580      590      600
          GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL

a951.pep  600      610
          KRHGIALPQPSRKPRK
          |||||

m951      610
          KRHGIALPQPSRKPRK
          610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

```

g952.seq (partial)
1      ..TTGTCTTATC GTTTGAATGC TGCACCGATG TTTAACGATA ATCCTGTTGT
51     TTACGAAAA ATCAAATTGC AGAGTTGGAA AGCGCGGCGG GATTTCATA
101    TTGTAAGACA GGATTGGAT TTTTCCTGCG GGGCGGCTTC GGTGGCGACG
151    CTTTGAACA ATTTTACGG GCAAAAGCTG ACGGAAGAAG AAGTGTGGA
201    AAAACTGGGT AAGGAACAGA TCGCGCGGTC GTTTGAGGAT ATGCGGCGCA
251    TTATGCCCCG TTTGGGTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301    CAGCTCGCGC AGTTGAAAT CCCCCTCATC GTGTATCTGA AATACGCAA
351    AGACGACCAT TTTTCGGTAT TCGCGGAGT GGATGGCAAT ACGGTTTTCG
401    TTGCCGACCC GTCGCCGGT CATGTTTCGA TGAGCAGGGC GCAGTTTTCG
451    GAGGCTTGGC AAACCCGTGA GGGAAATTG GCAGGCAAAA TTTTGCGCGT
501    CGTGCCGAAA AAAGCGGAGG CGATTTCAAA TAAATTGTTT TTCACACATC
551    ATCCAAGCGC GCAGACGGAG TTTGCAGTCG GACAGGTAAA ATGGTGCGCT

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601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)
 1 ..LSYRLNAAPM FNDNPVVYVK IKLQSWKARR DFNIVKQDLD FSCGAASVAT
 51 LLNNFYGQKL TEEVLEKLG KEQMRASFED MRRIMPD LGF EAKGYALSFE
 101 QLAQLKIPVI VYLKVRKDDH FSVLRGVDGN TVLLADPSPG HVSMSRAQFL
 151 EAWQTREGNL AGKILAVVPK KAEAISNKL FTHHPKRQTE FAVGQVKWWR
 201 AY*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq
 1 ATGATGAAGT TCAATATGT TTTCTGTG GCGTGTGTTG TCGTTTCTTT
 51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
 101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG CGCGGCGGGA TTTCAATATT
 151 GTAAAGCAGG ATTTGGATT TTTCTGTGGG GCGGCTTCGG TGGCGACGCT
 201 TTGTAACAA TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
 251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
 301 ATGCCTGATT TGGGTTTTGA GGCGAAGGGC TATGCCCTGT CTTTCGAGCA
 351 GCTCGCGCAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
 401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
 451 GCCGACCCGT CGCTGGGGCA TGTTTCAATG AGCAGGGCGC AGTTTTTGGA
 501 TGCTTGCAA ACCCGTGAGG GAAATTTGCG AGGTAAGATT TTGGCTGTCA
 551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
 601 CCAAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
 651 AGAGTAA

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep
 1 MMKFKYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKARRDFNI
 51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKLDKEQM RASFEDMRRI
 101 MPDLGF EAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDNTVLL
 151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTOH
 201 PKRQTEFTVG QIRQARAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952; 92.5% identity in 201 aa overlap

		10	20	30	40		
g952.pep		LSYRLNAAPMFNDNPVVYVKIKLQSWKARRDFNIVKQDLDFSCG					
m952		MMKFKYVFLACVVVLSYRLNAAPMFNDNPVVYVKIKVQSWKARRDFNIVKQDLDFSCG					
		10	20	30	40	50	60
	50	60	70	80	90	100	
g952.pep	AASVATLLNNFYGQKLTEEEVLEKLGKEQMRASFEDMRRIMPD LGFEAKGYALSFEQLAQ						
m952	AASVATLLNNFYGQTLTEEEVLKLDKEQMRASFEDMRRIMPD LGFEAKGYALSFEQLAQ						
	70	80	90	100	110	120	
	110	120	130	140	150	160	
g952.pep	LKIPVIVYLKVRKDDHFSVLRGVDGNTVLLADPSPGHVSMSRAQFLEAWQTREGNLAGKI						
m952	LKIPVIVYLKVRKDDHFSVLRGIDGNTVLLADPSLGHVSMSRAQFLDAWQTREGNLAGKI						
	130	140	150	160	170	180	
	170	180	190	200			
g952.pep	LAVVPKKA E AISNKLFFTHHPKRQTEFAVGQVKWWRAYX						
	: : : : :						
m952	LAVIPKKAETISNKLFFTOHPKRQTEFTVGQIRQARAE						
	190	200	210				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq
 1 ATGATGAAGT TCAATATGT TTTCTGTG GCGTGTGTTG TCGTTTCTTT

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51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGGCGGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATTT TTCCTGCGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCTCGT TTAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATT CTCCGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTC AATG AGCAGGCGC AGTTTNGGA
501 TGCTTGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTCG
551 TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1 MMKFYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDFSCG AASVATLLNN FYGQTLTEE VLKLLDKEQM RASFEDMRR
101 MPDLGF EAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

a952/m952 97.7% identity in 218 aa overlap

	10	20	30	40	50	60
a952.pep	MMKFYVFLACVVVLSYRLNAAPMFNDNPVVYGKIKVQSWKERRDFNIVKQDLDFSCG					
m952	MMKFYVFLACVVVLSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLDFSCG					
	10	20	30	40	50	60
a952.pep	70	80	90	100	110	120
	AASVATLLNNFYGQTLTEEVLKLLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ					
m952	AASVATLLNNFYGQTLTEEVLKLLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ					
	70	80	90	100	110	120
a952.pep	130	140	150	160	170	180
	LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSM SRAQFXDAWQTREGNLAGKI					
m952	LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSM SRAQFLDAWQTREGNLAGKI					
	130	140	150	160	170	180
a952.pep	190	200	210	219		
	LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAEX					
m952	LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAEX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1 ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51 CTCCGCCACC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCCGTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCCGTC GCCAACCTGC AAAGCGGTTC GCAACCTTC ACCGGCCACC
251 TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCGGGA CATCCGCTTC
301 GTTCCACCA AATTCAACTT CAACGGCAAA AACTTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACCGCCCC CGTCAAACCT AAAGCCGAAA
401 AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451 GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGGCGTGG ACTACCTCGT
501 TAACGCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAACAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

```
g953.pep
  1 MKKIIFAALA AAVGTASAT YKVDEYHANV RFAIDHFNTS TNVGGFYGLT
  51 GSVEFDQAKR DGKIDITIPV ANLQSGSQPF TGHLSADIF DAAQYPDIRF
 101 VSTKFNENGK KLVSV DGNLT MRGKTAPVKL KAEKFNCYQS PMAETEVCGG
 151 DFSTTIDRTK WGV DYL V NAG MTKNVRIDIQ IEAAKQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

```
m953.seq
  1 ATGAAAAAAA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC
  51 CTCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCG
 101 CCATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
 151 ACCGGTTCCG TCGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
 201 CACCATCCCC ATTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
 301 TTTGTTTCCA CCAAATTCAA CTTCAACGGC AAAAACTGG TTCCGTTGA
 351 CGGCAACCTG ACCATGCACG GCAAACCGC CCCCGTCAA CTCAAAGCCG
 401 AAAAAATCAA CTGCTACCAA AGCCCGATGG AGAAAACCGA AGTTTGTGGC
 451 GCGCACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
 501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
 551 CAGCCAAACA ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

```
m953.pep
  1 MKKIIFAALA AAAISTASAA TYKVDEYHAN ARFAIDHFNT STNVGGFYGL
  51 TGSVEFDQAK RDGKIDITIP IANLQSGSQH FTDHLKSADI FDAAQYPDIR
 101 FVSTKFNENG KLVSV DGNLT TMHGKTAPVK LKAEKFNCYQ SPMEKTEVCG
 151 GDFSTTIDRT KWGM DYL V NV GMTKSVRIDI QIEAAKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

```
m953/g953    93.0% identity in 187 aa overlap

      10      20      30      40      50      60
m953.pep    MKKIIFAALAAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK
             |||||:::|||| |||||:|||||
g953         MKKIIFAALAAAAVGTASA-TYKVDEYHANVRFAIDHFNTSTNVGGFYGLTGSVEFDQAK
             10      20      30      40      50

      70      80      90      100     110     120
m953.pep    RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKLVSV DGNL
             |||||:||||| || |||||
g953         RDGKIDITIPVANLQSGSQPFTGHLKSADIFDAAQYPDIRFVSTKFNENGKLVSV DGNL
      60      70      80      90      100     110

      130     140     150     160     170     180
m953.pep    TMHGKTAPVKLKAKEFN CYQSPMEKTEVCGGDFSTTIDRTKWGM DYL NVGMTKSVRIDI
             |||||:||||| :|||||
g953         TMRGKTAPVKLKAKEFN CYQSPMAETEVCGGDFSTTIDRTKWGV DYL V NAGMTKNVRIDI
      120     130     140     150     160     170

m953.pep    QIEAAKQX
             |||||
g953         QIEAAKQX
      180
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

```
a953.seq
  1 ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC
  51 CTCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCT
 101 CTATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
 151 ACCGGTTCCG TTGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
 201 CACCATCCCC GTTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
 301 TTTGTTTCCA CCAAATTCAA CTTCAACGGC AAAAACTGG TTCCGTTGA
```

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```

351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGCGGC
451 GGCGACTTCA GCACCACCAAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
1  MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
51  TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYDIR
101 FVSTKFNENG KKLVSVDGNL TMHGKTAPVK LKAKEFNCYQ SPMLKTEVCG
151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

a953/m953 97.3% identity in 187 aa overlap

	10	20	30	40	50	60
a953.pep	MKKIIIAALAAAAGTASAATYKVDEYHANARFSIDHFNTSTNVGGFYGLTGSVEFDQAK					
	: : : : : : : : : :					
m953	MKKIIFAALAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	60
	70	80	90	100	110	120
a953.pep	RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYDIRFVSTKFNFNKKLVSVDGNL					
	: : : : : : : : :					
m953	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYDIRFVSTKFNFNKKLVSVDGNL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a953.pep	TMHGKTAPVKLKAKEFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
	: : : : : : : : :					
m953	TMHGKTAPVKLKAKEFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
	130	140	150	160	170	180
a953.pep	QIEAAKQX					
m953	QIEAAKQX					

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
1  ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
51  GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
101 AATATCAATT TGCAGATGAG AAACAGGCTT TTTATTTTGA ACGCGCCGCC
151 CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251 TTAACAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301 TACCGCTCT CAAACAGGC TGCACAAGAT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTTAGAT AAGGAAAGTT
401 ATCAAAATTA CCGAAAATCA ATGCAAGAAT GCCGTAAAC AATAACGGAA
451 GCTGAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
1  MKKFYFVLLA LGLAACQEQE SQKADAEQYF FANKYQFADE KOAFYFERAA
51  RFRVLQQLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDDP
101 YRVCKQAAQD AEILMKSMVT SGGGTTDLDD KESYQNYRKS MQECKRTITE
151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

```
g957.seq (partial)
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTGT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAATAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCGG GGGGatgaag gcgaacagtc ttgtggtcgg
801 ctatgatgcg gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaacc ccaaagtgtc gaatattatt tgaaaaacgg aaatcttttt
901 attgcccaat cttcgacggt aaccttgaaa acggatggcg taacggcgga
951 tatgcaaacc tatcatgctg aacaaacggt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

```
g957.pep (partial)
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT EVPENPNFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGFLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YNDRPFVSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS VDNGKKPQSV EYYLKNGNLF
301 IAQSSTVTLK TDGVTADMQT YHAQOTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

```
m957.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTGT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAAC TGGGATGACG
251 GTCCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CGGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAATAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATCGG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTT
901 ATTGCACAAT CTTGACGGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GGCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGGAATAAT TGGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

```
m957.pep
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT EVKPNPNFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGFLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YNDRPFVSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
```

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251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
 301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEAAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFAVAKLARLFRNA					
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKPNFAVAKLARLFRNA					
	10	20	30	40	50	60
g957.pep	70	80	90	100	110	120
m957	70	80	90	100	110	120
	130	140	150	160	170	180
g957.pep	130	140	150	160	170	180
m957	130	140	150	160	170	180
	190	200	210	220	230	240
g957.pep	190	200	210	220	230	240
m957	190	200	210	220	230	240
	250	260	270	280	290	300
g957.pep	250	260	270	280	290	300
m957	250	260	270	280	290	300
	310	320	330			
g957.pep	310	320	330			
m957	310	320	330	340	350	360
m957	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAAAA	AATCAAACC	GGTACTGTTG	TCATTTTTTG	CACTTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAAATCCGA	ATGCTTTTGT	GGCGAACTT
151	GCCCCCTGT	TCCGAAATGC	CGACAGGCGG	GTTGTCATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAAACG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTTGATGC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCTCGGGT	GTTATCAGAT	GGCCCAGGTA	TATTGGCGGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGACTCGCGC	GATTCTGTGT	TTTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAAACAGT	CTTGTGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAA	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC

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```

951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTC TC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

a957.pep

```

1 MFKKFKPVLL SFFALVF AFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51 ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL POKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10	20	30	40	50	
m957	10	20	30	40	50	
a957.pep	60	70	80	90	100	110
m957	60	70	80	90	100	110
a957.pep	120	130	140	150	160	170
m957	120	130	140	150	160	170
a957.pep	180	190	200	210	220	230
m957	180	190	200	210	220	230
a957.pep	240	250	260	270	280	290
m957	240	250	260	270	280	290
a957.pep	300	310	320	330	340	350
m957	300	310	320	330	340	350
a957.pep	360	370				
m957	360	370				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

g958.seq

```

1 TTGGCTCGTT TATTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51 TTTCGGCAGC CATTGCGCCG CCGATACCGT TGCGGCGGAA GAGGCGGACG

```

```

101 GCGGTGTGCG AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAAGCT
151 TCCGATTGTA CCCTCGGTTT GACCTGCCTG TTTTGAGTA ACGAAAGCGG
201 CAGCCCCGAG AGAACCAGAG CCGCCGTCCA AGGACGCGGC GAAGCATCCG
251 TCCCCGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TGCGCGCGGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTCCGC CTCCAACAGG ACGGTACGCT GATTTCGGGC
451 GAAACCTGA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACGT
501 CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAGC GTCAGCCGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCTAATC
601 AACACCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAACCCGAT CGGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCCTTCG
701 TGTTCCGCGG CGTTCCTCTT TTCTATACGC CTTGGGCGGA CTTCCCGCTT
751 GACGGCAACC GCAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCCGGTTC
801 GGACGGCGTT TCCCTTTCCG TCCCTATTA TTCAACCTT GCCCCAACT
851 TCGATGCCAC TTTCGCCCCC GGCATTATCG GCGAACGCGG CGCGACGTTT
901 GACGACAAAT TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GCGGGGTGTC
1051 GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCCGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGGCGCGAG GCGGCGGGGA GGCAGCCTGA ATGCCGCGCT TTCGTTTCAG
1201 AAATACCAGA CGCTGGCAA CCAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCGGCCAA
1351 GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAATGGG ATTTTCAGCA
1401 CAGCTGGGGC TACGTCCGCC CCAAACCTCG GCTGCACGCC ACTTATTACA
1451 GCCTCGACAG TTTCCGCGGC AAAGCATCCC GCAGCGTCGG GCGCGTTTTG
1501 CCGGTTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCCGCGCCTG TTCTACAAC
1601 ATATTCCTGC CAAATCTCAA AACGACCTGC CCAATTTCTG TTCGTGCGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACGCCGCCA ACAGCCTTTC CACCGCCGTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTGAG
1801 AAATTCCTAT TCAAGGATGA TCGGTTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCCG ACTGGGTGGC ATTCGCCTCC GCGGCGATAG
1901 GCGGGCGTTT CACCTCGAC AGCAGCATCC ACTACAACCA AAACGACAAA
1951 CGCGCCGAAC ATTACGCCGT CGGCGCAGGC TACCGCCCCG CCCCAGGAAA
2001 AGTGTGAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGGCGGACGG TTCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTGCTCC GCTACAATA
2151 CCGGTTTGAA GCCAAAAAAC CGATAGAAAT GCTTGCCGGT CAGAGAATACA
2201 AAAGCAGTTG CCGGTGCTGG GCGCGGGGCG GTGACGCCCA ACGTACGTT
2251 ACCGCGGAAA ACACCTACAA AAACGCCGTC TTTTTCCTAC TTCAGTTGAA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCGCG AGGACGGATG GATGTCGCGG
2351 TTCCCGGCTA CATCCCGGCC CACTCTCTTT CCGCCGGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

g958.pep

```

1 LARLFSLKPL VLALGFCEGT HCAADTVAAE EADGRVAEGG AQAASESAQA
51 SDLTLGSTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRMEGQS
101 KVKVRAEGSV IIERDGAVLN TDWADYDQSG DTVTVGDRFA LQDQGTILRG
151 ETLTYNLDQQ TGEAHNVNME TEQGGRRLQS VSRTEMLGE GRYKLTETQF
201 NTCASAGDAG YVKAASVEAD RGKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLRPD YSGQTDLTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSLNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSDHGRQ
451 DGSRLVVYPG IKWDFNSWVG YVRPKLGLHA TYYSLDSFGG KASRSVGRVL
501 PVVNIIDGTT FERNTRLFEG GVVQTIEPRL FYNYIPAKSQ NDLPNFDSSSE
551 SSFGYGQLFR ENLYYGNDRI NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGVSFGKNPR SRSDWVAFAS GGIGGRTFLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLQADGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRVY
751 TGENTYKNAV FFSLQLKDLN SVGRNPAGRM DVAVPGYIPA HSLSAGRNRK
801 P*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

m958.seq

```

1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCCTCTG
51 CTTCCGCGAC CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGCCGA ACCCATACAG

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1371

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTGTCA GTAACGAAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAACCG
351 GACGACCCTC AATACCGATT GGGCGGATTA CGACCAGTCG GGCGACACCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGCGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGCATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACGTAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCG
701 TCGTGTTCGG CGGCGTTCCC ATTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCGTCTT GTTCCCTCAC TGTCGCCGGG
801 TTGCGGAGCG GTTTCCTTTT CCGTTCCTTA TTATTTC AAC CTTGCCCCCA
851 ATCTCGATGC CACGTTCCGG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CTTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTC ACAAAGTCTC GCACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGCGCGCG GCGGCGAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAACCGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTGAGTGC GCGTAAAAAC ACCGCGAGGG
1301 CGCAAAATCG CGTGTCGCA CAATTTACCC GATTACGCCA CGACAGCCGC
1351 CAAGACGGCA GCGCCCTGGT CGTCTATCCC GACATCAAAAT GGGATTTCAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATTT TCAACATCGA CAGCGGCGCA ACTTTTGAGC GGAATACGCG
1551 GATGTTCCGG GGAGAAGTCC TGCAAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTTCGTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCGCGCGCC GTGCAAAGCC
1751 GTATTTTGG ACGGCGGACG GGGGAAGAGC GTTTCGCGCG CGGCATCGGT
1801 CAGAAATCT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCC CGCAACCGTT CCGACTGGGT GGCATTGGCC TCCGGCAGCA
1901 TCGGCGAGCG CTTTCATCCT GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCGC AGAAGTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCT AACGCCCCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAA GTCCGCTGAC GCGCAACCTG TCGGCGGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAA AACCAGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGCGCGG GCGTGTACGC CCAAGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTGC
2351 CCGTTCCTCG CTATATCACC GCCCACTCTC TTTCCGCGCG ACGCAACAAA
2401 CGACCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```

m958.pep
1  LARLFLSKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51  PLSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTL NTDWADYDQS GDTVTAGDRF ALQQDGLTLR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRRLO SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFFVFGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VLSVPYYFN LAPNLDATFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWOHR HDISDTLQAG
351 VDFNQVSDG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGS LNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QFTRFSDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGA TFERNTRMFG GEVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYQQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGVSQKKP RNRSDWVAFS SGISGRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGKVL NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVLA GAEYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRKN
801  RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

1372

m958/g958 89.3% identity in 802 aa overlap

	10	20	30	40	50	60
m958.pep	LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC					
g958	LARLFSLKPLVLALGLCFGTHCAA-DTVAEEADGRVAEGGAQGASESAQASDLTLGSTC					
	10	20	30	40	50	
	70	80	90	100	110	120
m958.pep	LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL					
g958	LFCSNESGSPERTEAAVQGSGEASVPEDYTRIVADRMEGQSKVKVRAEGSVIIERDGAVL					
	60	70	80	90	100	110
	130	140	150	160	170	180
m958.pep	NTDWADYDQSGDVTAGDRFALQQDGTLRGETLTYNLEQQTGEAHNVMEIEQGGRRRLQ					
g958	NTDWADYDQSGDVTTVGDRFALQQDGTLRGETLTYNLDQQTGEAHNVRMETEQQGGRRRLQ					
	120	130	140	150	160	170
	190	200	210	220	230	240
m958.pep	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKIGIVAKHAAFFVGGVVP					
g958	SVSRTAEMLGEGRYKLTETQFNTCSAGDAGWYVKAASVEADRGKIGIVAKHAAFFVGGVVP					
	180	190	200	210	220	230
	250	260	270	280	290	300
m958.pep	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSPYYFNLAPNLDATFAPSVIGERGAV					
g958	LFYTPWADFPLDGNRKSGLLVPSVSAGSDGVSLSPYYFNLAPNFDATFAPGIIGERGAT					
	240	250	260	270	280	290
	310	320	330	340	350	360
m958.pep	FDGQVRYLRPDYAGQSDLTWLPDCKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
g958	FDGQIRYLRPDYSGQDLTWLPDCKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
	300	310	320	330	340	350
	370	380	390	400	410	420
m958.pep	YYRDFYGNKEIAGNVNLRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
g958	YYRDFYGGEEIAGNVNLRVWLDYGGRAAGGSLNAGLSVQKYQTLANQSGYKDEPYAIM					
	360	370	380	390	400	410
	430	440	450	460	470	480
m958.pep	PRLSVEWRKNTGRAQIGVSAQFTRFSDHSDRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
g958	PRLSADWHKNAGRAQIGVSAQFTRFSDHSDRQDGSRLVVYPGIKWDFSNSWGYVRPKLGLH					
	420	430	440	450	460	470
	490	500	510	520	530	540
m958.pep	ATYYSLNRFSGQEARRVSRTLPIVNIDSGATFERNTRMFGGEVLQTLERLFFNYIPAKS					
g958	ATYYSLDSFGGKASRSVGRVLPVVNIDGGTTFERNTRLFGGGVVQTIERLFFNYIPAKS					
	480	490	500	510	520	530
	550	560	570	580	590	600
m958.pep	QNDLPNFDSESSFGYGQLFRENLYYGNDRINTANSLSAVQSRILDGATGEERFRAGIG					
g958	QNDLPNFDSESSFGYGQLFRENLYYGNDRINAANSLSTAVQSRILDGATGEERFRAGIG					
	540	550	560	570	580	590
	610	620	630	640	650	660
m958.pep	QKFYFKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA					
g958	QKFYFKDDAVMLDGSVGKNPRSRSDWVAFASGGIGGRFTLDSSIHYNQNDKRAEHYAVGA					
	600	610	620	630	640	650
	670	680	690	700	710	720
m958.pep	SYRPAQGGKVLNARYKYGRNEKIYLSKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
g958	GYRPAPGGKVLNARYKYGRNEKIYLDQDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
	660	670	680	690	700	710

1373

	730	740	750	760	770	780
m958.pep	EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
	:					
g958	EAKKPIEMLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR					
	720	730	740	750	760	770

	790	800
m958.pep	MDVAVPGYITAHSLSAGRNRKP	
g958	MDVAVPGYIPAHSLSAGRNRKP	
	780	790

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

a958.seq

```

1   TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCAGC CATTCGCGCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCCGA ACCCATAACG
151 CCTACCGAGC TGAGCCTCGG TTCGACCTGC CTGTTTGTGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GCGGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTC CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAATCG
351 GACGACCCTC AATGCCGATT GGGCGGATTA CGACCAGTCG GCGGACACCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCGG
451 GCGGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAAACCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
701 TCGTGTTCGG CGGCGTTCCT ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGGA ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCGCGCGG
801 TTCGGACGGC GTTTCCTTTT CCGTTCCTTA TTATTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTTCGG CCGGGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCCTATC
1001 AGGCGAAATG CAGCACCAGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTC AACAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTTATGGCG CAGGGCGGCG GCGGCGAGCC TGAATGCCCG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAAACGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAAC ACCGCGAGGG
1301 CGCAAAATCG CGTGTCGCC CAATTTACCC GCTTCAGCCA CGACAGCCGC
1351 CAAGACGGGA GCCGCTTCGT CGTCTATCCC GACATCAAAAT GGGATTTTCAG
1401 CAACAGCTGG GGTACGTCC GTCCCAAACT CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CGGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCCATG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGCG
1551 GATGTTCCGG GCGGAGTCC TGCAAACCCCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTTCGTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTT CTGAAAACCT TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCGCGCGCC GTGCAAAAGCC
1751 GTATTTTGGA CGGCGCGACG GGGGAAGAGC GTTTCGCGCG CGGCATCGGG
1801 CAGAAATTCT ACTTCAAAA CGACGCAGTC ATGCTTGACG GCAGTGTCGG
1851 CAAAAAACCG CGCAGCCGTT CCGACTGGGT GGCATTTCGCC TCCAGCGGCA
1901 TCGGCAGCCG CTTATCCTC GACAGCAGCA TCCACTACAA CCAAACGAC
1951 AAACGCGCCG AGAATACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCGGTCG TCCGTTACAA
2151 CTACGGTTT GAAGCCAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGGCGCGG CGGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTCT GCAGAAACCC CGCAGACAGG ATGGATGTCT
2351 CCGTTCCCG CTATATCCCC GCCCACTCTC TTTCCGCCG ACGAACAAA
2401 CCGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

a958.pep

```

1   LARLFLKPL VLALGFCFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PTSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQQDGTLLR
151 GETLTYNLEQ QTGEAHNVRM ETEHGGRRLO SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFVFGGVP IFYTPWADFP

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1374

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251 LDGNRKSGLL VPSLSAGSDG VLSVPPYYFN LAPNLDTFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QTRFSDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLTQLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSGVKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GAEEKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFESLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRKN
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

	10	20	30	40	50	60
a958.pep	LARLFS	LKPLVL	ALGFCF	GTHCAA	ADAVAA	EETDNPTAGGSVRSVSEPIQPTSLSLGSTC
m958	LARLFS	LKPLVL	ALGFCF	GTHCAA	ADAVAA	EETDNPTAGESVRSVSEPIQPTSLSLGSTC
	10	20	30	40	50	60
a958.pep	LFC	SNESGS	PERTEAA	VQSGEAS	IPEDYTR	IVADRM
m958	LFC	SNESGS	PERTEAA	VQSGEAS	IPEDYTR	IVADRM
	70	80	90	100	110	120
a958.pep	EGSQVQ	VRAEGN	VVVERN	RTTL		
m958	EGSQVQ	VRAEGN	VVVERN	RTTL		
	70	80	90	100	110	120
a958.pep	NADWAD	YDQSGD	TVTAGD	RFALQD	GTLRGE	TLTYNLEQQTGEAHNV
m958	NTDWAD	YDQSGD	TVTAGD	RFALQD	GTLRGE	TLTYNLEQQTGEAHNV
	130	140	150	160	170	180
a958.pep	MEHGG	RRLQ				
m958	MEHGG	RRLQ				
	130	140	150	160	170	180
a958.pep	SVSR	TAEM	LGE	GHYKL	TETQ	FNTCSAGDAGWYVKAASVEADREKIGVAKHAA
m958	SVSR	TAEM	LGE	GHYKL	TETQ	FNTCSAGDAGWYVKAASVEADREKIGVAKHAA
	190	200	210	220	230	240
a958.pep	FGGVP					
m958	FGGVP					
	190	200	210	220	230	240
a958.pep	IFYTPW	ADFP	LDGN	RKSGLL	VPSLS	AGSDGVLSVPPYYFN
m958	IFYTPW	ADFP	LDGN	RKSGLL	VPSLS	AGSDGVLSVPPYYFN
	250	260	270	280	290	300
a958.pep	LAPNL	DTFA	PAPG	VIGER	GAV	
m958	LAPNL	DTFA	PAPG	VIGER	GAV	
	250	260	270	280	290	300
a958.pep	FDGQ	VRYLR	PDYAG	QSDLTW	LPHDKK	SGRNNRYQAKWQHRH
m958	FDGQ	VRYLR	PDYAG	QSDLTW	LPHDKK	SGRNNRYQAKWQHRH
	310	320	330	340	350	360
a958.pep	DISDT	LQAGV	DFNQ	VSDSG		
m958	DISDT	LQAGV	DFNQ	VSDSG		
	310	320	330	340	350	360
a958.pep	YYRD	FYGN	KEIAG	NVN	LNRRV	WLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM
m958	YYRD	FYGN	KEIAG	NVN	LNRRV	WLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM
	370	380	390	400	410	420
a958.pep						
m958						
	370	380	390	400	410	420
a958.pep	PRLS	ADWR	KNTG	RAQIG	VSAQ	FTRFSDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH
m958	PRLS	VEWR	KNTG	RAQIG	VSAQ	FTRFSDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH
	430	440	450	460	470	480
a958.pep						
m958						
	430	440	450	460	470	480
a958.pep	ATYY	SLNR	FGSQE	ARRV	SRTL	LPIVNIDSGMTFERNTRMFGGGVLTQLEPRLFYNYIPAKS
m958	ATYY	SLNR	FGSQE	ARRV	SRTL	LPIVNIDSGMTFERNTRMFGGGVLTQLEPRLFYNYIPAKS
	490	500	510	520	530	540
a958.pep						
m958						

1375

	490	500	510	520	530	540
	550	560	570	580	590	600
a958.pep	QNDLPNFDSSSESSFGYQQLFRENLYYGNDRIANTANSLSAAVQSRILDGATGEERFRAGIG					
m958	QNDLPNFDSSSESSFGYQQLFRENLYYGNDRIANTANSLSAAVQSRILDGATGEERFRAGIG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a958.pep	QKFYFKNDVAVMLDGSVGKKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
m958	QKFYFKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA					
	610	620	630	640	650	660
	670	680	690	700	710	720
a958.pep	SYRPAQGVNLNARYKYGRNEKIYLSKSDGSYFYDKLSQDLDSAQWPLTRNLSAVVRNYGF					
m958	SYRPAQGVNLNARYKYGRNEKIYLSKSDGSYFYDKLSQDLDSAQWPLTRNLSAVVRNYGF					
	670	680	690	700	710	720
	730	740	750	760	770	780
a958.pep	EAKKPPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
m958	EAKKPPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
	730	740	750	760	770	780
	790	800				
a958.pep	MDVAVPGYIPAHSLSAGRNRKRPX					
m958	MDVAVPGYITAHSLSAGRNRKP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAARAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEQ KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep

```

1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEQ KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

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m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MNIKHL	LLTSAAT	LLSISAP	ALAHHD	GHGDD	DDHGHA
g959	MNIKHL	LLTAAAT	LLGISAP	ALAHHD	GHGDD	DDHGHA
	10	20	30	40	50	60
	70	80	90	100	109	
m959.pep	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQEY	KVVVD
g959	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQEY	KVVVD
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

```

1  ATGAAGTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

```

1  MNFKRLLLTA AATALMGISA PALAHHDGHG DDDHGHAHO HSKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MNFKRL	LLTAAAT	ALMGISA	PALAHHD	GHGDD	DDHGHA
m959	MNIKHL	LLTSAAT	LLSISAP	ALAHHD	GHGDD	DDHGHA
	10	20	30	40	50	60
	70	80	90	100	109	
a959.pep	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQEY	KVVVD
m959	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQEY	KVVVD
	70	80	90	100		

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

```

1  ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51 TAAGCCCCC TTGTTTGAAG CTCCGCGGCT CCTGCCGAGC TTCACCGACC
101 CCGTTGTGCC CAAGCTCTCT GCTCCCGGCG GCTACATTGT CGACATCCCC
151 AAAGGCAATC TGAAGACCGA AATCGAAAAG CTGGCCAAAC AGCCCCAGTA
201 TGCCTATCTG AACACGCTCC AAGTAGCGAA AAACGTCAAC TGGAAACCAGG
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGG CTTAACCAGG
301 GCCCGTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGC
351 GGGAGTCGGA GCCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG
401 ATGCCGCCTT TGCCTCACTC GCTTCTCAGG CTTCCGTATC GCTCATCAAC
451 AATAAAGGCG ATGTCGGCAA AACCCTGAAG GAACTGGGCA GAAGCCGCAC
501 GGTAAAAAAT CTGTTGTAG CGCGCGCAAC GGCAGCGCTA TCCAACAAAC

```

1377

```

551 TCGGTGCTCT TCCCTTGCC ACTTGAGCG AAACCCCTTG GGTAAACAAC
601 CCAACGTTA ACCTGGCCAA TCGGGCAGT GCCGCGCTGA TCAACACCGC
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAAT ATCCTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCC CAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG GCGAATAAGG GCAAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTCGGG GAGGCTTTGG TTAAAAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGC ACAAACCGCA CAAACGCGG TAGAAAATAA TGCGGTTAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTATTTCGA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTAG
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGAAAAA CAGCTGGCTC AAATTCAGA
1401 AAAGACAACG CTTCCGACGC AGCAAGGGCA GTCTGCTCTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAAAA ACCGGTGATA GGTTTTATT AGATGGCCAA
1501 CATAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAC TTAAGTTTGT
1551 TCTAAATATG GATGGTTTCG TTAACCAAAT GAAACTGGG GCAGCAAAAG
1601 GTCGTAAATT AAACCTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

m960.pep

```

1 MQVNIQIPCM LYRRGSVKPP LFEAPRLPS FTDPVVPKLS APGGYIVDIP
51 KGNLKEIEK LAKQPEYAYL KQLQVAKNVN WNQVQLAYDK WDKQEGLTR
101 AGAAIALAV TVVTAGAGVG AALGLNGAAA AAADAFAFSL ASQASVSLIN
151 NKGDVGKTLK ELGRSRTVKN LVVAAATAGV SNKLGLASSLA TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSKDNLEAN ILAALVNTAH GEAAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKQDGA IGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTLFDETL
401 LDNDARAVID IVVGTGLNRA NKGEAAQVKV EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPEFG QLAQISEKTT LPTQOGQSVF LVKRNOGLLK TGDRFYLDGQ
501 HKNHLEVFDK NGNFKFVLNM DGSLNQMKTG AAKGRKLNK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

m961.seq

```

1 ATGAGCATGA AACACTTTC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51 CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCGTCAAT
301 GAAAACAAAC AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTTGCTGA AGAGACTAAG ACAATATATCG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CCGCCAATGA AGCCAAACAG ACGCCGAAG AAACCAACA
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAGCCCG
701 AAGCTGCCGC TGGCAGAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCCTGTTCC AACCTTACAA CGTGGGTCCG TTCAATGTAA CGGCTGCAGT
951 CGGCGGCTAC AAATCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTTCCTCCG CAGCCTACCA TGTCCGCGTC AATTACGAGT GGTA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

m961.pep

```

1 MSMKHFAKV LTTAILATFC SGALAATSDD DVKKAATVAI VAAYNNGQEI

```

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```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEAENDIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV DAKVAAETAA GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPYNVGR FNVTAAVGGY KSESAVAIGT GFRETENFAA KAGVAVGTS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet
a961.pep not found yet

g972.seq not found yet
g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTAC ATTCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTTCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GATGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAAAT CTCGTTTTGT TCGTGTTTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCTG GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTGTAG AAAATTAAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCCGGGAT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATTCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGKLEIP QRRGKQDGVF
51  VDWSIFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGXQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICKRKF NMPVPERFDQ RKKKLNLTFE
301 HKLHYAKNAV GKLVNFMIE M GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVVHQNVDDYD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTAC ATTCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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1379

```

251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTTCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTTCAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GCATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTTAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAGGCGAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATTT GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAATTTCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

```

a972.pep
  1 LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKKGKLEIP QRRGKQDGVF
 51 VDWISFTFHE DTLKLVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFQGGQRTV LVELKGTGCS VASPGWELRL
151 KQFLDDSIPT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFPICRKF NMPVPERFDQ RKKTLNLTFE
301 HKLHYAKNAV GKLNVNFIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPTYDVE
401 KERKQYELSL KVIHQNVVDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

	10	20	30	40	50	60
m972.pep	LTNRGGAKLK	TXSKSSERMS	EVEYFSHFIS	DGKKGKLEIP	QRRGKQDGVF	VDWISFTFHE
a972	LTNRGGAKLK	TNSKSSERMS	EVEYFSHFIS	DGKKGKLEIP	QRRGKQDGVF	VDWISFTFHE
	70	80	90	100	110	120
m972.pep	DTLLKLVSGC	PLFSDAEYMY	VLSRKLEEIL	GFGITRKCKS	RGNKFYESMY	RLGSDDVDYGE
a972	DTLLKLVSGC	PLFSDAEYMY	VLSRKLEEIL	GFGITRKCKS	RGNKFYESMY	RLGSDDVDYGE
	130	140	150	160	170	180
m972.pep	VHFGXQRTV	LVLEKGTGCS	VASPGWELRL	KQFLDDSIPT	RITRIDLALD	FFDGEYTPDQ
a972	VHFGGQRTV	LVLEKGTGCS	VASPGWELRL	KQFLDDSIPT	RITRIDLALD	FFDGEYTPDQ
	190	200	210	220	230	240
m972.pep	ALLDHDNGFF	DNSNQRPKSE	TIGTAWRNED	GSGKTFYVGR	KKNSRFVRVY	EKGRQLGDKE
a972	ALLDHDNGFF	DNSNQRPKSE	TIGTAWRNED	GSGKTFYVGR	KKNSRFVRVY	EKGRQLGDKE
	250	260	270	280	290	300
m972.pep	SKWVRFEIQF	NYGDIEIPLD	ILINQGSYFC	GAFFPICRKF	NMPVPERFDQ	RKKTLNLTFE
a972	SKWVRFEIQF	NYGDIEIPLD	ILINQGSYFC	GAFFPICRKF	NMPVPERFDQ	RKKTLNLTFE

1380

	310	320	330	340	350	360
m972 . pep	HKLHYAKNAVGLVNFMIEMGFNDSEIVESLKADSGFPGGLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGLVNFMIEMGFNDSEIVESLKADSGFPGGLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972 . pep	HEQPDIDLEIELDELGVIAFKNSDKFDRKRLFSPDYDVEKERKYQEYLSKVYHQNVDDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFDRKRLFSPDYDVEKERKYQEYLSKVYHQNVDDYD					
	370	380	390	400	410	420
m972 . pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

g973 . seq

```

1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATACCG
251 CCTACGTCAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CCTGCCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCACC TTTGAAGACA TCATCGAGCa aatcgtcggt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTCGGTACG GAatacggca gcgaagaagc cgacaccatc ggcggtTGG
701 TCATTCAGGA ATTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTAtc
751 ggcgGTTTGC agttcacgct CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcggttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

g973 . pep

```

1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQFHLKSVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFPGT EYGSEADTI GGLVIQELGH LPVRGEKVLI
251 GGLQFTVARA DNRRHLTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

m973 . seq

```

1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCG
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTTCCGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTTTA AAGAAAACGA CAGCATCGAG CGCATACCG
251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCGCCGTCT
401 TCGTCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTCATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTCm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

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1381

651 CTTCGGCACG GAATACAGCA kCGAAGAAGC CGACACCATT GGCGGCCTGG
 701 TCATTCAAGA GTTGGGACAT CTGCCCCTGC GCGGCGAAAA AGTCCTTATC
 751 GGCGGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973 .pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLLRLE
 51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG EIEDEFDEDD SADNIHAVSS
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVL
 251 GGLQFTVARA DNRRLHTLMA TRVK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

	10	20	30	40	50	60
m973 .pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLLRLEKVLDFSDLEV					
	:					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLTRLEKVLDFAELEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973 .pep	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	:					
g973	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973 .pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	:					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973 .pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
	: : : : :					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFGTEYGSEEADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973 .pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	:					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973 .seq

1 ATGACGCGC CACAACCGAA AACAAATTT TTTGAACGCC TGATTGCCCG
 51 ACTGCGCCG GAACCGGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
 201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG
 251 CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCGTCAT CGGTGAAGAC
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAAATATAT
 351 GTTCAACCCG GAGCAGTTCC ACCTCAAATC GATATTGCGC CCTGCCGTCT
 401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCC

1382

```

601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCACG GAATACAGCA GCGAAGAAGC CGACACCATC GCGCGCCTGG
701 TCATTTCAGGA ATTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
751 GGCGGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
  1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLLRLE
  51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
 201 ERWRIHAATE IEDINAFFGT EYSSEADTI GGLVIQELGH LPVRGEKVL
 251 GGLQFTVARA DNRRLHTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLLRLEKVLDFSDLEV					
	:					
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLLRLEKVLDFSDLEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
a973	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
	: : : :					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFFGTEYSSEADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
a973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
  51 TGCCTGCGGC GGTCAAGGCA AAGATGCCGC CGCGCTGCC GCCAACCCCG
 101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
 151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
 201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATTCAAACAC CAGCCGTGGG
 251 ACAGCCTTTT CCCCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
 301 GGCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
 351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
 401 CTTCCTCCGA AGATTTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
 451 CACACGGGCG ATTTCTCCGT TTCCAACTC TTGGGCAACG ACAATCCGAA
 501 AATCGCGCGC TTCGAAAACG TCCCCCTGAT TATCAAGAA CTGGAACG
 551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
 601 AAAAAACAAC CGGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
 651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
 701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
 751 AAGATCTACG CCAAATATTT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

```

1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

```
g981.pep
1   MKKWIAAALA CSALALSACG GQGKDAAPA ANPGKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK MNMKVGVVTG
151 HTGDFSUSKL LGNDNPKIAR FENVPLIIKE LENGGLDSV SDSAVIANVY
201 KNNPAKGMDV VTLPDFTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GGQAAK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

```
m981.seq
1   ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAGGGCA AAGATACCGC CGCGCCTGCC GCCAACCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAATAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTA AACACGCGC ATGCGGACGT TGTGATGTCG
301 GCGCTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCTCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAAACGGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGA TTCGTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG
601 AAAACAATC CGGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATTACG CCAAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

```
m981.pep
1   MKKWIAAALA CSALALSACG GQGKDTAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK MNMKVGVVTG
151 YTGDFSUSKL LGNDNPKIAR FENVPLIIKE LENGGLDSV SDSAVIANVY
201 KNNPAKGMDV VTLPDFTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/g981 98.1% identity in 266 aa overlap

```

      10      20      30      40      50      60
981.pep MKKWIAAALAC SALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF
      |||
g981     MKKWIAAALAC SALALSACGGQGKDAAPAANPGKVYRVASNAEFAPFESLDSKGNVEGF
      |||
      10      20      30      40      50      60

      70      80      90      100     110     120
981.pep DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE
      |||
g981     DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE
      |||
      70      80      90      100     110     120

      130     140     150     160     170     180
981.pep ITQVVLVPKGKKVSSSEDLKMNMKVGVVTGYTGDFSUSKLLGNDNPKIARFENVPLIIKE
      |||
g981     ITQVVLVPKGKKVSSSEDLKMNMKVGVVTGHTGDFSUSKLLGNDNPKIARFENVPLIIKE
      |||
      130     140     150     160     170     180

      190     200     210     220     230     240
981.pep LENGGLDSVVS DSAVIANVYKNNPAKGMDVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
      |||
g981     LENGGLDSVVS DSAVIANVYKNNPAKGMDVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
      |||
      190     200     210     220     230     240

      250     260
981.pep EKVRESGEYDKIYAKYFAKEDGQAAKX
      |||
g981     EKVRESGEYDKIYAKYFAKEGGQAAKX
      |||
      250     260
```

1384

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGT CAGGGTA AAGATGCCGC CGCGCCCGC GCAAATCCCC
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCC GCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACC AAG TCGTCCTCGT TCCGAAAGGC AAAAAATAT
401 CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGG TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAAAACAATC CGACCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1  MKKWIAAALA CSALALSACG GQKDAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KISSSEDLK NMNKVGVTG
151 YTGDFS SVSKL LGNDNP KIAR FENVPLI KE LENGGLDSV SDSAVIAN YV
201 KNNPTKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALACSALALSACGGQKDAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALACSALALSACGGQKDAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
	130	140	150	160	170	180
m981.pep	ITQVVLVPKGKGVSSSEDLKNNMKVGVTGYTGDFS SVSKLLGNDNP KIARFENVPLI KE					
a981	ITQVVLVPKGKGISSSEDLKNNMKVGVTGYTGDFS SVSKLLGNDNP KIARFENVPLI KE					
	130	140	150	160	170	180
m981.pep	LENGGLDSVVS DSAVIAN YVKN NPAGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVVS DSAVIAN YVKN NPAGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
m981.pep	LENGGLDSVVS DSAVIAN YVKN NPAGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVVS DSAVIAN YVKN NPAGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	250	260				
m981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
a981	KKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1  atcgcatcgc aaaaccttcg attcgacaat cgattcctcc aaaaaatggt
51  caacggcgTg aatattttgc cggccgcCga ttgggtagcC ttgGGcgCgCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCG GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAGT CCGGTCCAAA ACCAAcgaCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAAgcga TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCCGCTtt ggttgAAGAg cTGAAAAACA
401 TCGCCAAACC TTGCGATACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTT TTGCTGTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCCGTGTT GGAACAAGTG GCGAAAGCCA GCCGCCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGCGC ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 GCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTtccGAAG Aagtcggcct GTCTTTGGAA AAAGcgactT TGgacgaCTT
951 Gggtcaaacc aaACGcatCG AAATCGGtga agaaaacact ACCGTCATcg
1001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAACCTGGCAG GAGGCGTGGC AGTGATCAAA GTCGGCGCGG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TCGCGCGCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCCTGC CAAAGTAACC
1501 CGTTCGCGC TGCAACACGC CGCGTCTAtc GCCGGTCTGA TGCTGACGAC
1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1601 TGGGGGGAAT GGGCGGTATG GCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1  IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG DKAVAALVEE LKNIAKPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVNVNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGVV
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENLH TGNADQDAGV QIVLRAVES P
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYGMIG MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGM GMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1  ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCG GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAGT TCGGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGAAAAA CAAATCGCTG CTTTGACAA

```

651	TCCGTTTGTA	TTGTTGTTCC	ACAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCGTGTTTT	GGAAACAAGTG	GCAAAAGCCA	GCCGTCCGCT	GTTGATTATC
751	GCTGAAGACG	TAGAAGGCGA	AGCCTTGCGC	ACTTTGGTCG	TGAACAACAT
801	CCGAGGACATC	CTGAAACC	TTGCCGTCAA	AGCCCTTGGC	TTCCGGCGACC
851	GCCGCAAAGC	GATGTTGCAA	GACATCGCCA	TCCTGACCGG	CGGCGTGGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCTTTGGAA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAAACC	ACCATCATCG
1001	ACGGCTTTTG	CGACGCGAGC	CAAAATCGAAG	CGCGTGTTGC	CGAAATCCCG
1051	CAACAAATCG	AAACCGCAAC	CAGCAGTTAC	GCAAAAGAA	AAC TGCAAGA
1101	GCGCGTGCT	AAATTGGCAG	GCGGCGTGGC	AGTCATCAA	GTGCGTGCCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	ACCGCGTGGA	AGACGCGCTG
1201	CACGCTACCC	GCGCAGCCGT	TGAAGAAGGC	GTGGTTGCAG	GCGGCGGCGT
1251	AGCCCTGTTG	CGTGCCCGTG	CTGCTTTGTA	AAACCTGCAC	ACCGGCAATG
1301	CGCACCAGA	CGCAGGCGTA	CAAATCGTTA	TGCGCGCGGT	TGAGTCTCCG
1351	CTGCGCCAAA	TCGTTGCCAA	CGCAGGCGGC	GAACCCAGCG	TGGTTGTGAA
1401	CAAAGTATTG	GAAGGCAAAG	GCAACTACGG	TTACAACGCT	GGCAGCGGCG
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCGC	TGCAACAAGC	CGCATCTATC	GCCGGCTTGA	TGCTGACCAC
1551	TGATTGTCATG	ATCGCTGAAA	TCCCCGAAGA	CAAACCGGCT	GTGCCTGATA
1601	TGGGCGGCAT	GGGTGGTATG	GGCGGCATGA	TGTAA	

m982.seq

Homology with a predicted ORF from *N. gonorrhoeae*

m982.pep MAAKDVFQGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDFRGGPHITKDGVTVAKEI
:::| | | | | | | | | | | | | | | | | | | | | |

1387

g982	IASQNLRFDNRFLOKMNNGVNILPAADWVALGAKGRNVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
m982.pep	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
g982	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
g982	DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
m982.pep	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
g982	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTG
	250 260 270 280 290 300
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTG
	250 260 270 280 290 300
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
g982	ISEEVGLSLEKATLDDLQAKRIEIGEENTTVIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
m982.pep	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKLEGGKNGYGYNA
	430 440 450 460 470 480
g982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKLEGGKNGYGYNA
	430 440 450 460 470 480
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM
	490 500 510 520 530 540
g982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

a982.seq	1	ATGGCAGCAA	AAGACGTACA	ATTCGGCAAT	GAAGTCCGCC	AAAAAATGGT
	51	AAACGGCGTG	AACATTTTGG	CAAACGCCGT	GCGCGTAACC	TTGGGTCCCA
	101	AAGGCCGCAA	CGTGGTGGTT	GACCGCGCTT	TCGGCGGCC	GCACATCACC
	151	AAAGACGGCG	TAACCGTCGC	CAAAGAAATC	GAAGTCAAAG	ACAAGTTTGA
	201	AAATATGGGC	GCGCAAATGG	TGAAAGAAGT	GCGGTCCAAA	ACCAACGACG
	251	TGGCGGGCGA	CGGTACGACT	ACCGCCACCG	TATTGGCGCA	ATCCATCGTT
	301	GCCGAAGGTA	TGAAATACGT	TACCGCCGGT	ATGAACCGA	CCGACCTGAA
	351	ACGCGGTATC	GACAAAGCCG	TCGCGGCTTT	GGTTGAAGAG	CTGAAAAACA

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401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGCGAAAAA CAAATCGCCG GCTTGGACAA
651 TCCGTTTGTA TTGCTGTTTC ACAAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTGC CGAATCCGCG
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAACCTGGCAG GCGGCGTGGC AGTAATCAAA GTCGCTGCCG
1151 CGACCGAAGT GGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGTTGCAG GCGGCGCGCT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351 CTGCCCAAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGTTGTGAA
1401 CAAAGTGTTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTATC GCCGGCCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGCGGCAT GGGTGGTATG GGCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

```

a982.pep
  1 MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
 51 KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFLDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGTV
301 ISEEVGLSLE KATLDDLQGA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALNLH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVNVKVL EGKGNYGYN A GSGEYDMIE MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGGM GMM*

m982/a982 99.3% identity in 544 aa overlap

          10          20          30          40          50          60
m982.pep  MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHITKDGVTVAKEI
a982      MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          10          20          30          40          50          60

          70          80          90          100         110         120
m982.pep  ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG I
a982      ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          70          80          90          100         110         120

          130         140         150         160         170         180
m982.pep  DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
a982      DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          130         140         150         160         170         180

          190         200         210         220         230         240
m982.pep  KLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
a982      KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
          190         200         210         220         230         240

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	250	260	270	280	290	300
m982.pep	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
a982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982.pep	RARAALLENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNKVLEGGKNGYGYNA					
a982	RARAALLENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNKVLEGGKNGYGYNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPMGGMGGM					
a982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPMGGMGGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCCTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCCACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAAGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTTC	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTT
501	GGATGTCCAA	TCCGATGTGC	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCGT	CAAAATCGGC	AATCCCAAAA	ATTGAAACC	GGGCGAATGG
601	GTGCGTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701	TCATCCAAAC	CGACGTGCCC	ATCAATCCGG	GCAATTCGGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTGCG	CGAACAGCTG	AAAAACACCG	GCAAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTCAAGG	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCCT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGCGGCAT
1101	TACGCCGGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	ccgagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAGcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcgtacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

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1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGGTCatgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

```

g986.pep
  1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
101 EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVAGM GSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

```

m986.seq
  1 GTGTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGCACAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCCGGC
201 AGTCGTCAAT ATTCAAGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCG
251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
301 GAATTTTTCA AACGCCTCGT CCCGAATATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GGCGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGTACAT CCTGACCAAT ACCCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCGGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCCG
651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGCGGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTGCG CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGCGGCGG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CAGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GCGGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCAATCC GCAGGCATTA CCCTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

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This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

```

m986.pep..
  1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
101 EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVAGM GSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

m986.pep	10	20	30	40	50	60
	VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
g986	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	10	20	30	40	50	60
m986.pep	70	80	90	100	110	120
	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
g986	VQSEGPVVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
m986.pep	130	140	150	160	170	180
	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
m986.pep	190	200	210	220	230	240
	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
m986.pep	250	260	270	280	290	300
	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
g986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
g986	AGITLQTHTDSSGKHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1   GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCCGCCTC
51  GCTGGCAGGC TGCACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACTG GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAAGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCA
251 GCAATGCCGA AACCATTCC GACCCGCTTG CCGACAGCGA CCGGTTCTAC
301 GAATTTTTC AACCCTCGT CCCGAACATG CCCGAAATCC CCAAGAAGA
351 AGCAGATGAC GNGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCGGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGGCGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCCG
951 TTTGGACAAA GCCGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGCGCTG CGGCGGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GGCGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAC CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1   VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPEEADD GGLNFGSGFI ISKDGYYLTN THVVTGMGSI
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ

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301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGHLVVVR VSDAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMMLLPDFAQL					
a986	VFKKYQYLALAALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMMLLPDFVQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
a986	VQSEGPVVNIQAAPAPRTQNGSSNAETDSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGDNSVTAGXVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQKNTGKVQRGQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLVVVRVSDAERAGLRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
a986	AGITLQTHTDSSGGHLVVVRVSDAERAGLRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987.seq
 1 ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCCTCCTTC TCTGTTCATG

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51  TTCTTCATGG TTGCCCCAC TGGAAGAAGC GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTTGG CGCAACGaCA TTTCGGCAG GCTGCTGTTC
301 AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTT
351 ggacgacaAC AACAcgcgcg gcttgagca tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCCTGTTCA ACCCCTtctgt CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCgcCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTTCGACCG TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT GATCAGCGAC AGCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAAACTG GTGCAAGGACG GCATAGACGT TACCGTCTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACCT TACGAGCTGC
1151 AACCACAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacg gCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCGG TTCCGCACGG CTAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 AccctCGCG AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAACGCA TCGCCGAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

```

g987.pep
1  MKTRSLISLL CLLLCSCSSW LPPLERTES RHFNTSKPVL LDNLIQIRHT
51  PHNNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAERG VRVRLLLDDN NTRGLDDLLL ALDSHPNI*V RLFNPFVLRK
151 WRALGYLDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 VTSLSHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHDPATRK TYPNEPEAKL WKRIA AKILS
501 LLPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

```

m987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCAC TGGAAGAAGC GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCGGCAG GCTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCgcCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTTCGACCG TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCCT CATCAGCGAC GACCTGCAA AAGGACTCGA CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCCA
951 AAAAAGCGTC TATCTGGTTT CACCTATTT CGTTCCACACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCACAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGGT TCGTTCAACC TCGACCCCGG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1 MKTRSLISLL CLLLCSCSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAAERG VVRVRLDDN NTRGLDDLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTFPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIA AKILS
501 LLPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

```

m987.pep      10      20      30      40      50      60
MKTRSLISLLCLLLCSCSSWLPPEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY
|||||
g987          10      20      30      40      50      60
MKTRSLISLLCLLLCSCSSWLPPEERTESRHFNTSKPVLLDNILQIRHTPHNGLSDIY
|||||

m987.pep      70      80      90      100     110     120
LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLDDN
||:|||||
g987          70      80      90      100     110     120
LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLDDN
|||||

m987.pep     130     140     150     160     170     180
NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI
|||||
g987         130     140     150     160     170     180
NTRGLDDLLLALDSHPNIXVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI
|||||

m987.pep     190     200     210     220     230     240
LGGRNIGDEYFKVGEDTVFADLDILATGSVGEVSHDFDRYWASHSAHNATRIIRSGDIG
|||||
g987         190     200     210     220     230     240
LGGRNIGDEYFKVGEDTVFADLDILATGSVGEVSHDFDRYWASHSAHNATRIIRSGNIG
|||||

m987.pep     250     260     270     280     290     300
KGLQALGYNDETSRHALLRYRETVEQSPYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR
|||||
g987         250     260     270     280     290     300
KGLQALGYNDETSRHALLRYRETVEQSPYQKIQTGRIDWQSVQTRLISDPAKGLDRDR
|||||

m987.pep     310     320     330     340     350     360
RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVL TNSLQATDVA

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1396

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|||||
g987      RKPP|IAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDIVTVLTNSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          |||||
g987      AVHSGYVVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNT|EMGVVIESPKIAEQMERTLADTT|PAYAYRVTLDRHNLQWHPATRK
          |||||
g987      SFNLDPRSARLNT|EMGVVIESPKIAEQMERTLADTT|PEYAYRVTLDKHNRLQWHPATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
          |||||
g987      TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
          490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAGC CGTCATTTC
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCCGGCCG ACTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCGCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCGCGCG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCTCTAC CAAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAAGCGT C TATCTGTTT CACCCTATTT CGTCCCCACA AAATCCGCGC
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTCTG
1051 ACCAACTCGC TACAGCGGAC CGACGTTGCC GCGTCCATT CCGGTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCACAACCA TGCCGTCCTT GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACTG
1301 AAATGGGCGT TGTTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1  MKTRSLISLL CLLLCSSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAAERG VVRVRLLDN NTRGLDLLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTFD PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPP|IAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGDIVTVL

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
 451 TLADTSPEYA YRVTLDRHNR LQWHD PATRK TYPNEPEAKL WKRIA AKILS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
a987	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLA AERGVRVRLLLDDN					
a987	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLA AERGVRVRLLLDDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m987.pep	NTRGLDDLLALD SHPNIEVRLFPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
a987	NTRGLDDLLALD SHPNIEVRLFPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGESVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGESVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVTRRLISDDPAKGLDRDR					
a987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRRLISDDPAKGLDRDR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m987.pep	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA					
a987	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m987.pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m987.pep	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNR LQWHD PATRK					
a987	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNR LQWHD PATRK					
	430	440	450	460	470	480
	490	500	509			
m987.pep	TYPNEPEAKLWKRIA AKILSLLPIEGLLX					
a987	TYPNEPEAKLWKRIA AKILSLLPIESLLX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq

1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

1398

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51' AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTCGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgaggcg
251 CagtTTGCGc gGCGgacaag ctgGATTTGG TCAAATGccg Cgtcgaggcg
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTTCGT TTATACGAAC GCCAgatgcy tggTGtcatG CAcggcgaca
401 ccgttACCGT CCGTCCTGCg ggtatggaCC GCAGGGGccg ccgcGAaggg
451 acgtttctGG ATATTGTCGA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTGGAA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAt cgAAATTGCC GTGCGCAAGC ATCATTTCGC GCAccgaTTC
751 AGTGAagcgt gtGcCAATC CGcgaAAAA ATtccccgacc ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTGTG CGACCTTCCT TTGGTAACGA
851 TAGACGGCGA AACGGCGCGC GATTTTCGACG ACGCGGTGTT TGCCGAAAAA
901 GTCGGACGCA ATTACGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCCGCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGATTT CCCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAAATAC CGCTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGAAAA
1201 TGGCTTTCAG ACGGCATCGG GAATCCGCAC AAAGCCCAA TCGACACGCT
1251 TTACAAGCTG TTTAAATTT TGCAGAAAAA ACGTCTGGCG CGCGGGGCGG
1301 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAAA TTGTCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGGCGA ATGTTTGC GC CGGATTTT CTGTTGAAAA
1451 ACAAACATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGCGCAAC CCCTCGCCGA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCGG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGGAAAAA CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGAAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTCCGTGAA ATATTTGAAG GcaaaatCtc ccggggtgtg
1951 gcaaaTtttg gaATATTTGT CACTTTGGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGTTCG CCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGAG AAAGCGGCAG GCGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGCGG GGAAAGGGAA ATCGAAAACC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GGAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1 MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIELLER KGVPSKIESL
51 ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGEFVP LMPMDEGDFV LYERQMRGVM HGDTVTVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGKIE VYPEQNRPAV AKIEVLGDY ADSGMEIEIA VRKHHLPHRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VGRNRYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMIFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSQWALGVH TSFCERRADD AGRDVENWLK TYMRDKVGE IFEGKISRGV
651 ANFGIFVTLD DIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPVAV AESGKKAKKP VPIKVKRRKG KS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```
m988.seq (partial)
1  ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51  CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TCGGAAAAAA ATCCCGTCC ATGTACGCAA
351 AAGCGATTTC AAAGGCCGCG TCGATTTCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451 GTCGGACGCA ATTACCGTCT GGTCGTGGCG ATTGCGGATG TCAGCCATTA
501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATTT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGA
751 TGGATTTCAG ACGGCATCGA CCATCCGTAC AAAGCCCAA TCGACACCCT
801 TTACAACTC TTCAAATCC TTCAGAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTC CTGTTGAAAA
1001 ACAAGCATA GCGCTTTGTT CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051 CTCGCCACCC TCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGCGCG
1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201 CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCCTA
1251 CGAAGCATA GCGCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1301 CCGTACACCG CGCCATCAA GCGGTGTTGA ATCAGCAAAC CTACACGCCA
1351 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1451 TCGCGGATAA GGTCGGCGAA GTATTGGAAG GTAAAATCTC CGGCATGACC
1501 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGTT
1551 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
1601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCAACAT GGGGGACAGG
1651 GTTGCCGTCC GGGTCGCCCC TGCCGATTTC GATGACGGAA AAATCGATT
1701 TGTCTGATT GCCGGGGGGA GCGGCAGGG GCGGAAAGTT AAATCATCCG
1751 CGTCTGCCAA ACCGGCAGGG ACGCGGGGA AAGGAAGCC GAAACCGCC
```

1400

1801 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
 51 SGQVIVGEIE VYPEQNRPAV AKIEVLGDY ADSGMEIEIA VRKHHLPHQF
 101 SEACAKAAKK IPVHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPD AE LLQVMMLRSM
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQOTYTP
 451 KKSQWALGVH TSFCERRADD ASRDVENWLK TYMRDKVGE VFEGKISGMT
 501 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGPKTA
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKKRKGK S*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGVMHGD	TVTVRPAGMDRRGRREGTFLDIVERAQSKVVGRFYMDRGVAILEPED				
	130	140	150	160	170	180
m988.pep		40	50	60	70	80
		KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA				
g988		KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA				
	190	200	210	220	230	240
m988.pep		100	110	120	130	140
		VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK				
g988		VRKHHLPHRFSEACAKSAKKIPDHVRKSDLKGRVDLCDLP LVTIDGETARDFDDAVFAEK				
	250	260	270	280	290	300
m988.pep		160	170	180	190	200
		VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRMIPLPENLSNGICSLNPDV				
g988		VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRRMIPLPENLSNGICSLNPDV				
	310	320	330	340	350	360
m988.pep		220	230	240	250	260
		ERLCMVCDMVVTYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL				
g988		ERLCMVCDMVVTYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSDGIGNPHKAQIDTLYKL				
	370	380	390	400	410	420
m988.pep		280	290	300	310	320
		FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
g988		FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
	430	440	450	460	470	480
m988.pep		340	350	360	370	380
		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPD AE				
g988		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPD AE				

	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQITYTP					
g988						
	LLQVMMLRSMQQAVYEPHCEGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNKRKITYTP					
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	509
	KKSWQALGVHTSFCERRADDASRDVENWLKTYMYMRDKVGEVFEGKIS-GMTSFGIFVTLD					
g988	:	:	:	:	:	:
	NKSWQALGVHTSFCERRADDAGRDVENWLKTYMYMRDKVGEIFEGKISRGVANFGIFVTLD					
	610	620	630	640	650	660
m988.pep	510	520	530	540	550	569
	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
g988						
	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
m988.pep	570	580	590	600	610	629
	IAGSGRGRKVKSSASAKPAGTAGKGKPKTAAEKKTARGGKVRGRGASAAAESRKKAKKP					
g988			:	:	:	:
	IAGESGRRRKVKLSASAKPAGAAGKGKSKTTAEKKTARCGKVRGRGVFAVAESGKKAKKP					
	730	740	750	760	770	780
m988.pep	630	640				
	VPIKVKRRKGKXS					
g988						
	VPIKVKRRKGKXS					
	790					

a988.seq

1	ATGAATAAAA	ATATTAAATC	TTTAAATTTA	CGGGAAAAAG	ACCCGTTTTT
51	AAGTCGTGAA	AAACAGCGTT	ATGAACATCC	TTTGCCAGT	CGGGAATGGA
101	TAATCGAGCT	GCTTGAACGT	AAAGGCGTAC	CATCCAAGAT	TGAAGCTTTG
151	TACGCGGAAT	TGTCGATTAA	GGAAGAAGAG	TACGAATTTT	TCGAACGTCG
201	TCTGAAGGCG	ATGGCGCGGG	ACGGTCAGGT	TTTAATCAAC	CGTTCGGGGC
251	CGGTTTGCGC	GGCGGACAAA	TTGGATTGCG	TCAAATGCCG	TGTCAAGGCG
301	CACAAAGACC	GCTTCGGTTT	CGCCGTCGCC	CTCACGCCCG	CCAAAGACGG
351	TGATTTTGTC	TTGTACGAAC	GCCAGATGCG	CGGCATTATG	CACGGCGATA
401	TTGTCACTGT	TCGTCCTGCC	GCCATGGACG	TAGGGGCCCG	CCGCGAAGGG
451	ACGGTTCCTG	ATATTGTCGA	ACGCGCGCAA	AGCAAAGTGG	TCGGCCGTTT
501	CTANATTGGAT	AGGGGCGTGG	CGATTTTGGA	GCCGGAAGAC	AAGCGTCTGA
551	ACCAAAGCAT	CGTATTGGAA	CCGGACGGCG	TGGCGCGTTT	CAAACCTGAA
601	TCGGGTCAGG	TGATCGTCGG	GCAAAATTAG	GGTTATCCTG	AGCAAAACCG
651	GCCGGCAGTG	GCAAAAATCA	TCGAAGTTTT	GGGCGATTAT	GCCGACACGG
701	GCATGGAGAT	TGAAATTGCC	GTGCGCAAGC	ATCATTTGCC	GCACCAATTC
751	AGTGAAGCGT	GTGCCAAAGC	CGCGAAAAAA	ATTCCCGACC	ATGTACGCAA
801	AAGCGATTTG	AAAGGCGCGG	TCGATTTGCG	CGACCTGCCT	TTGGTAACGA
851	TAGACGGCGA	AACGGCTCGA	GATTTTGACG	ATGCGGTGTT	TGCGGAAGAA
901	ATCGGACGCA	ATTACCGTCT	GGTCGTGGCG	ATTGCCGATG	TCAGCCATTA
951	TGTCCGCCCC	GATGACGCTA	TCGACACGGA	CGCTCAGGAA	CGCAGCACCA
1001	GTGTTTACTT	CCCGCGCCCG	GTGATTCCCA	TGTTGCCGGA	AAACCTGTCC
1051	AACGGCATCT	GCTCGCTCAA	TCTCATGTCT	GAGCGTTTGT	GTGTTGTGTG
1101	CGATATGGTT	ATCACTTACG	CGGGCAATAT	CAGAAGATAC	CGCTTGTACC
1151	CCGCCGTGAT	GCGCTCTCAT	GCCCGCCTGA	CCTACAACCA	AGTTTGAAAA
1201	TGGCTTTCAG	GCGGCATCGA	GCATCCGTTT	AAAATCCAAA	TCGACACGCT
1251	TTACAAATCT	TTCAAAATCC	TTCAGAAAAA	CGGTTCGAA	CGCGGGGCGG
1301	TGGAGTTTGA	CAGCATCGAA	ACCCAAATGC	TTTTTCAGCA	CAACGGTAAG
1351	ATTGAAAAAA	TCGTCCCCGT	TGTCCGCAAC	GATGCCACAC	AGCTGATTGA
1401	AGAATTGTAT	TTGGCGGCAA	ACGTTTGCGC	AGCGGATTTT	CTGTTGAAAA
1451	ACAAGCATAC	CGCATTTGTT	CGCAACCAAT	TGGGGCCCCC	GCCCCAAAAA
1501	CTCGCCGCCT	TGCGCGAGCA	GCTCGGTCGT	TTGGGGCTTC	AACTTGGCGG
1551	CGGCGACAAC	CCGTGCGCGA	AAGACTATGC	CGCGCTTGCC	GGACAGTTTC

a988.pap

1	MNKNIKSLNL	REKDPFLSRE	KQRYEHLPLS	REWIIELLER	KGVPSKIEAL
51	VRELSIKEEE	YEFFERRLKA	MARDGQVLIN	RRGAVCAADK	LDLVKCRVKA
101	HKDRFGFAVP	LTPAKDGDFV	LYERQMRGIM	HGDIVTVRPA	GMDGRGREG
151	TVLDIVERAQP	SKVVGRFXMD	RGVAILEPED	KRLNQSIVLE	PDGVARFKPE
201	SGQVIVGEIE	VYPEQNRPAV	AKIEVLGDY	ADSGMEIETA	VRKHHLPHQF
251	SEACAKAAKK	IPDHVRKSDL	KGRVDLRDL	LVTIDGETAR	DFDDAVFAEK
301	IGRNYRLVVA	IADVSHYVRP	DDAIDTDAQE	RSTSVYFPRR	VIPMLPENLS
351	NGICSLNPHV	LETVCVCDMV	ITYAGNIKEY	RFYPVMRSH	ARLTYNQVWK
401	WLSGGIEHPF	KTQIDTLYKL	EKILQKKRFE	RGAVEFDSIE	TQMLFDDNGK
451	IEKIVPVVRN	DAHKLIEECM	LAANVCAADF	LLKNHPTALF	RNHLGPTPEK
501	LAALREQLGL	LGLQLGGGDN	PSPKDYAALL	GQFKGRPDAL	LLQVMMLRSM
551	QQAVYEPHCD	GHEFLGAEAY	AHFTSPIRRA	PDLTVHRAIK	AVLNQMTYTP
601	KKSQWALGVH	TSFCERRADD	ASRDVENWLK	TYVMRDKVGE	VFEGKISGMT
651	SFGIFVTLDG	THIDGLVHIS	DLGEDYFNFR	PEIMAIIEGER	SGIRFNMGDR
701	VAVRVARADL	DDGKIDFVLI	AGSGSRGRKV	KSSASAKPAG	TAGKGPKFTA
751	AEKKTARGGK	VRGRGASAAA	ESRKKAKKPV	PIKVKKKRKG	S*

m988/a988 97.0% identity in 641 aa overlap

	10	20	30
m988.pep	TVLDIVERAQSKVVGRFYMDRGVAILEPED		
a988	LYERQMRGIMHGDIIVTRPAGMDGRGRREGTVLDIVERAQSKVVGRFXMDRGVAILEPED		
	130	140	150
	160	170	180
	40	50	60
	70	80	90
m988.pep	KRLNQSIIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDIADSGMEIEIA		
a988	KRLNQSIIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDIADSGMEIEIA		
	190	200	210
	220	230	240
	100	110	120
	130	140	150
m988.pep	VRKHHLPHQFSEACAKAAKKIPVHVRSDDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK		
a988	VRKHHLPHQFSEACAKAAKKIPDHVRSDDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK		
	250	260	270
	280	290	300
	160	170	180
	190	200	210
m988.pep	VGRNRYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVIPMLPENLSNGICSLNPDV		
a988	IGRNRYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFPRRVIPMLPENLSNGICSLNPHV		
	310	320	330
	340	350	360
	220	230	240
	250	260	270
m988.pep	ERLCMVCDMVVITYAGNIKEYRFYPVMRSHARLTYNQVVKWISDGIDHPYKAQIDTLYKL		
a988	ERLCVVDVMVITYAGNIKEYRFYPVMRSHARLTYNQVVKWLSGGIEHPFKTOIDTLYKL		

1403

	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAV	EFESVETQMI	FDDNGKIEKIV	PVVRNDAHKL	IEECMLAANV	CAADF
a988	FKILQKKRFERGAV	FDSIETQML	FDDNGKIEKIV	PVVRNDAHKL	IEECMLAANV	CAADF
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHL	GPTPEKLATL	REQLLGLQL	GGGDNPSPK	DYAALVEQF	KGRPDAE
a988	LLKNKHTALFRNHL	GPTPEKLAAL	REQLLGLQL	GGGDNPSPK	DYAALAGQF	KGRPDAE
	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQQA	VYEPHCDGH	FGLAYEAYAH	FTSPIRRYP	DLTVHRAIK	AVLNQQTYTP
a988	LLQVMMLRSMQQA	VYEPHCDGH	FGLAYEAYAH	FTSPIRRYP	DLTVHRAIK	AVLNQQTYTP
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	510
	KKSWQALGVHTS	FCERRADDAS	RDVENWLKTY	YMRDKVGEV	FEGKISGMTS	SFGIFVTLDG
a988	KKSWQALGVHTS	FCERRADDAS	RDVENWLKTY	YMRDKVGEV	FEGKISGMTS	SFGIFVTLDG
	610	620	630	640	650	660
m988.pep	520	530	540	550	560	570
	IHIDGLVHISDL	GEDYFNFRPE	IMAIEGERSG	IRFNMGDRV	AVRVARADL	DDGKIDFVLI
a988	IHIDGLVHISDL	GEDYFNFRPE	IMAIEGERSG	IRFNMGDRV	AVRVARADL	DDGKIDFVLI
	670	680	690	700	710	720
m988.pep	580	590	600	610	620	630
	AGGSGRGRKVKSS	ASAKPAGTAG	KGKPKTAAE	KKTAGGKVR	GRGASAAE	SRKKAKKPV
a988	AGGSGRGRKVKSS	ASAKPAGTAG	KGKPKTAAE	KKTAGGKVR	GRGASAAE	SRKKAKKPV
	730	740	750	760	770	780
m988.pep	640					
	PIKVKKRKGSX					
a988	PIKVKKRKGSX					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989.seq

```

1  ATGACCCCTT TCACACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51  TGCCGCGCA TCTGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCCG ACGCGTCGAC CATCTTCTAC
151 AATCCCGCCG GCCTGACCAA ACTCGACAGC AGCCAGATT TCCGTCAACGC
201 CAACATCGTG CTGCCCAGCA TTCATTATGA AGCAGATTCC GCCACCGACT
251 TTACCGGGCT TCCCGTCCAA GGTCTATAAA ACGGCAAAAT CACCAAAACC
301 ACGGTCGCAC CCCACATTTA CGGCGCATAC AAAGTCAACG ACAATCTGAC
351 CGTGGGCTTG GCGGTGTACG TCCCCTTCGG CTCTGCCACC GAATACGAAA
401 AAGATTCCGT GTTGCGCCAC AACATCAACA AACTCGGTCT GACCAGCATC
451 GCCGTCGAAC CTGTCGCCGC GTGGAAACTC AACGAACGCC ATTCCTTCGG
501 CGCAGGCATC ATCGCCCAAC ATAATTCCGC CGAACTGCGC AAATATGCCG
551 ACTGAGGAAT CCCAAAAAAA GCGCAAATGC TGCAAGCAAC ACCTTCTAAT
601 CCTACTGCCG CTGCTCAAAT CAAGGCCGAC GGACACGCCG ATGTCAAAGG
651 CAGCGATTGG GCGGTCGGCT ACCAACTGGC GTGGATGTGG GACATCAACG
701 ACCGCGCGCG CGTGGGCGTG AACTACCGTT CCAAAGTTTC ACACACGCTC
751 AAAGGCGATG CCGAATGGGC GGCAGACGGC GCGGCGGCGA AACAACAGTG
801 GAATGACAA ATGCTCACAC CGCTCGTTA CACGGCGAAT GAAAAAGCCA
851 GTGTCAAAAT CGTAACGCCT GAGTCTTTGT CCGTACACGG CATGTACAAA

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1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAAC TTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGT TTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAAGT GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCCGCAAC GCCGACTacC
1151 GCATGAACAG CCTGCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGACCGG GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TGCACGCTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989.pep
  1 MTPFTLKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
 51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNNDLTVGL GVIYVFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWK L NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAAQIKAD GHADVKGSDW GVGYQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGM YK
301 VSDKADLFGD VTWTRHSR FN KAELFFFEKEK NIANGKKS DR TTITPNWR NT
351 YKVGLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWF SAGM
401 KYHIGKNHV V DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CAREFKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989.seq
  1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
 51 TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATT CAT TATGAGCGCG
251 ATTCGCCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTT C GAAAAGCGGC
301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACCTAA CCGTGTAGCC GAAGCTGCAA AAATTCAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAAC TAC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGCGGAA TGAAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCCGGCGA
951 CGTAACTTGG ACGCGCCACA GCCGCTTCGA TAAGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCCTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCCG
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCCG CCGGTATGAA ATACCATATC GGTAAAAACC ACGTCGTCGA
1251 TGCCGCCTAC ACCCACATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACCACG CCGACATCAT CCGTCTGCAA TACACCTACA AATTCAAATA
1401 A

```

This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989.pep
  1 MTPSALKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
 51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKT TVAPH IYGAYKVN D LTVGLGVYV FGSATEYEK D SVLRHNINKL
151 GLTSIAVEPV AAWKLND R HS FGAGIIAQ HT SAELRKYAD W GIKSKAEILT
201 AKPPKPNGVA EAAKIQAD GH ADVKGS DWGF GYQLAWMW DI NDRARVGV NY
251 RSKVSHTLKG DAEWAADG AA AKAMWSTML A ANGYTANE KA RVKIVTPES L
301 SVHGM YKVSD KADLFGDVTW TRHSRFDKAE LVFEKEKT VV KGKSDRTTIT

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1405

351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI
 401 WFSAGMKYHI GKNHVVDAA YTHIHINDTSY RTAKASGNDV DSKGASSARF
 451 KNHADIIGLQ YTYKFK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989.pep	MTPFTLKKTVLLLGTAF	AAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL			
m989	MTPSALKKTVLLLGTAF	AAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL			
	10	20	30	40	50
	60	70	80	90	100
g989.pep	TKLDSSQISVNANIVLPSI	HYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN			
m989	TKLDSSQISVNANIVLPSI	HYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN			
	70	80	90	100	110
	120	130	140	150	160
g989.pep	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVA	AAWKLNERHSFGAGIIAQHN			
m989	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVA	AAWKLNDRHSFGAGIIAQHT			
	130	140	150	160	170
	180	190	200	210	220
g989.pep	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGS	DWVGQYQLAWMWDI			
m989	SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGS	DWVGQYQLAWMWDI			
	190	200	210	220	230
	240	250	260	270	280
g989.pep	NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKQQW	NDNMLTPLGYTANEKASVKIVTPES			
m989	NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIVTPES				
	250	260	270	280	290
	300	310	320	330	340
g989.pep	LSVHGMVKVSDKADLFGDVTWTRHSRFNKAELFFEKEKNIANGKKS	DRTTITPNWRNTYK			
m989	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTVVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	360	370	380	390	400
g989.pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRI	WFSAGMKYHIGKNHVDA			
m989	VGFSGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRI	WFSAGMKYHIGKNHVDA			
	360	370	380	390	400
	420	430	440	450	460
g989.pep	AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq
 1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTACTGCTCG GCACTGCCTT
 51 TGCCGCGCA TCCGCACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG
 101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
 151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA
 201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG
 251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTC GAAAAGCGGC

1406

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301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 ACGCCATTCC TTCGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAAC TA CCGTTCCAAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GGCGAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTCG GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCCAAC
1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTTCCTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC
1201 TCCGCCGGCA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCGC
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCACG GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTTCCGCACG TTTCAAAAAC
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

a989.pep

```

1 MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERSH FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGSWDWFGYQ LAWMWDINDR ARVGVNYSK
251 VSHTLKGDAE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMVKVSDKA DLFGDVTWTR HSRFDKAE LV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVFGF GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVDDAAYTH IHINDTSYRT AKASGNDVDS KGASSAREFN
451 HADIIGLQYT YKFK*

```

m989/a989 93.1% identity in 467 aa overlap

```

          10      20      30      40      50      60
m989.pep  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
          |||
a989      MTPSALKKTVLLLGTAFAAASQASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
          10      20      30      40      50      60

          70      80      90      100     110     120
m989.pep  TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          |||
a989      TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          70      80      90      100     110     120

          130     140     150     160     170     180
m989.pep  LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT
          |||
a989      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERSHFGAGIIAQHT
          130     140     150     160     170     180

          190     200     210     220     230     240
m989.pep  SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWFGYQLAWMWDI
          |||
a989      SAELRKYADWGIMEKAKALKETPPNPT---KAAQIKADGHADVKGSDWFGYQLAWMWDI
          190     200     210     220     230

          250     260     270     280     290     299
m989.pep  NDRARVGVNYSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTAN EKARVKIVTPES
          |||
a989      NDRARVGVNYSKVSHTLKGDAEWAADDAMAKQLWDANKLALLGYTPSEKARVKIVTPES

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1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTVVKGKSDRTTITPNWRNTYKV					
a989	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTIIVNGKSDRTTITPNWRNTYKV					
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSAREFKNHADIIGLQYTYKFKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1  ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CCGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGCG GGTAAAAAGT CAATTACAGG ATTTATACAA AACCAAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCGAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTTCCTGTTT GGCTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTTGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CAAAACGGC GGATTCCGGT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCTCG
1051 CAAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CGGCGTGATG
1201 GGCGGCAGGG CCGGCCAGCA CGCATCAGT AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TGTATTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCCTGCGG AACGCTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTCAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTCGGAATA GGCAATAATG TGCGGTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GGCGGCTTTA CCGACACGCA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTTCGGG AAAAAACCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGGCG CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLQKQMP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLPQ
501 QAQFTYLGVN GGFTDSEGTA VGLLGSQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLFL*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

a990.seq

```

1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCCTACCA AAATCGGCCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAACACTACA AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTTAAGAAG CAATTACAGG ATTTATACAA AACAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCAC GTCCGCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GCGTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGCGCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAACAAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGCGGGA
951 AGCGGTTTTA TATGCCAAC AGGCTTATGC GGCAAATACT TTGTTCTGGG
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GCGGCGCAA AGGCGTGCAA ATCGGCGCGC
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGCAAT CCGGCTGATG
1201 GCGGCGAGGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGTT ATGGCGGGGG TGTATTGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCCTGCGG AACGCTACAA
1401 AACCAGAGGT TGGACGGCTT CTGTGCAAGG CCGCTACAAC GCGCTGTGG
1451 CGGAAGGCGT TGTCGAAAAA GGCAATAATG TGCGGTTTTA CCTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGCGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCGC
1601 GCATTGCGGC AAAAAACCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

a990.pep

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITDLY GDNLKDAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVQ IGGEVFVRQN EGSRLAIGVM

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1409

401 GGRAGQHASV NGKGGAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
 451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLQF
 501 QAQFTYLGVN GGFTDSEGTA VGLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
 551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
 601 YGKRTDGDKE AALSLKWLF*

m990/a990 96.0% identity in 619 aa overlap

m990.pep	10	20	30	40	50	60
	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQQGKNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQQGKNYN					
	10	20	30	40	50	60
m990.pep	70	80	90	100	110	120
	SGILAVDNMPVVKYITEKYGADLKQAVKSQLQDLYKTRPEAWAENKKRTEEAYIAQFGT					
a990	SGILAVDNMPVVKYITDITYGDNLDKAVKKQLQDLYKTRPEAWEENKKRTEEAYIEQLGP					
	70	80	90	100	110	120
m990.pep	130	140	150	160	170	180
	KFSTLKQTMPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
a990	KFSILKQKNPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
	130	140	150	160	170	180
m990.pep	190	200	210	220	230	240
	MTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRESDEP					
	190	200	210	220	230	240
m990.pep	250	260	270	280	290	300
	ALTFEDKVSQSGVVLERRPENLKTLDGRKLIAAKTADSGSFAFKQNYRQGLYELLKQC					
a990	ALTFEEKVSQSGVVLERRPENLKTLDGRKLIAAEKADSNSFAFKQNYRQGLYELLKQC					
	250	260	270	280	290	300
m990.pep	310	320	330	340	350	360
	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
a990	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
	310	320	330	340	350	360
m990.pep	370	380	390	400	410	420
	RSHQNIRGGAAADGWRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHASVNGKGGAGSD					
a990	RSHQNIRGGAAADGRRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHASVNGKGGAGSY					
	370	380	390	400	410	420
m990.pep	430	440	450	460	470	480
	LYGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
a990	LHGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	430	440	450	460	470	480
m990.pep	490	500	510	520	530	540
	ALVAEGIVGKGNVRFYLQFQAQFTYLGVNGGFTDSEGTA VGLLGSGQWQSRAGIRAKTR					
a990	ALVAEGVVGKGNVRFYLQFQAQFTYLGVNGGFTDSEGTA VGLLGSGQWQSRAGIRAKTR					
	490	500	510	520	530	540
m990.pep	550	560	570	580	590	600
	FALRNGVNLQFPFAAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					
a990	FALRNGVNLQFPFAAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					

1410

	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLFX					
a990	YGKRTDGDKEAALSLKWLFX					
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

```
g992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGCGCGTTG  GGTATACGG
101 GATATGACAG  TGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCACGTCAG  GGGACGTGGG  TTTCGACGCG  CCCGTTCCGC  GACGGGCATC
201 GGCGAAATCC  GGCCACAGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGATACCC  TCACGTCATC  GACGCGCAGC  GCGCGAAACA  TAAATTCGG
301 ATGGCGTATA  TCGACGCACC  GGAGATGAAA  CAGGCTTACG  GTACACGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAGGG  TAGGAAAGTC  AGTGTACGTG
401 TGTTTGAAAC  CGACCGCTAT  CAGCGCGAAG  TGGCGCAGGT  ATCCGCCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATT
501 TAAAAGTTAT  GCTAAGAAG  AGCAGGATAA  GCGGATTTT  GCCGACTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGTACCGC  CGGGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATTCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA
```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```
g992.pep
1  MFRHRHLKN  MQIKKIMKWL  PVALSLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GTAGDVGFDA  PVRRRASAKS  GHSYTGTVSK  VYDGDTLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDSVGEWL  GIW*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

```
m992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GTTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGGCGGGCAG  GGGACGCGGG  TTCCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GGCGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCT  TCACGTTATC  GACGCGCAGC  GCGCGAAACA  CAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTGCGCG
401 TGTTCGATAC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATT
501 TAAAAGTTAT  GCTAAGAAG  AGCAGGATAA  GCGGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGTACCGC  CGAGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA
```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```
m992.pep
1  MFRHRHLKN  MQIKKIMKWL  PVALSLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGDTLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDAVGEWL  GIW*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

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	10	20	30	40	50	60
m992.pep	MFRRRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
g992	MFRRRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
g992	PVRRRASAKSGHSYTGTVSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVSVRVFDTDRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF					
g992	LRAAAEGRKVSVRVFETDRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF					
	130	140	150	160	170	180
	190	200	210	220	230	
m992.pep	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIWX					
g992	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMSVGEWLGIWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

```
a992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCT  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCGCGGCAG  GGGACGCGGG  TTCCGACGCG  CCGGCCCGCC  GCCGAGCATC
201 GGCGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCT  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGCGGGAAGG  CAGGAAAGTC  AGCGTCCGCG
401 TGTTTCGACAC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCCGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATT
501 TAAAGTTAT  GCTAAAGAAC  AGCAGGATAA  GCGGATTATT  GCCGATTATG
551 CCGACGCTCA  AATTCAGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGGGCAGGCA  GGAGCGCGCG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTTGGT
701 AA
```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

```
a992.pep
1  MFRRRHRLKN  MQIKKIMKWL  PVALSLLGAL  GYTGYGSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGD TLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFDTDRY  QREVAQVSVG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDAVGEWL  GIW*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRRRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
m992	MFRRRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
m992	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

a992.pep      LRAAAEGRKVSVRVFDTDRYQREVAQVSVGKTDNLMQVQDGAAWHYKSYAKEQQDKADF
               |||
m992          LRAAAEGRKVSVRVFDTDRYQREVAQVSVGKTDNLMQVQDGAAWHYKSYAKEQQDKADF
               |||
               130      140      150      160      170      180

               190      200      210      220      230
a992.pep      ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIX
               |||
m992          ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIX
               |||
               190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1   CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATCCG ATGGTGGAAA
101 TTACCGGGCA GTATCTGCAC TATATTGCC AAATGGAAG CTATCAGTTT
151 GATTGGCGCG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGTC TTGCCTACGA GCAAATGAAA
301 CTGGCGGCGC AGGGTTTGA CGCGCTGCCG CGTGCGGGAC GGGATTTCCG
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCGAGG
401 TTTACATCGC CGATTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCTTT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTTCGGC ACACGGGGCG GCGCGGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1   LKVVVLGSFQG PLDLLLYLIR KQIDVLDIP MVEITGQYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTAEVDE EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLSVRAQMT AILRRLNEHG ICRFHAFNFP EQGAAYVIVN
201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1   TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATCCG ATGGTGAAGA
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGTC TGGCTTACGA ACAGATGAAG
301 CTGGCGGCGC AGGGTTTGA CGCGCTGCCG CGAGCCGAC GGGATTTCCG
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCCAA GAAACCATCT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCTGTCAC
601 TTCATCGCAC TGTTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGAGGCG GCGCGGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1   LKVVVLGSFQG PLDLLLYLIR KQIDVLDIP MVKITEQYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNGHG ICRFHDLFNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

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m993/g993 93.1% identity in 248 aa overlap

	10	20	30	40	50	60
m993.pep	LKVVLGSFQGPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQIETYQ	FDLAAEYLLMA			
g993	LKVVLGSFQGPLDLLLYLIRKQNI	DVLDIPMVEITGQYLHYIAQMEAYQ	FDLAAEYLLMA			
	10	20	30	40	50	60
m993.pep	70	80	90	100	110	120
	AMLIEIKSRLLLPRTETVEDEEADPRAELV	RRLAYEQMKLAAQGLDALPRAGRDFAWAY				
g993	70	80	90	100	110	120
	AMLIEIKSRLLLPRTETVEDEEADPRAELV	RRLAYEQMKLAAQGLDALPRAGRDFAWAY				
	130	140	150	160	170	180
m993.pep	LPLEIAVEAKLPEVYITDLTQAWLGILSRAKHTRSHEVIKETISVRAQMTAILRRLN	GHG				
g993	130	140	150	160	170	180
	LPLEIAAETKLPEVYIADLMQAWLGILSRAKHTRSHEVIQETLSVRAQMTAILRRLN	EHG				
	190	200	210	220	230	240
m993.pep	ICRFHDLFNPQGAAYVVVNFIALLELAKEGLVRIVQEDGFGEIRISLNHEGAHSDGISG					
g993	190	200	210	220	230	240
	ICRFHALFNPQGAAYVIVNFIALLELAKEGLVGIVQEDGFGEIRISLNHEGAHSDGIFG					
	249					
m993.pep	TRGGRDVF					
g993	TRGGRDVF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

1	CTGAAAGTCG	TATTGAGCAG	TTTTCAAGGC	CCTTTGGATC	TGCTGCTCTA
51	CCTTATCCGC	AAGCAGAACA	TCGATGTTCT	CGATATCCGC	ATGGTGAAGA
101	TTACCGAACA	GTATCTGCAC	TACATCGCCC	AAATAGAAAC	CTATCAGTTT
151	GATTTGGCGG	CGGAATATCT	TTTGATGGCA	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCCTG	CTGCTGCCGC	GTACCGAAAC	CGTCGAAGAC	GAAGAAGCCG
251	ACCCGCGTGC	CGAGTTGGTG	CGCCGCTGCG	TGGCTTACGA	GCAGATGAAG
301	CTGGCGGCAC	AAGGGTTGGA	TGCGCTTCCT	CGTGCGGGCC	GGGATTTCGC
351	ATGGGCATAC	CTGCCACTGG	AAATTGCCGT	CGAAGCCAAG	CTGCCCGAAG
401	TCTATATTAC	CGACTTGACG	CAGGCGTGGC	TGAGTATTTT	GTCTCGGGCA
451	AAACATACCG	GCAGCCACGA	AGTTATCAAA	GAAACCATCT	CCGTGCGCGC
501	GCAAAATGACG	GCAATCCTGC	GCCGTTTGAA	CAAACACGGG	ATATGCAGGT
551	TTCACGACCT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GGTCGTCAAC
601	TTCATCGCAC	TGTTGGAGCT	TGCCAAAGAA	GGTTTGGTCG	GAATCGTACA
651	GGAAGTCGGT	TTCGGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTACAGACG	CATTTCCGCG	ACACGGGGCG	GGCGCGATGT	GTTCTAA

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

1	LKVVLSSFQG	PLDLLLYLIR	KQNI	DVLDIP	MVKITEQYLH	YIAQIETYQF
51	DLAAEYLLMA	AMLIEIKSRL	LLPRTETVED	EEADPRAELV	RRLAYEQMK	
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAVEAK	LPEVYITDLT	QAWLSILSRA	
151	KHTRSHEVIK	ETISVRAQMT	AILRRLNKHG	ICRFHDLFNP	EQGAAYVVVN	
201	FIALLELAKE	GLVGIVQEVG	FGEIRISLNH	EGAHSDGISG	TRGGRDVF*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

	10	20	30	40	50	60
a993.pep	LKVVLSSFQGPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQIETYQ	FDLAAEYLLMA			
m993	LKVVLGSFQGPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQIETYQ	FDLAAEYLLMA			

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
m993	70	80	90	100	110	120
a993.pep	130	140	150	160	170	180
m993	130	140	150	160	170	180
a993.pep	190	200	210	220	230	240
m993	190	200	210	220	230	240
a993.pep	249					
m993	249					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1   ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGC TTCTACCGC
51  CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTTCC GAAGGAAGCA
101 CCGTGCTTGC CTTGGGCGAT TCGCTCACCT TCGGCTACGG AGCAAACCCC
151 GCGGAATCCT ACCCGCGCA ACTGCAAAAA CTGACGGGT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACGTCCGC GCAAGCCCTA TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAA CCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TGCGCAAAGT TCCCGAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AAAAGGAAAA CATCCCGCC GTCTCGTCG
401 GCGTGCCGCA CATCACACTG GCGCGTTGT TCGGCATT T GAGCGACCAT
451 CCGTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CGCGTGGCG GAAATTTTGG GCAATAATA TCTGAAATCC GACCAAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTG CCGAAATTT GAATCAATTT
601 TTGAGAAAAC ATGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1   MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPAQLQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG
101 NDFLRKVPEE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
151 PLYEDLSEFY GIPLFGGAWA EILGNNNLKS DQIHANGKGY RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1   ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGC TGCTTACCGC
51  CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTTCC GAAGGAAGCA
101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCTT
151 GCGGAATCCT ACCCGCGCA ACTGCAAAAA CTGACGGGT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCTGC CCAAGCCCTG TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAA CCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TGCGCAAAGT TCCAAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AGAAGGAAAA CATCCCGCC GTCTCGTCG
401 GCGTGCCGCA CATCACACTG GGTGCGTTGT TCGGCATT T GAGCGATCAT
451 CCGTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGC TGTTCGGCGG
501 CGCGTGGCG GAAATTTTGG GCGATAATA TCTGAAATCC GACCAAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTG CCGAAGATT GAATCAATTT
601 TTGAGAAAAC AGGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1   MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPAQLQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG

```

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101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHTL GALFGHLSDH
 151 PLYEDLSEY GIPPLFGGAWA EILGDNLLKS DQIHANGKGY RKFAEDLNQF
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

m996.pep	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK					
g996	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK					
m996.pep	70	80	90	100	110	120
	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
g996	70	80	90	100	110	120
	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEEQTRANIAKII					
m996.pep	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITLALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGDNLLKS					
g996	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITLALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGNNLLKS					
m996.pep	190	200				
	DQIHANGKGYRKFAEDLNQFLRKQGFR					
g996	190	200				
	DQIHANGKGYRKFAENLNQFLRKHGFRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGCGCA	GGCGCGTTGC	TCCTTACCGC
51	CTGCGGCAGA	AAATCCGCCC	GAACCCACGC	CAAAATTCCC	GAAGGAAGCA
101	CCGTACTTGC	CTTGGGCGAT	TCGCTTACCT	TCGGCTACGG	CGCAAACCCC
151	GGCGAATCCT	ACCCCGCGCA	ACTGCAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACATCCG	CCAAGCCCTG	TCGCGCCTGC
251	CCGCGCTGTT	GGCACGCAAA	CCCAAGCTTG	TGATTGTCGG	CATAGCGGCG
301	AACGACTTTC	TGCGCAAAAGT	TCCCAAGGAG	CAGACCCGCG	CCAATATCGC
351	GAAAATCATC	GAAACCGTGC	AGAAGGAAA	CATCCCCGCC	GTCCTCGTCG
401	GCGTGCCGCA	CATTACCTTG	GGCGCGTTGT	TCGGGCATT	GAGCGATCAT
451	CCGCTGTATG	AGGATTTGTC	CGAGGAATAC	GGCATTCCGC	TGTTCCGCGG
501	CGCGTGGGCG	GAAATTTTGG	GCGATAATA	TCTGAAATCC	GACCAATATC
551	ACGCCAACGG	CAAAGGCTAT	CGGAAATTG	CCGAAGATT	GAATCAATT
601	TTGAGAAAC	AGGGGTTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

1	MNRRTFLLGA	GALLLTACGR	KSARTHAKIP	EGSTVLALGD	SLTFGYGANP
51	GESYPAQLQK	LTGWNIVNGG	VSGDTSQAAL	SRLPALLARK	PKLVIVGIGG
101	NDFLRKVPKE	QTRANIAKII	ETVQKENIPA	VLVGVPHTL	GALFGHLSDH
151	PLYEDLSEY	GIPPLFGGAWA	EILGDNLLKS	DQIHANGKGY	RKFAEDLNQF
201	LRKQGFR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

a996.pep	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK					

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```

|||||
m996      MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK
          10      20      30      40      50      60

          70      80      90      100     110     120
a996.pep   LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
          |||||
m996      LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
          70      80      90      100     110     120

          130     140     150     160     170     180
a996.pep   ETVQKENIPAVLVGVPHITLGALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGDNNLKS
          |||||
m996      ETVQKENIPAVLVGVPHITLGALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGDNNLKS
          130     140     150     160     170     180

          190     200
a996.pep   DQIHANGKGYRKFAEDLNQFLRKQGF
          |||||
m996      DQIHANGKGYRKFAEDLNQFLRKQGF
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCGCGG TTGTCCGCGG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GAAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGGCGTGT TCGGCCTGAT GAAAACCATC GGTTTCAGACC
251 CCGTGCCGCG CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCGCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAAGTGTCTG
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGGG CAGCCCTTGG TCTGGGGCGC GCTCAACACG CCTTTGAAAA
551 CCGCAAGCCT GCGCGTGTGG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGcCTGcC GCGCCCGCTG ACcGGCATtg CCGAcggcAC
951 ggcaCaatgG CTGCTTTgcc cgGGGCAGGC tccggactgc CcccaaAacg
1001 aagTCTCCGC cGTCAttagc GTTTCGGAcc GCGtcggcgC Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGFGLD NGQHILLGAY RGVLRMLKTI GSDPRAAFRL VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGGPDT
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFFAN
351 R...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCGAGG CTGTCCGCGG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGGCGTGT TCGGCCTGAT GAAAACCATC GGTTTCGGATC
251 CCGTGCCGCG CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCGCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAAGTGTCTG
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGGCG AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGGG CAGCCCTTGG TTTGGGGCGC GCTCAACACG CCTTTGAAAA

```

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```

551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCCTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCCGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACGCTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCCTGCC CGCCCCGCTG ACCGGCCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGAGGCT CGGACTGCCT GAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCCG GACTTGTCTG GTTTCACCG GCACCGCATC
1201 TTCCCCGCCG GCGACTACCT CCACCCGGAC TACCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

m997.pep

```

1 MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGFGLD NGQHILLGAY RGVRLMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVL
201 KKS GSDYLLP KODLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQVW LLCRGRGLP ENEVSAVISV SDRVGAFAFR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPP DLWLHRRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

	10	20	30	40	50	60
g997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
g997.pep	70	80	90	100	110	120
	NGQHILLGAYRGVRLMKTI GSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVRLMKTI GSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
g997.pep	130	140	150	160	170	180
	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
g997.pep	190	200	210	220	230	240
	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC					
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC					
	190	200	210	220	230	240
g997.pep	250	260	270	280	290	300
	RLNTLPDGKVLVNGEAFDAAILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
m997	RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
	250	260	270	280	290	300
g997.pep	310	320	330	340	350	
	AEPVRLPAPLTGLADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFAFR					
m997	AEPVRLPAPLTGLADGTQVWLLCRGRGL-GLPENEVSAVISVSDRVGAFAFR					
	310	320	330	340	350	

1418

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTC A TCGGCGCAGG
51  CTGGGCCGGC TTGTCCGCGC CCGTTACCTT GGCGCGGCAC GCCGACGTTA
101 CCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGGCGTGT TCGCCTGAT GAAAACATC GGTTCAGACC
251 CCCATGCCGC CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAATGCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAACAGGATT TGGGCGCAAT
651 CGTGCGCGAA CCCGCTTGG CCGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCATATGC CGTCTGAACA CCCTCCCGGA CGGGAAGTG
751 CTCGTCAACG GCGAACCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCGGAACCCG TCCGCTTGCC TGCCCGCTG ACCGGAAGTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCGAGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCGCATT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCCG GATTGTCTGT GGTTCACCG GCACCGCATC
1201 TTCCCCGCCG GCGACTACCT CCACCCAGAC TACCCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVLRIMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPFDDA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLR
301 AEPVRLPAPL TGLADGTVQW LLCRGRLGLP ENEVSAVISV SDRVGAFANR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPD DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

```
a997/m997 98.2% identity in 437 aa overlap

      10      20      30      40      50      60
a997.pep MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD
          |||
m997     MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD
          |||

      10      20      30      40      50      60
a997.pep NGQHILLGAYRGVLRIMKTIGSDPHAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL
          |||
m997     NGQHILLGAYRGVLRIMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL
          |||

      70      80      90      100     110     120
a997.pep TVAQWLKQRNVPRAAVMQFWQPLVWGALNTPLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAE
          |||
m997     TVAQWLKQRNVPRAAVMQFWQPLVWGALNTPLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAE
          |||

      130     140     150     160     170     180
a997.pep ARRVPFAFKA KLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT
          |||
m997     ARRVPFAFKA KLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT
          |||

      190     200     210     220     230     240
a997.pep PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAE PALAELQRLGADIRLETRIC
          |||
m997     PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAE PALAELQRLGADIRLETRIC
          |||
```


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```

m997      PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

           250      260      270      280      290      300
a997.pep  RLNTLPDGKVLVNGEFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           |||||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           250      260      270      280      290      300

           310      320      330      340      350      360
a997.pep  AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVHADL
           |||||
m997      AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

           370      380      390      400      410      420
a997.pep  KRILPHLGEPEAVRVITEKRATTAADAPPPDLSWLHRHRIFPAGDYLHPDYPATLEAAVQ
           |||||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLSWLHRHRIFPAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

           430
a997.pep  SGFASAEACLQSLSDAVX
           |||||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTTATC
51  AGCCTGCAAC CAACAATCAA AAACGGCACA AGCCGAAGAA CCTGTCCAAA
101 GTATCCAGGC TGCTGATTGT ACCGCCCAA TGGACATCAC AGTTGAACAA
151 TATCTCATCA ATTTGGAGCA AGCATTAAA ACTCAGAACG TCTCAACAAA
201 AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
251 TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301 ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351 ACAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAGGCAG
401 TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCGGA AGCAGGAAAA
451 CAACTTTTTA CAGCTTTAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
501 AGCAACAGCG CAAAAGACG TTCCGGCAGA TGGTATTTTA TATAGCGTTG
551 TTTTGTAAAA AGAAACAAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI CVSIVLSACN QSKTAQAEF PVQSIQAADC TAPMDITVEQ
51  YLINLEQAFK TQNVSTKIHN KNIVKTDGKY DLTLMVDFGA IALKLDEQKQ
101 IRAISVGYIL KTDGEKGQNL VNNAINGLHS IQAVLSLTTT DKLGESEAGK
151 QLFATLTVV KESNOTGATA QKDV PADGIL YSVVFEKETN TIAIIGRKQF
      *

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.